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A; Molecule type: mRNA
A; Residues: 27-81,'L',83-103 <RYA2>
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A;Accession: S04892
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C; Species: Homo sapiens (man)
C; Date: 28-May-1986 #sequence_revision 01-Sep-1995 #text_change 08-Dec-2000
C; Storaski, M.; Sandell, L.J.
C; Storaski, M.; Sandell, M.; S
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R;Su, M.W.; Lee, B.; Ramirez, F.; Machado, M.; Horton, W.
Nucleic Asids Res. 17, 9473, 1989
A;Title: Nucleotide sequence of the full length cDNA encoding for human type II procolla
A;Reference number: S06715; MUID:90067946; PMID:2587267
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A; Molecule type: DNA
A; Molecule type: DISSA
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A;Residues: 7-28, 'R',99-157,'P',159-440,'G',442-456,'E',458-640,'A',642-831,'PA',834,'F'
A;Cross-references: EMBL:X16711; NID:930040; PIDN:CAA34683.1; PID:930041
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A, Residues: 1.28, R(')99-1487 <SUZ>
A, Cross-references: EMBL:X16468; NID:929515; PIDN:CAA34488.1; PID:929516
A; Note: alternative splice form 1
R; Vikkula, M.; Metsearanta, M.; Syvaenen, A.C.; Ala-Kokko, L.; Vuorio, E.; Peltonen, L.
Biochem. J. 285, 287-294, 1992
A; Title: Structural analysis of the regulatory elements of the type-II procollagen gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           collagen alpha 1(II) chain precursor [validated] - human
N'Alternate names: procollagen alpha 1(II) chain
N'Contains: chondrocalcin; collagen alpha 1(II) chain precursor splice form 1; collagen
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A;Note: this translation is not annotated in GenBank entry HSPROCOE1, release 111.0
R;Nunez, A.M.; Kohno, K.; Martin, G.R.; Yamada, Y.
A;Nunez, A.M.; Kohno, K.; Martin, G.R.; Yamada, Y.
A;Title: Promoter region of the human pro-alpha-1-(II)-collagen gene.
A;Reference number: A24828; MUID:87031574; PMID:3021582
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                                                                                                                                                                                                                                                                                                                                          --GlyLeuArgProHisAspGl 1184
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                                                                       .- 11177
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                                                                                                                                                                                                  176 GCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCA
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1184 uGluValGluAlaThrLeuLysSerLeuAsn----
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A;Molecule type: DNA
A;Residues: 1-28 <VIK>
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A; Residues: 1-103 <RYA>
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A, Molecule type: protein
A, Residues: 243-261;575-590;756-763, 'X', 765-779 <FRA>
R;Tiller, G.E.; Weis, M.A.; Polumbo, P.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Ey
Am. J. Hum. Genet. 56, 388-395, 1995
A;Title: An RNA-splicing mutation (G+5IVS20) in the type II collagen gene (COL2A1) in
A; Reference number: 138867; MUID:95150028; PMID:7847372
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A; Residues: 630-640, A', 642-785 < VIK2>
A; Cross-references: EMBL:X16158; NID:929951; PIDN:CAA34278.1; PID:91335018; PIDN:CAA3
A; Cross-references: EMBL:X16158; NID:929951; PID:91335024
B; Bogaert, R.; Tiller, G.E.; Wels, M.A.; Gruber, H.E.; Rimoin, D.L.; Cohn, D.H.; Eyre
J. Biol. Chem. 267, 22522-22526, 1992
A; Title: An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II) chain
A; Reference number: A44309; MUID:93054548; PMID:1429602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Organization of the exons coding for Pro alpha-1(II) collagen N-propeptide c A;Reference number: A30147; MUID:89233138; PMID:2714801 A;Accession: A30147
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A; Residues: 171-172, 'C', 174-175 <ALA>
A; Note: mutant sequence from a family with family with primary generalized osteoarthr
R; Diab, M.; Wu, J.J.; Eyre, D.R.
Biochem. J. 314, 327-332, 1996
A; Title: Collagen type IX from human cartilage: a structural profile of intermolecula
A; Reference number: $64673; MUID:96195147; PMID:8660302
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A; Residues: 188-189, X', 191-195;1224-1230, X', 1232-1236 <DIA>
R; Franc, S.; Marzin, E.; Boutillon, M.M.; Lafont, R.; Lechene de la Porte, P.; Herbag
Eur. J. Biochem. 234, 125-131, 1995
A; Title: Immunohistochemical and biochemical analyses of 20000-25000-year-old fossil
A; Reference number: S63514; MUID:96096730; PMID:8529631
                                                                                                                                                                                                                                                                                                                                                        A;Note: alternative splice form 2; splicing appears to be under developmental regulat R:Su, M.W.; Benson-Chanda, V.; Vissing, H.; Ramirez, F. Genomics 4, 438-441, 1989
                                                             cysteine-rich domain in the amino-terminal prop
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A; Residues: 104-157, Pr. 7159-236 <SUM>
A; Residues: 104-157, Pr. 7159-236 <SUM>
A; Cross-references: GB: 403065; GB: 403066; GB: M25655; GB: M25656; GB: M25730; GB: M32168;
B; Ala-Kokko, L.; Baldwin, C.T.; Moskowitz, R.W.; Prockop, D.J.
Proc. Natl. Acad. Scil. U.S.A. 87, 655-6568, 1990
Proc. Natl. Acad. Scil. U.S.A. 87, 655-6568, 1990
A; Title: Single base mutation in the type II procollagen gene (COL2A1) as a cause of A; Reference number: A94227; MUID: 90370826; PMID: 1975693
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A; Cross-references: EMBL:U15195; NID:9557053; PIDN:AAB60370.1; PID:9557054
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A; Residues: 501-676, A', 678-783, A', 785-831, 'PA', 834, 'F', 836-1214 < RAM>
A; Cross-references: EMBL:X13783; NID:g30037; PIDN:CAA32030.1; PID:g930050
R; Vikkula, M.; Peltonen, L.
FEBS Lett. 250, 171-174, 1989
J. Biol. Chem. 265, 10334-10339, 1990
A;Title: Differential expression of a cysteine-rich dom:
A;Reference number: A35428; MUID:90285153; PMID:2355003
A;Accession: A35428
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A;Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 541-560 <SAN3>
A;Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A;Accession: I37251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 CysValGlnAspGlyGlnArgTyrAsnAspLysAspValTrpLysProGluPro----
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                     A;Status: translated from GB/EMBL/DDBJ
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A; Note: this translation is not annotated and this publication is not cited in GenBank e Note: untant sequence associated with perinatal lethal hypochondrogenesis
R;Tiller, G.E.; Rimoin, D.L.; Murray, L.W.; Cohn, D.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3889-3893, 1990
A;Title: Tandem duplication within a type II collagen gene (COLZAI) exon in an individua A; Reference number: S16502; MUID:90251662; PMID:2339128
A;Accession: S16502
                                                                                                                                                                                                                                                                                                                                                          A.Cross-references: EMBL:M37126; NID:9180808; PIDN:AAA52037.1; PID:9180809
A.Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R.Cheah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveld, F.G.; Solomon, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 2555-2559, 1985
A.Title: Identification and characterization of the human type II collagen gene (COL2A1)
A.Reference number: A02858; MUID:85190534; PMID:3857598
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A; Residues: 1296-1358
A; Residues: 1296-1358
A; Cross-references: GB:MI2048; NID:g180017
A; Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A; Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the
A; Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with the
B; Sangiorgi, F.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez,
Nucleic Acids Res. 13, 2207-2225, 1985
A; Title: Isolation and partial characterization of the entire human pro alpha 1(II) coll
A; Reference number: 137249; MUID:85215609; PMID:2987845
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 7-28, 'K', 99-114;541-578;786-802;1055-1056, 'N', 1058-1068, 'T', 1070-1109;1200-1
A; Status: translated from GB/EMBL/DDBJ
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Nucleic Acids Res. 12, 1025-1038, 1984
A;Title: Isolation and characterization of genomic clones corresponding to the human typ
A;Reference number: A21733; MUID:84118798; PMID:6320112
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A;Residues: 1245-1295 <STR1>
A;Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g4378975
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A; Residues: 1032-1056, Nv, 1058-1068, Tr, 1070-1487 <CHE>
A; Residues: 1032-1056, Nv, 1058-1068, Tr, 1070-1487 <CHE>
A; Cross-references: GB:J00116; NID:g180395; PIDN:AAA51997.1; PID:g180396
B; Ellma, K.; Vuorio, T.; Vuorio, E.; Vuorio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 'XE',1244-1246,'N',1248,'X',1250-1265;1295-1305;1395-1408 <VAN>
A;Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal
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R; van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
Bochem. J. 237, 923-925, 1986
A;Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
A;Reference number: A57033; MUID:87099927; PMID:3800925
A;Accession: A57033
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A;Note: the GenBank PID is based on an incorrect reading frame
A;Accession: 137250
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                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1164-1184,'GPSGKDGANGIPGPI',1185-1199 <TIL2>
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A, Molecule type: DNA
A, Residues: 894-909, 'PE' <STR2>
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A: Residues: 7-28 <SAN2>
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213

N;Alternate names: sucrose carrier protein; sucrose permease C;Species: Spinacia oleracea (spinach) C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jul-2000	Qy 955 CCCCACCAGCAGAAGGCTGTCGGCCCCCTGTTGTCGCCCCACTGC ::	CCCCACCGAGCCAGAAGGCTGTCGGCCCCTTCTTGTCGCCCCACTGCTGTCCATG 1014 :::
R.Riesmeler, J.W.; Willmitzer, L.; Frommer, W.B. EMBO J. 11, 4705-4713, 1992 A:Title: Isolation and characterization of a sucrose carrier cDNA from spinach by funct	Qy 1015 CCGGCCCGCTTGCCGAACCTGGCCCCCTGCTTCCCCGGCTGCACCAGCTGT	ACCTGGCCCCTGCTTCCCCGGCTGCACCAGCTGTG 1074
	OY 1075 CTGCCGCATGCCCCGCACCTGCGCCGGCTCTTCGTGGCTCAGCTGTGCACTGGATGG 1	U
Avisos references, Emplianital NID:galis / PID:galis / PID:galis / PID:galis / C. Superfamily: common tobacco sucrose transport protein C:Keywords: transmembrane protein	1135	
3.32e-12 Length: 32.00 Matches:	308	
Best Local Similarity: 23.47% Mismatches: 200 Query Match: 2.10% Indels: 145 DB: 2 Gaps: 21	DD 328 FQD 328 FQD QY 1255 CAGCCTGGGGCTGTTCCTGCAGTGCGCCATT	F
US-09-759-143-110 (1-3410) x S28052 (1-525)	342	
Qy 310 CCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGTTGGCCTGGA 369	OY 1315 GCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTT-	GCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTT 1368
370 GGTGTGTTGGCCGCAGCATCACCTATGTGCCGCCCCCCCCCC	OY 1369 CCCTGTGGCTGCCGGTGCCATGCCTGTCCTGTCCTGTCC	CCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGGGCCGTGGTGACAGCTTCAGC 1428
41 lAlaSerValAlaAlaGlyValGlnPheGlyTrpAlaLeuGlnLeuSerLeuLeuThrPr	1429	
VY 40v ICTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC		
	Qy 1489 CTACCACCGGGAGAAGCAGGTGTTCCTGCCC ::: :::	CTACCACCGGGAAAGAGAGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAG 1548 ::: ::: -HispheargaspSerHisHislleMet
CTATGGCCGCCGCCCCTTCATCTGGGCACTGTCTGGGCATCCTGTTTTTTTT	Qy 1549 CAGTGAGGACAGCCTGATGACCAGCTTCCTC	CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 1608
Db :::	405	405
Qy 586 TCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGCCCGGATCCC 634	Qy 1609 TAATGGACACGTGGGTGCTGGAGGCAGTGGC Db 406GlySerAla	TAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTCTGCGG 1668
-AGGCCCCTGGAGCTGGCACTGCTCGTGGGCGTGGGGCTGCTGACTT :::	Qy 1669 GGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGGTGGGTG	GGTGGTGGGTGAGCCCACGAGGCCAGGGT 1728 ::: aValLeuGlyIleProLeuAlaileThrPh 436
	Qy 1729 GGTTCCG	GGCCGGGCCATCTGCCT 1752
CCGGGACCACTCGCCAGGCTACTCTGTCTATCATCATCATCACTTGGGGGCTG rGlnThrLy8ThrArdTyrAlaAsnAlaPhePheSerPhePheMetAlaLeuclyAsn11	Qy 1753 GGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTG	GCTGTCCCAGGTG1795 ::: :: ValProGInMetPheValSerValThrSe 476
802 CCTGGGCTACCTCCTGCCATTGACTGGGACAC	Qy 1796	rGlyProTrpAspAlaMetPheGlyGlyGlyGlyAsnLeuProAlaPheValValGlyAlaVa 496
	OY 1822 IGTCCAGCTCAGCCAGTCTGTCACTGCCTAT	T 1852
	Db 496 IAlaAlaThrAlaSerAlaValLeuSerPhe	: e 506
Oy 896 -CTCATCTTCCTCACCTGCGTAGCACCACACTGCTGGGCTGAGGAGCCAGGCTGGG 954	REGULT 22 S43142 suit 12 suit 142 suit 142 suit 142 suit 144 N'Alternate names: suit 146 C', Species: Ricinus communis (castor bean)	

us-09-759-143-110.rpr

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCTCATCCCAAGGGCC-----GGCTGGCTAGCAGGG----CTGCTGTGCCCGGATC 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGCCCCTGGAGCTGCCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCC 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  693 AGGIGITICACICCACIGGAGGCCCIGCICICIGACCICITC---CGGGACCCGGACC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      750 ACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGGCTGCCTGGGCT 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 ysThrargThralaAsnAlaLeuPheSerPhePheMetAlaValGlyAsnValLeuGlyT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||:::|||
201 yrAlaAlaGlyAlaTyrThrHisLeuTyrLysLeuPheProPheThrLysThrThrAlaC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               846 TGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     906 TCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCCACCGAGC 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTATIGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCT 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405 CICIGCIGCIGGAAGIGGGGGTAGAGGAAGIICAIGACCAIGGIGCIGGGCAIIGGIC 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 CAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGAC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                   231 AGCAGITCIGGAGIGCCIGAACGGCCCCCT-----GAGCCCIACCCGCCTGGCCCACIA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 TGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTGG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 TCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 alAlaSerIleAlaAlaGlyIleGlnPheGlyTrpAlaLeuGlnLeuSerLeuLeuThrP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || ::: :::|||:::
61 roTyrValGlnLeuLeuGlyIleProHisThrTrpAlaAlaPheIleTrpLeuCysGlyP 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 MetValAlaGly-AlaAlaGlu---ProAsnSerSerPro-LeuArgLysValValMetV 41
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-May-2000 C;Accession: S43142
R;Weig, A.; Komor, E.
B;Weig, A.; Komor, E.
B;Weig, A.; Komor, E.
B;Date Library, March 1994
A;Pescription: A sucrose carrier from Ricinus communis.
A;Reference number: S43142
A;Accession: S43142
A;Accession: S43142
A;Accession: S43142
A;Accession: J633 AWEI>
A;Residues: 1-533 AWEI>
A;Residues: 1-533 AWEI>
A;Cross_references: EMEL:Z31561; NID:g468561
C;Superfamily: common tobacco sucrose transport protein
                                                                                                                                                                                                                                                                    533
147
102
236
126
22
                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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Db	241 erLeuThrValLeuAlaLeuSerTyrVal	LysGluLysProTrpSerP 257
QY	966 CAGCAGGGCTG	TCGCCCCCTCTTGTCGCCCC 1
qq	oAspGlnAlaVa	AspThrAlaSerGlnAlaSerSerSe
Qy	1002 ACTGCTGTCCATGCCGGGCCCGCTTG	GCTTTCCGGAACCTGGGC
qq	등	euGlyAlaPheLysAsnLeu 292
Qy	1056 CCCGGCTGCACCAGCTGTGCTGCCGCAT	CGCATGCCCCGCACCTGCGCCGGCTCTTCGTGGCTG 1115
qq	293	tTrp1leLeuLeu
Qy	1116 AGCTGTGCAGCTGGATGGCACTCATGACC	CTTCACGCTGTTTTACACGGATTTCGTGGGCG 1175
Оb	PhePr	PheLeuLeuPheAspThrAspTrpMetGlyA 323
οy	1176 AGGGCTGTACCAGGGCGTGCCCAGAGC	CTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATG 1235
Dp	323 rgGluValTyrGlyGlyAspSe	γr
ΟŸ	1236 ATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTC	SCIGITUCCIGCAGIGCGCCAICTCCCIGGICT 1295
qq	<a>C	euGlyPheT 36
Qy	1296 TCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCT.	ATTTGGCCA 13
qα	361 hrSerLeuGlyValGluValLeuAlaAr	gllyvalGlyGlyvalLysArgLeuTrpG 380
Qy	GT	4
qa	380 lylleValAsnPheValLeu	_
Qy	SACAGCTTCAGCCGCCCTCACCGGG	ACCTTCTCAGCCCTGCAGATCCTGCCCTACA 14
QQ	396 alThrLysGlnAlaGluSerThr	403
Qy	CCTCTACCACCGG	GTICCIGCCCAAATACCGAGGGGACA 15
Op	404	ArgArgPheAlaThrValS 410
Qy	6 CTGGAGGTGCTAGCAGTGAGGACAGCC ::	SATGACCAGCTTCCTGCCAGGCCCTAAGCCTG 15
qq	rGlyGl	- 416
Qy	CTAATGGACACGTGG	GCTGGAGGCAGTGGCCTGCTCCCACCTCCAC 16
qq	417	
Qy	rerecerere	rcrccgracGrgGrgGrgGgrgGgrgAGCCCA 17
QQ	421SerGlyValLysAlaGlyAl	laLeuPheAlaValMetGlyValProG 43
Qy	.1716 CCGAGGCCAGGGTGGTTCCG	
qa	438 lnAlaIleThrTyrSerIleProPheAla	aLeuAlaSerIlePheSerAsnThrSėr
Qy	1740 GGGCATCTGCCTGGACCTCGCCATCCTGGATAGT	GGATAGTGCCTTCCTGCTGTCCCAGGTGGCCC 1799
QQ	ly lyglnglybeuserb	SerlleVallleProGln
Qy	۲١.	CTCAGCCAGTCTGTCACTGCCTATA 18
qq		LeuPheGlyGlyGlyAsnLeuProAlaPhe
Qy	GGT	SCCATTTACTTTGCTACACA
qq	31G	3ly11ePheAlaLeuThr
Oy	1914 ACAAGAGCGACTTGGCCAAATACTCAGCG	G 1942
4	::: ::: 013	 527

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A) Cross-references: GB:J03051; NID:g179695; PIDN:AAA51858.1; PID:g179696
A;Note: the authors translated the codon GAA for residue 1460 as Gln, and GAG for res
C;Comment: Prolines and 1ysines at the third position of the tripeptide repeating uniare 5-hydroxylated and subsequently O-g1ycosylated.
C;Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Map position: 2q31-2q31 A May 1064/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 144 A intrans: 341, 812/3; 830/3; 846/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 144 C:Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV), alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among ength, is formed with desmosine cross-links made from lysine and allysine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3068 GGTCCTGCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGGGAAAGTTGGGGGGTAGGGGA 3009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3008 AAGTTGGGG---GTAGGGGAAATTTTGGGCAGTGCCTTCATCAGCCCAGTCCTAGAGAGA 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2951 ---GTAGAGGG-----------AGTGGAAGTGGGGGGAACCAGGCTGGG 2916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 ProThrGlyProProGlyGluProGlyAspProGlyProMetGlyProIleGlySerArg 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216 GlyPro---ValGlyProArgGlyProGlnGlyLeuGlnGlyGlnGlyGlyAlaGly 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 GlyProGluGlyProProGlyLysProGlyGluAspGlyGluProGlyArgAsnGlyAsn 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                            A:Cross-references: GDB:119064; OMIM:120190
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A; Molecule type: DNA
A; Residues: 1449-1463, 'E', 1465-1495,'A'
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29.16%
25.40%
5.21%
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F;187-208/Region: nonhelical
F;209-1225/Region: helical
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Best Local Similarity:
                                                                                                                                                                                                                                                                            A; Gene: GDB:COL5A2
                                                                                                                                                                                                                                            C; Genetics:
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                                                                              C; Species: Homo sapiens (man)
C; Date: 31-Jul-1989 #sequence_revision 28-Jul-1995 #text_change 31-Dec-2000
C; Date: 31-Jul-1989 #sequence_revision 28-Jul-1995 #text_change 31-Dec-2000
C; Accession: A31427; A5455; S415643; A25874; I55239; I59025; A25374; A30017
R; Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
J. Biol. Chem. 264, 2735-2738, 1989
A; Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms to the struct A; Reference number: A31427; MUID:89123368; PMID:2914927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: GB:MS8529; NID:9180834; PIDN:AAC41699.1; PID:9553235
R:Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Ber Bur. J. Blochem. 221, 987-995, 1994
A)Title: Diversity in the processing events at the N-terminus of type-V collagen. A;Reference number: S43642; MUID:94237164; PMID:8181482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Molecule type: mRNA AREA (MES)
A; Residues: 1002-1226 (RE2>
A; Residues: 1002-1226 (RE2>
A; Residues: 1002-1226 (RE2>
A; Residues: 1002-1226 (RE3>
A; Residues: 1002-1226 (RE3>
A; Note: part of this sequence were determined by protein sequencing
A; Note: part of this sequence were determined by protein sequencing
A; Rismanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad Sci. 10.S.A. 82, 3385-3389, 1985
A; Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
A; Reference number: 159025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: I59025
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1003-1034 <RES>
A; Cross-references: GB:M1135; NID:g179693; PIDN:AAA51857.1; PID:g179694
A; Note: part of this sequence were determined by protein sequencing
A; Mote: part of this sequence were determined by protein sequencing
A; Mote: part of this sequence were determined by protein sequencing
A; Mote: Dat. Chem. 260, 11216-11222, 1985
A; Fitle: Complete primary structure of the human alpha-2 type V procollagen COOH-termine
A; Reference number: A25374; MUID:85289337; PMID:2411731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Wolecule type: protein
A; Residues: 288-291, 'P', 293-294, 'X', 296-297; 606, 'X', 608-617 < MOR>
A; Residues: 288-291, 'P', 293-294, 'X', 296-297; 606, 'X', 608-617 < MOR>
R; Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
Nucleic Acids Res. 15, 181-198, 1987
A; Title: The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrill
A; Reference number: A25874; MUID: 87146331; PMID: 3029669
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:304478; NID:g179697; PIDN:AAA51859.1; PID:g179698
A;Experimental source: placenta
R;Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gene Expr. 1, 29-39, 1991
A;Title: HomoLogy between alpha2(V) and alpha1(III) collagen promoters and evidence for A;Reference number: A54555; MUID:92314691; PMID:1820205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
A;Title: Genetic distance of two fibrillar collagen loci, COL3Al and COL5A2, located on A;Reference number: A30017; MUID:89138450; PMID:3224983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Title: Partial covalent structure of the human alpha 2 type V collagen chain. A.Reference number: 155239; MUID:85182703; PMID:2985598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA; DNA
A; Residues: 398-1496 <WEL>
A; Cross-references: GB:X04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Molecule type: mRNA
A.Residues: 1227-1417, 'r', 1419-1437,'S', 1439-1496 <MYE>
A.Cross-references: GB:M11718; NID:g180912; PIDN:AAA52058.1; PID:g180913
A.Experimental source: normal fibroblasts
R.Tsipouras, P.; Schwart*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: rhabdomyosarcoma cell line R; Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M. J. Biol. Chem. 260, 5533-5541, 1985
                                                  collagen alpha 2(V) chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-463 <WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-32 <GRE>
                                                                                                                                                                                                                                                                                                                              A; Accession: A31427
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Db 275 Qy 2864 Db 294 Qy 2804 Db 307 Qy 2729 Qy 2729 Db 341 Qy 2669 Db 354 Qy 2648 Db 374 Qy 2588 Qy 2588 Db 383			513
2864 294 2804 307 2767 326 2729 341 2669 354 2688 374 374 378	TCTACCTTCCTTCAACCCTTGGGTAACGGTTTGGAATTATCGTTTGGGATG		
294 294 307 307 2729 341 2669 354 2689 374 378	### AGENCE AND CONTROLLED TO STATE AND ADDRESS OF THE STATE OF THE STA		
2804 307 2767 326 2729 341 2669 354 2588 333	AGTAGATUTCCAAGGTCCTGGGTTAGGCATTTGGG		
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2729 341 2669 354 2648 374 2588	AGCCCAATGACCAGCTATCTCAGGGGACCTGATTGTTGGGGATCCCCCACCCTACCAAA	8 8 8 8 8	
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2648 374 2588 383			
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2588.	4 oGlySerSerGlyPheProGlyAsn 382	ě	
383	TGTCTCTGTGATGGCAAC	;	
	::: 3 -ProGlyMetLysGlyGluAlaGlyProThrGlyAlaArgGlyProGluGl 399	a a :	
Oy 2528	GGTGGATCAGCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCC 2469	δο ?	1499 CCCGGTGGTAGAGGAGG
399 a	lli:: 9 yProGlnGlyGlnArgGlyGluThrGlyProProGlyProValGlySerProGlyLeuPr 419	gg ,	
Oy 2468	CTCAGGACTCTTCCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCAT 2409	δ t	1463 TCTGCAGGGCTGAGAAGGTGAACCCGGTGA
Db 419	9 oGlyAlaileGly 423	aa :-	
Qy 2408	8 CCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGTTAAGGGGCCTTAGAGA 2349	ò á	
Db 424		ag ::	ernery
Qy 2348	TGGGAAACCAGGTGACTGAGTTTATTCAGC	À 5	
Db 425	pGlyThr	3 8	
Оу 2288	8 ACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTC 2229	Š	
Db 435		3 8	
Qy 2228	8 CAGTGCATGGAGCCCTTCTGGCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGG 2169	Š 7	
Db 444	GlyProProGlySerProGlyProGlnGlySerThrGlyProGl	3 8	
Qy 2168	CCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAGAGGGAC 2124	S d	
Db 462	2 yAsnSerGlyLeuProGlyAspProGlyPheLysGlyGluAlaGlyProLysGlyGl 481	<u>a</u> :	ProGlyProserGlyIn
Oy 2123	3 GCCCCAGCCCCCAGCTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAGAGCC 2064	Š á	1184 ACA
Db 481	l uProGlyProHisGlyIleGln	a :	
Qy 2063	ACATTACTTTGGCAGCAACAGAAACTG	Š d	1139 TGAGTGCCATCCAGCTGCACAGCTCAGCCA
Db 489		ž O	
7	-CCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTT	7 g	785 GluGlyThrAlaGlyAsnAspGlyAlaGly
Db 499	499 sArgGlyProArgGlyAspProGlyThrLeuGlyProPro 512	à0	

1946	TCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAA 1887
513	
 1886 516	TGGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTG 1835
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 1781 555	GGA
 1721 567	
1664	AGAGCGCGGGTGGAGGTGGGAGCGCCTCCAGCACCCACGTGTCCATTAGG- 1606
 1605	AAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCT 1554
 1553 624	CACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT 1500
 1499	CCCGGTGGTAGAGGGAGG
 1463 655	
 1403	TGTGGGACAGGCATGTGGCCACCGGCAGCAAAG
 1364	CTGCC::: ::: GlyAspGlnGlyValPr
 1316	
 1259	
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1184	ACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCA
763	GluArgGlyIleAlaGlyThrProGlyProLysGlyAsp775
776	
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1019	

qq		qa
ογ	959 TGGGGCCCAGCGCTGCTCCTCACCACCAGTGTGGCTGCTGCTACGCAGGTGAGGAAGA 900	oy da
ρp	810GlyGluLysGlyGluProGlyProArg	
٥٧ و	899 TGAGGGTGAGCGCAAAGAGGCACTCCT	da da
, vo		RESULT 2
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οy	848 CCAGGGCACTGGTGTCCCAGTCAATGGCAGGCAGGTAGCCCAGGCAGCAGCAAGAC 789	N;Contai C;Specie
QQ		C; Date: C; Access
οy	GACAGT	R; Zhidko FEBS Let
QQ	877	A:Title: hain.
Οy	740CCCGGAAGAGGT 729	A; Kelere A; Access
Dβ	892 LeuLysGlyGlyArgGlyThrGlnGlyProProGlyAlaThrGlyPheProGlySerAla 911	A; Morecu A; Residu
οy	728 CAGAGAGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGCAGCCCCA 669	R;Kimura
QQ	oglyProAlaGlyAlaProGly	A;Title:
Qy	TGAGCAGTGCCAGGGGCCTGGGATCCGGGCA	A; Netere A; Access
qq	929 LeuGlyGluProGlyLysGluGlyProProGlyProArgGlyAspProGlySerHisGly 948	A; Molecu A; Residu
Qy	614 CTGCTAGCCGGCCCTTGGGATGAGAAAGAGGTCAGCAGGATGCCCAAGGACAGTG 555	A; Cross : A; Note: C; Commen
Dp	949 ArgValGly 960	ed and s
οy	554 CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTA 495	A; Gene:
Ob	096	A; Map po
Óγ	494 GGAGCGGACACAGACCAGCCCAGCCACCAATGCCCAGCATGGTCATGAACT 435	A; Incloud
qq	961 GlyProGlyAspLysGlyAspProGlyGluAspGlyGlnProGlyProAspGly 978	3(XI) C
ογ	434 TCTCCTCTACCCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGCGGCCAAAC 375	C; Functi
qq	979ProProGlyProAlaGlyThrThrGlyGlnArgGlyIleVal 992	A; Descri A; Note:
δ	3TTAC	C; Superi C; Keywor
qa	993 GlyMetProGlyGlnArgGlyGluArgGlyMetProGlyLeuProGlyProAlaGlyThr 1012	E; 1-234/ E; 1-187/
Οy	344 CCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGCC	F; 255-30 F; 306-34
qq	1013 ProGlyLysValGlyProThrGlyAlaThrGlyAspLySGlyProProGlyProValGly 1032	F; 343-13 F; 429-43
ογ	305 TCACCCACACACCATAGTGGGCCAGGCGGGTAGGCTCAGGGGCCGTTC 249	E; 44/-44 E; 1257-1
οp	1033 ProProGlySerAsnGlyPro-ValGlyGluProGlyProGluGlyProAlaGlyAsnAs 1052	F;1337-1 F;1381-1 E:1403-1
Qy	248 AGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCAGAAGCTGCGGCCTCTCCTTG 189	F; 1403-1 F; 109-16
QQ	oglyArgAspG	F; 426, 12
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DP	1066	F;942/MO F;942,10
Qy	128 TCCAGCTICTCAGCCCATGCTCAACACCTGCTGCTGGGGCACCTCAGTGGGACACGT 69	F;1427,1 F;1460/B

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7-130/Region: cell attachment (R-G-D) motif
7-449/Region: cell attachment (R-G-D) motif
7-449/Region: cell attachment (R-G-D) motif
7-57-1239/Region: cell attachment (R-G-D) motif
557-1380/Region: cell attachment (R-G-D) motif
557-1380/Region: cerboxyl-terminal nonhelical telopeptide
881-1546/Domain: carboxyl-terminal propeptide (fragment) #status predicted
103-1546/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #status
103-1546/Domain: fibrillar collagen carboxyl-terminal homology (fragment) #status
103-153,151-1545/Disulfide bonds: #status predicted
6,1266/Modified site: 5-hydroxylysine (Lys) #status predicted
103-1033,1299/Modified site: carbohydrate (Lys) (covalent) #status atypical
12,1033,1299/Rodified site: 5-hydroxylysine (Lys) #status experimental
12,1033,1299/Binding site: carbohydrate (Lys) (covalent) #status experimental
12,1033,1299/Binding site: carbohydrate (Lys) (covalent) #status predicted
12,1033,1299/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 references: EMBL:L18987; NID:9306439; PIDN:AAA35498.1; PID:9306440
1, T.; Cheah, K.S.E.; Chan, S.D.H.; Lui, V.C.H.; Mattel, M.G.; van der Rest, M. Chem. 264, 13910-13916, 1989
The human alpha2(XI) collagen (COL11A2) chain. Molecular cloning of cDNA and ance number: A32645; MUID:89340485; PMID:2760050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             references: GDB:119788; OMIM:120290
sation: 6p21.3-6f21.3
ss: 1302/3; 1320/3; 1322/3; 1350/3; 1440/1; 1477/3
the list of introns is incomplete
*x: type XI collagen may be a heterotrimer of two alpha 1(XI) chains (see PIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular cloning of PARP (proline/arginine-rich protein) from human cartila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         references: GB:J04974; NID:g180714; PIDN:AAA52034.1; PID:g180715 parts of this sequence were determined by protein sequencing it: Prolines and lysines at the third position of the tripeptide repeating uniubsequently 0-g1ycosylated.
1076 oGlySerGln-GlyAlaProGlyThrProGlyProValGly---AlaProGlyAspAlaG 1095
                                                                                                                                                1095 lyGlnArgGlyAspProGlySerArgGlyProIleGlyHisLeuGlyArgAlaGlyLysA 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is: Homo sapiens (man)
07-Jun-1990 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
ion: S34790; A32645
                                                              n alpha 2(XI) chain precursor - human (fragment) hate names: procollagen alpha 2(XI) chain .ns: proline/arginine-rich protein (PARP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nce number: S34790; MUID:93314796; PMID:8325374
                                                                                                                                                                                                                                                                                            1115 rgGlyLeuProGlyProGlnGlyProArg 1124
                                                                                                                                                                                                                          38 GGCTGTCACCCGGAGCCAGCGCGTGCAGG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           va, N.I.; Brewton, R.G.; Mayne, R.
t. 326, 25-28, 1993
                                                                          68 CTCATCACTCAGATCCTGGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       le type: DNA; mRNA es: 586-1546 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56/Region: helical
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les: 1-663 <ZHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDB:COL11A2
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						οp	396 AlaGlyProAsp
Alignment S Pred. No.:	ent Scores: No.:	4.7e-12	Length:	1546		Qy	2350GATGGGA
Percent Simil	E Similarity:		Conservative:	588.		Ф	415 yPheAspGlyLe
Best Local S Query Match:	ocal Similarity: Match:	24.20% 5.21%	Mismatches: Indels:	479		Qy	2294 GTCTCAACTAGO
DB:			caps:	.0/		qq	422
08-09-7	59-143-110 (1-	3410) x CGHU2E	(1-1546)			QY	2234 GCATTCCAGTG
δλ	3224 TTATTGCA :::	AACGGCACTTAAAC	CCCCCCTGAGAGATAAC	TCCCTTAGCTCAGGCAGG	31.65	qq	 427 yHisArgGlyA
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Qy	3164 GGGTGCTC	CTGAGTTTCTGTGT	GAGATTCCCCAAGCACA	GGGTGCTCCTGAGTTTCTGTGAGATTCCCCAAGCACAGATATACTCTGGGGGCTGAGA	3105	7 E	
qa	232		HisGlyProArg	• ₁⊒	238	1 8	2131 AGAG
oy.	3104 TGGACAAAG		CTTGGGAAACCGCACT1	-GCTTGGGAAACCGCACTTTGTGCTTCTGGTCCTGCAGTA	3057	Š i	í
Q	 239 GlvGluLv	 SGlvGluProAlaV	 alLeuGluProGlyMet	 	257	qq	eGlyPr
1 2	, v	ACAGGGTTGTGGAGG	TGGTGGGAAAGTTGG	GCTCCAAACAAGGGTTGGGGAAAGTTGGGGAAAAGTTGGGGAAAAGTTGGGGGAAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAAGTTGGGGGAAAAGTTGGGGGAAAAAGTTGGGGGAAAAGTTGGGGGAAAAGTTGGGGGAAAAAGTTGGGGGAAAAAGTTGGGGGAAAAAGTTGGGGGAAAAAGTTGGGGGAAAAAA	2997	QY	2078 TGGCA
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3 8	, ,				2037	ΟŊ	2024 GCAGCCCCATG
ολ	ا م	rrrrgggcagrgccr	TCATCAGCCCAGTCCT	GGGGAAATTTTGGGCAGTGCCTTCATCAGCCCAGAGAGAG	293/	qq	486 pGlyProGlnG
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ογ		gggaaccaggcigggc :::	CAAGAGAAGAGGGGTG(AGTGGGGGAACCAGGCTGGGCCAAGAGAAGAGGGGTGGTTAAGGAAGCCGTTGAGACCT :::	2877	QQ	III 504 oGlyGlnGlnG
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οy	2876 GAAGCCCC	CCACCTCTACCTTCC	CTTCAACACCCTAACCT	GAAGCCCCACCTTTACCTTCAACACCCTAACCTTGGGTAACAGCATTTGGAATTA	2817	qq	 523 GlyProHisGl
QQ	300GlyPr	GlyThrSer	euMetLeuPro		310	ò	7
Qy	2816 TCATTTGGG	SGATGAGTAGAATTT -	TCATTIGGGATGAGTAGAATTICCAAGGICCIGGGITAGGCATITIGGGGG-	GGCATTTTGGGGGGCC	2763	: A	
οp	311 ArgPheG	ArgPhedlySerGlyGlyGlyAspLys	spLys	GlyProvalval	323	ò	7
Qy	2762 AGACCCC	AGGAGAAGAAGATTC	TGGCAATGATCAGCCC	AGACCCCAGGAGAAGATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGGGGA	2703	7 A	
Dp	324 AlaAlaG	InGluAlaGlnAlaG	lnAlaileLeuGlnGl	AlaAlaGlnGluAlaGlnAlaGlnAlaIleLeuGlnGlnAlaArgLeuAlaLeuArgGly	343	ò	
δλ	2702 CCTGATTC	GTTGGGGATCCCCCC	ACCTACCCAAATATTA	CCTGATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACACAAAAAAAA	2643	7 2	
qq	344 Pro	 	 ProGlyProMetGlyTyr		350	Q A	
è		TTCCCTTCTACTTTC	STTAAATAAATAAGTTA	CAATGGATTCCCTTCTACTTGATAAATAAGGTTAAATATTTAAATGCCTGTGTCTC	2583	Qy	
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δλ	22	GCAACAGAAGGACCA	AACAGGCCACATCCTGA	TGTGATGGCAACAGAGCCAACAGGCCACATTCTGATAAAAGGTAAGAGGGGGGGG	2323	qq	616 lyValProGly
Q		Thr	ThrGlyArgProGlyPro	; 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	356	Qy	1595 CAGGCTTAGGG
ΟŸ		AAAGACAGTGCTGTC	SGGCTGAGGGGACCTGGTTC	TCAGCAAAAAGACAGTGCTGTGGGGCTGAGGGGGACCTGGTTCTTGTGTTGCCCCTCAGG	2463	qu	 635 roThrGlyAsp
QQ	357		LeuGlyGlnProGlySerProGlyLeu-	ySerProGlyLeu	365	δò	1535 TGTCCCCTCGG
٠ م	2462 ACTCTTC	CCCTACAAATAAGT	CATATGTTCAAATCCCA	ACTCTTCCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGA	2403	Db	 655 lyLeuProGly
QΩ	366		LysGlyGl	LysGlyGluSerGlyAspLeuGlyProGln	375	ΔO	
δλ	2402 AACTCCCAT	AT			2394	Z qq	
qq	376 GlyProA	rgGlyProGlnGly	LeuThrGlySerLeuGl	${\tt GlyProArgGlyProGlnGlyLeuThrGlySerLeuGlyLySAlaGlyArgArgGlyArg}$	395	ογ	
Qy	2393	GCAAGA(GCTACATTAAACGAAGC	GCAAGAGCTACATTAAACGAAGCTGCAGGTTAAGGGGCTTAGA	2351	g Q	689

Qy	1391 ATGTGGCACCGGCACACAGGGAAAGCTG	Qγ
qa	::: 704GlnArgGlyProArgGlyAlaThrGlyLysSerGlyAlaLysGlyThrSerGly 721	QQ
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qq	868 GlyProAlaGlySerProGlyGluArgGlyAlaAlaGlySerGlyGlyProIleGly 886	Suci N;A]
δy	AGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGA	ກີ ທີ່ ນີ້
QQ	887ArgGlnGlyArgProGlyProGlnGlyProProGlyAlaAlaGly 901	C; AC R; Sa
٥y	CCACA	Subn A; De
Dp	902 GluLysGlyValProGlyGluLysGlyProlleGlyPro 914	A; Re
οy	TGAGCAGTGCCAGCT	A; Re
qq	915 ThrGlyArgAspGlyValGlnGlyProValGlyLeuProGlyProAlaGlyPropro 933	R; V.
Οy	641 GGGGCC FIGGGATCCGGGCACAGCCGTGCTAGCCAGCCGG 600	rtz, subm
qq	934 GiyValalaGiyGluAspGiyAspLySGiyGluValGiyValProGlyGlnLySGiyThr 953	A; De
Ογ	599CCCTTGGGA 591	A; AC A; St
Dp	954 LysGlyAsnLysGlyGluHisGlyProProGlyProProGlyProIleGlyProValGly 973	A; Mo
Οy	GGACAGTGCCCAGATGAAGGGCC	A; Ex
qa	974GlnProGlyAlaAlaGly	C; Ge A; Ge

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olecule type: mRNA sesions. NID:9407091; PID:9407092 Estducs: 1-512 cSAU>
coss-references: BMBL:X75382; NID:9407091; PID:9407092 Sockernecs: BMBL:X75382; NID:9407091; PID:9407092 Sockernecs: BMBL:X75382; NID:940719; NID: Li, Y.; Falm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel mitted to the EMBL Data Library, July 1998 mitted to the EMBL on a Abidopsis thaliana chromosome 1 BAC T22318 sequence, complete sequence number: 214202
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esidues: 1-490, A', 492-512 <VYS>
ross references: EMBL:AC003979; NID:g3172156; PID:g3287687; GSPDB:GN00059; ATSP:T2
sperimental source: cultivar Columbia
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pecies: Arabidopsis thaliana (mouse-ear cress)
ate: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000
ccession: S38196; T00773
auer, N.K.
mitted to the EMBL Data Library, October 1993
escription: SUC1 and SUC2: two sucrose transporters from Arabidopsis thallana.
ccession: S38196
                                       1059 ValGlyAsnLeuGlyProProGlyGluLys-----GlyGluProGlyGluSerGlySer 1076
                                                                                                                                                                                                                                                                                                                                     1025 GluThrGlyAspValGlyProMetGlyProProGlyProGlyProArgGlyProAla 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1077 ProGlyIleGln-----GlyGluProGlyValLysGlyPro-ArgGlyGluArg---- 1092
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530 CATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGA---GCGGGACACACAGA----- 480
                                                                                                                                     479 ------CCAGGCCCA---GCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCT 432
                                                                                                                                                                                                                                                                        401 GCACATAGGTGATGCCTGCGGCCAAAC-----375
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995 TCGCCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 GlyAlaPheLysGluLeu-----LysArgProMetTrpMetLeuLleVal 285
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                                                                                                                                                                                                          CGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCC 382
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                                                                                                                                                                                                                           GlyLeuValThrValAlaValPheLeuIle------GlyTyrAlaAlaAspIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 ValLysGluLysProTrpThrProGluProThrAlaAspGlyLysAla------
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                                                                          512
123
92
195
101
A:Introns: 419/3; 441/1; 455/3
C;Superfamily: common tobacco sucrose transport protein
C;Keywords: sugar transport
                                                                                      Matches:
Conservative:
Mismatches:
Indels:
                                                                          ength:
                                                                                                                                                  Gaps:
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                                                                     5.4e-12
323.50
42.07%
24.07%
5.04%
                                                                                                     Percent Similarity:
Best Local Similarity:
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                                                             Alignment Scores:
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probable sucrose-proton symporter SUC2 protein T22J18.12 - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
C; Accession: 686360
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001
C; Accession: 686360
C; Date: 02-Nov-2001
C; Accession: 686360
A; Hudjacs, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudjacs, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; St., Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: 686360
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A; Accession: Company A;
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C; Genetics:
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1175 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTÁT
                                                                                                                                                                                           346 MetSerLeuGlyValGluTrpIleGlyArgLySLeuGly---GlyAlaLySArgLeuTrp
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                                                                        306 ArgGluValTyrGlyGlyAsnSerAspAlaThrAlaThrAlaAlaSerLysLysLeuTyr
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A; Residues: 1-512 <STO>
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Length:

5.4e-12

Alignment Scores:

Pred. No.:

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		382	442	21.1	502	87	562	619	124	661	144	721	164	778	817	204	874	224	934	5 # 3	994 259	1054	269	1114	285	1174	305	1234	325	1294
323.50 Matches: 123 42.07% Conservative: 92 lty: 24.07% Mismatches: 195 5.04% Indels: 101 2 Gaps: 18	(1-3410) x G86360 (1-512)	CGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTTGGCC 	4 F	LeuGlnLeuSerLeuLeuThrProTyrValGlnLeuLeuGlylleProHisLysTrpAla	ACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGGTCCTAGGCTCA	SerLeulleTrpLeuCysGlyProlleSerGlyMetLeuValGlnProlleValGlyTyr	GCCAGTGACCACTGGCGTGGACGCTATGGCCGCCCGCCCTTCATCTGGGCACTGTCC	CAAGGGCCGGCTGGCTAGCAGGGCTG	5	CTGTGCCCGGATCCCAGGCCCTGGAGCTGGCACTGCTCATC	::: ::: HisSerMetGlyAspGlnLeuAspLysProProLysThrArgALaIleALaIlePheAla	CIGGGCGIGGGGCIGCIGGAGATICIGGCCAGGIGIGCTICACICCACIGGAGGCCCIGGIGILIII	LeuGlyPheTrpIleLeuAspValAlaAsnAsnThrLeuGlnGlyProCysArgAlaPhe	CTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCGAGGCCTACTCTGTCTATGCC	TTCATGATCAGTCTTGGGGGCTGCCTGGGCTAC	 aAlaGlySerTyrArgAsnLeuTy	CCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGAG	.:: :: :: :: :: :: :: :: :: ::	TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG	Consequent and the control of the co	orizonensocariocortes de la companya	TCGCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT	::: ::	CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCCGGCTCTTCGTGGCT	GlyalaPheLysGluLeuLysArgProMetTrpMetLeuLeuIleVal	GAGCTGTGCAGCTGGATGCCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC		GAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT	ArgGluValTyrGlyGlyAsnSerAspAlaThrAlaThrAlaAlaSerLySLysLeuTyr	GATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTC
arit mila	-143-110									į									TGCC		Vali	TCGC	-	CCCC	GlyA	GAGC	Thra	GAGG	ArgG	GATG
s at	59	323	383	48	443	99	503	563	108	620	125	662	145	722	779	185	818	205	875	۰ ۲	. 4	995	260	1055	270	1115	. 286	1175	306	1235
Score Perce Best Query DB:	US-09-7	Qy Db	δy	QQ	ογ	QQ	Qy Dp	Οy	QQ	οy	Dp	ογ	op G	Qy Dp	οy	qq	0λ	QQ	Oy Dp		S Q	٥y	QQ	Qy	qq	οy	Db	οy	QQ	οy

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procollagen type V alpha 2 - mouse
C; Species: Mus musculus (house mouse)
C; Date: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C; Accession: 149607
R; Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
R; Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
R; Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
R; Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
R; Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
R; Andrikopoulos, K.; Suzuki, H.R.; Solursh, M.; Ramirez, F.
R; Accession: 149607
R; Reference number: 149607
R; Stafus: preliminary; translated from GB/EMBL/DDBJ
R; Andrewsion: 1497 (ARES)
R; Molecule type: mRNA
R; Residues: 1-1497 (ARES)
R; Cross-references: GB:L02918; NID:g309180; PIDN:AAA37440.1; PID:g309181
C; Genetics:
R; Genetics:
C; Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology cFCC>
F; 1270-1497/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
                                                                 1295 ITCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCC 1354
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                                                                                                                                                           1355 AGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCGGTG 1414
                                                                                                                                                                                                                                                                                                                                         1415 ---GTGACAGCTTCAGCC------GCCCTCACCGGG------TTCACC 1447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------CAGGTGTTCCTGCCCAAATACCGA 1528
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1448 TTCTCAGCCCTGCAGATCCTGCCCTACACAGCCTCCCTCTACCACCGGGAGAAG--- 1504
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                                                                                                       346 MetSerLeuGlyValGluTrpIleGlyArgLysLeuGly---GlyAlaLysArgLeuTrp 364
                                                                                                                                                                                         365 GlyIleValAsnPheIleLeu------AlaIleCysLeuAlaMetThrValValVal 381
                                                                                                                                                                                                                                                                                            382 ThrLysGlnAlaGluAsnHisArgArgAspHisGlyGlyAlaLysThrGlyProProGly 401
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422 PheSer------IleProPheAlaLeuAlaSerIlePheSerThrAsnSerGly 437
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3160 GCTCCTGAGTTTCTGTGTGAGATTCCCCAAGCACAGATATACTCTGGGGGCTGAGATGGA 3101 	3100 CAAAGGCTTGGGAACCGCACTTGTGCTCCTGGTCCTGCAGTACCTCCAACAGGTTG 3041 ::: ::: ::: 2 GlnLysGlyGluProGlyLeuValProValValThrGlyIle 125	3040 TGGAGCTGGTGGGGAAAGTTGGGGGTAGGGGAAAGTTGGGGGAAATTTTGG 2984 	2983 GCAGTGCCTTCATCAGCCCAGTCCTAGAGAGAGAGGGGAGTGGAAGTGGGGGGAACC 2924	GAGA yHis	2863 CTACCTTCCACCACCCT	2839 TTGGGTAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGG- 2782 	TAGGCATTTTGGGGGGCCAG	212 rValGiyProValGiyProArgGiyProValGiyLeUGinGinGinGinGinGinGinGinGiyGiyAlaGi 232 2760ACCCCAGGAGAAGAAGATTCTGGCAATGATCAGCCCAATGACCAGCT 2714	232 yProAlaGlyProProGlyGluProGlyGluProGly-ProMetGlyProIleGlySer- 251	2713 ATCTCAGGGACCTGATTGTTGGGGATCCCCCACCCTACCAAATATTAGACACCAACAC 2654	AGAAAAGCTAGCAATGGATTCCCTTCTACTTTGTAAATAAA	263 263	GCCTGTGTCTCTGTGATGGCAACAGGAGGACCAACAG	3GGGGGGGGGAGAAAAAAAAAAAAAAAAAAAAAAAAAA		2476 TGTTGCCCTCAGGACTCTTCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGAG 2417	- TGTTTCATCCTAGAAACTCCCATGCAAGAGCTACAFT	302 isLysGly-LeuGluGlyProLysGlyGluIle312	2356 CITAGAGAIGGGAAACCAGGIGACIGAGITIATICAGCICCCAAAAACCCTICTCTAGGI 2297	AlaLysGlyGlu	2296 GTGTCTCAACTAGGAGGCTAGCTGTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCC 2237	CCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAAACCCC	335GlyGluArgGly 343
Qy Dp	Qy Db	Qy Db	Qy Db	Qy Db	Oy Dp	Qy Db	. Ko	a &	qa	oy 4	oy Oy	qq	δο d	a &	qa	O.Y Db	٥y	q	٥y	Db	δ. 64 64	2 6	7 A

Qy	2176 T	TGGAAGGCTTCCAGTCAGCCAGCCCTAGAGACTGGGGAGAGGGAGAGGGACG 2123
qa	344 Ar	gLeuGlyProGlnGlyAlaProGlyLysArgGlyAlaHisGl
Qy		CCAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACACAGGAGCAGCAGA 20
Dp	360 P	GlyLysProGlyProMetGlyPro
Qy	9 9 8	AGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCT 20
qq	377 -	pheproGlyAsnProGlyMetLysGlyGluArgGlyProHisGlyAla 39
Qy	2008 A	AACAGGAGGGGGAGCTGGGACCCAGTGAGGCAGGCCTCCACCCCAA 1961
qq	393 A	nGlyGlnAr
٥y	1960 T	STGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTG 19
Dβ	409 -	1 1
Qy	1900 T	GTAGCAAAGTAAATGGCGACCAGACCCTGCGGCAGACACCATATAGGCAGTGAC 1841
Db	418 -	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Qy	1840 A	AGACTGGCTGAGCTGGACAATGGAGCCATAAACAGGGATGGGGCCACCTGGACAGCAG 1781
qq	431 1	athrGlySerAlaGlyThrSerGlyProProGlyLeuAlaGlyProProGlySerProG 451
Qy	1780 G	AAGGCACTAT
qq	451 1	yproGlnGlySerThrGlyProGlnGlyIleArgGlyGlnSerGlyAspProGlyValP 471
Qy	1768 Ç	SATGGCGAGGT
QQ	471 r	roglypheLysGlygluAlaGlyProLysGlygluProGlyProHisGlyIleGlnGlyP 491
Qy	1730 -	CCACCC
Dp	491 r	olleGlyProProGlyGluGluGlyLysAr
Qy	1696 A	ACGIACGGAGACATCACAGGCAGAGGCCCGCAGAGCGCGGGGGGGGGG
QQ	510 1	MetGlyGluArgGl
Qy	1642 C	CAGGCCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGA
qq	530 I	ProLysGlyAl
Qy	1597 1	CAGCTTAGGCCTGCAGGAAGCTGGTCATCAGGCTGTCATCACTGCT 15
Db	550 3	.ysGlyGlyGlnGlyAspProGlyArg-ProGlyGluProGlyLeuProGlyAlaA 570
Qy	1546	TTGGGCA
qa	570 1	rgGlyLeuThrGlyAsnProGlyValGlnGlyProGluGlyLysLeuGlyProLeuGlyA 590
QY	1501	CTCCCGGTGGTAGAGGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAA 1442
QQ	590	laProGlyGluAspGlyArgProGlyProProGlySerIleGlyIleArg-GlyGln 608
Qy	1441	AAGCTGTCACCACGCCACACTGTGGG
qq	609	etGlyValProGlyProLysGlySerSerGlyA
Qy	1396	CAGGCATGTGGCACCGGCAG1377
QQ	629	yasnaladiyvalProGlyGlnArgGlyAlaProGlyLysAspGlyGluVal 64
Qy	1376	CCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 13
Db	649 (SerglyProvalGlyProProGlyLeuAlaGlyGluArgGlyGluAla 6
Qy	1322 (GCACCAGCCGGTCCATGACCAGAGAAGACCAGGGAGA 1284

299	
128	
687	7 GlyGlyLysAlaGlyAspGlnGlyValProGlyGluProGlyAlaVal 702
1223	3 GGGCCTCGGTGCCCGGCTCTGGCACGCCCTGGTACAGCCCCTCGCCACGAAAT 1164
1163	CCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACAGCTCAGCCACGAAGA
721	
1103	3 GCCGGCGCAGGGTGCGGGCCATGCGGCAGCACACAGCTGGT 1065
729	III 9 LysGlyMetAlaGlyHlsGlyProAspGlyProLysGlyAsnProGlyProThrGly 748
1064	4 GCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGC
1022	
769	
971	
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926	GTGTGGCTGCTACGC
809	
872	CCTCCTGGGTGCCCAGGTAGGGGG
848	
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864	
779) AGGCATAGACAGAGAGCTGGCGACAGTGGTCGGGT
878	
740	
968	
719) GGGCCTCCAGTGGAGTGAAGCACACGTGGCCACAGAAGTCCAGCAGCACCCCAGGA 660
629	
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599	CCCTTG
953	
539	GGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGA 480
963	::
479	CCAGGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCTCTTCTAACAACAAAAAAAA

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Collagen alpha 5(IV) chain precursor, renal splice form - human
N.Alternate names: procollagen alpha 5(IV) chain
N.Alternate names: procollagen alpha 5(IV) chain
N.Contains: collagen alpha 5(IV) chain precursor, leukocyte splice form
C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 21-Jul-2000
C.Accession: S22917; A54365; A57079; A37122; I54317; A34850; S18850; I56971; I76598;
R.Zhou, J.; Hertz, J.M.; Leinonen, A.; Tryggvason, K.
J. Biol. Chem. 267, 12475-12481, 1992
A;Title: Complete amino acid sequence of the human alpha-5(IV) collagen chain and ide
A;Reference number: S22917; MUID: 92316923; PMID: 1352287
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A;Title: Deletion of the paired alpha5(IV) and alpha6(IV) collagen genes in inherited A;Reference number: A57079; MUID:93361972; PMID:8356449
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A;Residues: 1-922 <ZH2>
A;Cross-references: GB:U04470; NID:g463378; GB:U04520; NID:g463428; PIDN:AAC27816.1;
A;Cross-references: GB:U04470; NID:g463378; GB:U04520; NID:g463428; PIDN:AAC27816.1;
                                                                                                                                                                                                                        |||| ||| ::: ||| 999 ArgGlyValThrGlyMetProGlyLeuProGlyProAlaGlyThrProGlyLysValGly 1018
                                                                                                                                                                                                                                                                                                                                              1058 ----ArgAspGlyAlaValGlyGluArgGly----------As 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1039 GlyPro-ValGlyGluProGlyProGluGlyProAlaGlyAsnAspGlyThrProGly-- 1057
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                                                         419 CTTCCAGCAGCAGAGGGGGCACATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAA 360
                                                                                                                  982 GlyProAlaGlyThrThrGlyGlnArgGlyIleVal------GlyMetProGlyGln 998
                                                                                                                                                                                  359 AGG-----TTAGCAGGTTGACCAGCAAGAGCTGGG 330
                                                                                                                                                                                                                                                                                                                 -----GGCTCACCCACAGCCTCT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 GCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 TAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 CTGGC---CGAGGCGCGCGGCTGTCACCCGGAGCCAGCGCGTGCTGGTTCCC 1
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A; Residues: 1-967 <2HO>
A; Residues: 1-967 <2HO>
A; Cross-references: 1-967 <2HO>
A; Cross-references: A: Trygyason, K.
B; Zhou, J.; Leinonen, A.; Trygyason, K.
A; Biol. Chem. 269, 6608-6614, 1994
A; Title: Structure of the human type IV collagen COL4AS gene.
A; Reference number: A54365; MUID:94165049; PMID:8120014
                                                                                                                                                                                                                                                                                                        329 CTTTCCGGTGCCGCAGCAGGC----
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A; Residues: 1-27 <ZH4>
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A) Cross-references: GB:237153; NID:q587203; PIDN:CAA85512.1; PID:q587204
R) Phhlajaniemi, T.: Pohjolainen, E.R.; Myers, J.C.
Biol. Chem. 265, 13758-13766, 1990
A) Title: Complete primary structure of the triple-helical region and the carboxyl-ter
A) Reference number: A37122; MUID:90337990; PMID:2380186

A; Accession: A37122 A; Molecule type: mRNA

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C; Function:
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A;Note: permature termination mutation from a patient with Alport syndrome; one other mu R;Lemmink, H.H.; Schroeder, C.H.; Brunner, H.G.; Nelen, M.R.; Zhou, J.; Tryggvason, K.; Genomics 17, 485-489, 1993
A;Title: Identification of four novel mutations in the COL4A5 gene of patients with Alport A;Reference number: I54188; MUID:94010948; PMID:8406498
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A; Residues: 1284-1291, TFLGYLACLV <GUO2>
A; Residues: 1284-1291, TFLGYLACLV <GUO2>
A; Cross-references: GB:569169; NID:9545095; PIDN:AAC60613.1; PID:9545098
A; Cross-references: GB:569169; NID:954007; PIDN:AAC60613.1; PID:9545098
A; Mote: frameshift mutation in patient with Alport syndrome
R; Myers, J.C.; Jones, T.A.; Pohjolainen, E.R.; Kadri, A.S.; Goddard, A.D.; Sheer, D.; Sc
Am. J. Hum. Genet. 46, 1034-1033, 1990
A; Title: Molecular cloning of alpha5(IV) collagen and assignment of the gene to the regilance number: A35335; MUID:90252791; PMID:2339699
A;Residues: 84-439, 'GS', 442-624, 'LALQ', 629-666, 'FR', 669-887, 'R', 889-1264,1271-1691 <PIH)
A;Cross-references: GB:J05558; EMBL:M58526; NID:g1314209
A;Note: submitted to the EMBL Data Library, February 1991
A;Note: the authors translated the codon GC for residue 115 as Val
R;Renieri, A.; Seri, M.; Myers, J.C.; Pihlajaniemi, T.; Massella, L.; Rizzoni, G.; De Ma
Hum. Mol. Genet. 1, 127-129, 1992
A;Title: De novo mutation in the COL4A5 gene converting glycine 325 to glutamic acid in
A;Reference number: I54317; MUID:93244772; PMID:1363780
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A;Residues: 1448-1477 <MYE>
R;Residues: 1448-1477 <MYE>
R;Nakazato, H.; Hattori, S.; Ushijima, T.; Matsuura, T.; Koitabashi, Y.; Takada, T.; Yos
Kidney Int. 46, 1307-1314, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:M63455; EMBL:M63456; EMBL:M63457; EMBL:M63458; EMBL:M63459; EMB
B; EMBL:M64470; EMBL:M63472; EMBL:M63473; NID:9177922; PIDN:AAA51558.1; PID
R;Guo, C.; Van Damme, B.; Van Damme-Lombaerts, R.; Van den Berghe, H.; Cassiman, J.J.; M
Kidney Int. 44, 1316-1321, 1993
A;Title: Differential splicing of COLAA5 mRNA in kidney and white blood cells: a complex
A;Reference number: IS6971; MUID:94133540; PMID:8301933
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A,Reference number: 156975; MUID:95156853; PMID:7853788
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A;Molecule type: mRNA
A;Residues: 313-324, Pz', 326-330 <REN>
A;Residues: 313-324, Pz', 326-330 <REN>
A;Residues: GB:S59334; NID:9299946; PIDN:AAD13909.1; PID:g4261609
A;Cross-references: GB:S59334; NID:9299946; PIDN:AAD13909.1; PID:g4261609
B;Hostikka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeyhtyae, M.; Shows, T.B.; Tryggvason, K.
B;Hostikka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeyhtyae, M.; Shows, T.B.; Tryggvason, K.
A;Hostikka, S.L.; Eddy, R.L.; Byers, M.G.; Hoeyhtyae, M.; Shows, T.B.; Tryggvason, K.
A;Title: Identification of a distinct type IV collagen alpha chain with restricted kidne
A;Reference number: A34850; MUID:90160375; PMID:1689491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: BMBL:M31115; NID:g180824; PIDN:AAA52045.1; PID:g180825
R;Zhou, J.; Hostikka, S.L.; Chow, L.T.; Tryggvason, K.
Genomics 9, 1-9, 1991
A;Title: Characterization of the 3' half of the human type IV collagen alpha-5 gene that A;Reference number: A37969; MUID:91169491; PMID:2004755
A;Accession: S18850
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A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1595-1602 <NAK>
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A; Residues: 1604-1607, 'VHDAYKC' <LEM>
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A; Residues: 924-1264,1271-1691 <ZH3>
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A; Residues: 914-1264,1271-1691 <HOS>
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A; Residues: 1258-1276 <GUO1>
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A; map position: Xq22 Xq22
A; Introns: 27/3; 47/3; 77/3; 92/3; 107/3; 128/3; 146/3; 155/3; 182/3; 203/3; 215/3; 2
A; Introns: 27/3; 47/3; 77/3; 92/3; 1006/1; 1036/1; 1082/3; 1125/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 1155/1; 
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A; Note: frameshift mutation from a patient with Alport syndrome; five other mutations C; Comment: Prolines and lysines at the third position of the tripeptide repeating uni
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F.1583-1687/Domain: collagen IV carboxyl-terminal repeat <CT2>
F.29,32,38,40,124,451,481,484/Disulfide bonds: interchain #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          591 --GlyGluProGlyGlyIleThrPheLysGlyGluArgGlyProProGlyAsnProGlyL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 GGCGCCTGGCTGATTCCTAGGCAGTTGGCGGCAGCAAGGA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 CATGGGCTGAGAAGCTGGACCGGCACCAAAGGGCTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-759-143-110 (1-3410) x S22917 (1-1691)
                                                                                                                                                                                                                                                             A;Gene: GDB:COL4A5; ATS
A;Cross-references: GDB:120596; OMIM:303630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 TGGGTGAGCCG------
                                                                       C;Comment: Prolines and lysines at ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.79e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323.00
30.90%
25.59%
5.03%
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           195
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Qy	398 GTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGAGAGATCATGACCATGGT 450	qa	006
Qy	CATTGGTCCAGTGCTGGGCTGTGTGTCCCGCTCCTAGGCTCAGCC	Qy	1460 CAGATCCTGCCCTAC
QQ	638 lyValAlaGLyAsnProGlyGlnProGlyIleProGlyProLys 652	qq	901
οy	506 AGTGACCACTGGCGTGGACGCTATGGCCGCCGCCCCTTCATCTGGGCACTGTCCTTG 565	Οy	1520 AAATACCGAGGGGAC ::
Ob	653	QQ	rg
οy	566 GGCATCCTGCTGAGCCTCTTCTCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGC 625	Ολ	CCAG
QQ	653 lyAspProGlyGlnThrIleThrGlnProGlyLySProGlyLeuP 668	QQ	929GlyGlnPro
٥y		δ V	
qa	668 rodlyAsnProGlyArgAspGlyAspValGlyLeuProGlyAspProGlyLeuProGlyG 688	g G	
٥y	674 CTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCT- 732	δλ	1700 GTGGTGGGTGAGCCC
. q q	688 lnProGlyLeuProGlyIleProGlySerLysGlyGluProGlyIleProG 705	qa	960 u-GlySerLysGlyG
λλ	733CTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTGTGTGTGCC 778	δλ	1739 CGGGGCAT
q	705 lylleGlyLeuProGlyProProGlyProLysGlyPheProGlyllePro 721	qa	980 roLysGlyTyrGlnG
λ	779 ITCATGATCAGTCTTGGGGGGCTGCCTGGGCTACCTCCTGCCTG	Qy	1784 CTGTCCCAGGTGGCC
q	722	qa	1000 lyLeuProGlyProP
λi	839 AGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGC 877	δy	1844 ACTGCCTATATGGTG
ą	736 iuGlyProProGlyProGlyPheProGlyProLysGlyGluProGlyPheAlaLeup 756	අු	1018GlyL
ہ		δλ	
Q	756 roGlyProProGlyProProGlyLeuProGlyPheLysGlyAlaLeuGlyProLysGlyA 776	QQ	
>-	938 GAGGAGGCAGCGCCCCACCGAGCAGCAGCAGGGCTGTGGGCCCCCTCCTTGTCG 997	δδ G	1964 GGGTGGAGGCCTGC
c	776 spArgGlyPheProGlyProProGlyProProGlyArgT 789	3 8	
>-	998 CCCCACTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCC 1057	δ á	2024 CCGGGCTGGCCGCCA
Q	789 hrGlyLeuAspGlyLeuProGlyProLysGlyAspValGlyProAsnGlyGlnProGlyP 809	an .	
_		δŏ.	2084 TGCTGCTGAGGTGCG
٥	809 roMetGlyProProGlyLeuProGlyIleGlyValGlnGlyProProGlyProProGlyI 829	qn	1061
,	1106 TICGIGGCIGAGCIGIGCAGCIGGAIGGCACICAIGACCIICACGCIGITITACACGGAI 1165	δλ	2144 GTCTCTAGGGCTGCC
۵	829 leProGlyProlleGlyGln	οp	1072 -SerileGlyLeuPı
> -		Ολ	2201 AGGGAGGCCA
۵	841	q	1091 oglyAsnProGlyIl
>-	1226 AGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATC 1285	Ολ	2237 GGACTCTGCAGGTGG
م		QQ	1111 rProGlyAlaLysGl
~		Qy	2297 ACCTAGAGAAGGGTT
0	::: 	qa	1121ProGlyPh
	1346 TATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCC 1399	Qy	2357 CCCCTTAACCTGCAG
	882 eubroGlyLysAlaGlyAlaSerGlyPheProGlyThrLysGlyGluMetGlyMet- 900	qa	1133 s
	1400 CACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTG 1459	Οy	2417 CTCCTCCATGGGATT

06	0	006
146	0 CAGATCCTGCCCTACACACTGGCCTCCCTCACCACGGGAGAAGCAGGTGTTCCTGCCC	1519
06	1	915
152	0 AAATACCGAGGGAACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTG ::	1579
158	0 CCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGGGGGG	9
	orgenecacenceaccaccaccaccaccacacacacacacaca	946 1699
94		9
170	0 GTGGTGGGTGAGCCCACCGAGGGTGGTTCCGGGC	1738 980
173	9 CGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1	1783
178	4 CTGTCCCAGGTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1 :::	1843
84	ACTGCCTATATGGTGTGCGGCGAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1	90
01	GlyLeuIleGlyProProGlyLeuLysG 1	1027
190,	4 GTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGGGTAGAAACTTCCAGGACATTG 1: ::: 7 lythr	1963
1964	GGGTCCCAGCTCCCGCTCTGTTAGCCCCATGGGGCTG 2	020
3	TINGENERAL TREETO GIVETOGINATION VALGINATA TREETOGINALIAN TO TO TO TO THE TOTAL TREETOGINATION TO THE TREETOGI	0.4
105(Codest tolerated the state of t	090
2084	TGCTGCTGAGGTGCGTAGCTGCAGCTGGGGGCGTCCTCTCTCT	143
1061	GlyileSer 1	.071
14	GTCTCTAGGGCTGCCTGAGGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATAC 2	20
) i	-serileGlyLeuProGlyLeuProGlyProLysGlyGluProGlyLeuProGlyTyrPr 1	091
2201	AGGGAGGCCAGAAGGCTCCATGCACTGGAATGCGG 2 1 1 1 1 1 1 1 1 1	236
2237	GGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACAC 2	29
1111	rProGlyAlaLysGlyGlnProGlyLeu1	H
2297	ACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACTGGTTTCCCATCTCTAAG 2	356
1121	ProdlyPheProdlyThrProdlyProProGlyProLy 1	133
35	CCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACA 2	416
13	sGlyIleSer-Gly1	137
2417	CTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAACA 2	476

1		*. BAFORDAGO DIUMBOY. B01387. MITD.7204049. DMID.4673951
QQ	114	387
Qy	2477 CACAAGAACCAGGTCCCTCAGGCCCACAGCACTGTCTTTTGCTGATCCACCCCCTCTT 2536	A; Molecule type: protein A; Residues: 146-294 <f12></f12>
qq	roGlyGluProGlyProValGlyGlyGlyHisProGlyGlnProGlyProPro	A; Experimental Source: SKin R; Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
ολ	ACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGGCATT	Eur. J. Blocknem. 38, 390-400, 13/3 A,Title: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7
අු		A; Reference indired: Apilia A
δo i	TAAATATTTAACTTATTTATTTAACAAAGTAGAAAGGGAATCCATTGCTAGCTTTCTGTG 2000	A; Resident 215-562 - Vector A; Resident 21 - Source: Skin
a :		
දු දි		A;Title: The covalent structure of collagen. The amino-acid sequence of the 112 resid A;Reference number: A91201; MUID:73042276; PMID:4343808
Å	TGGTCATTGGGGTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGG 2764	A;Accession: A91201 A;Molecule type: protein
: 점	:::	A; Residues: 563-675 <wen> A; Experimental source: skin condt D . Ctark M . Knahn K</wen>
δ	TGGAAATTCTACTCATCCCAAATGATAATTCCA 2824	Kirletzek, F.F.) Rearout, F.W., Wender, F., Stark, W., McChar, C. Burry Burry Burry Burry Burry Burry 1972 a.m. 1972
. q	1186 GlnProGlyPheGlyAsnProGlyPro	A; Reference number: A91200; MUID:73042275; PMID:4343807
Οy	GAAGGAAGGTAGAGGGTGGGGCTTCAG 2878	A; MCCESION: AZZZO A; Molecule type: protein A: Residues: 676-758 <f14></f14>
q	1196GlyLeuProGlyLeuSerGlyGlnLysGlyAspGlyG 1208	A; Experimental source: skin a. Morper pro-726 is the only 3-hydroxybroline and the only hydroxylated proline in pos
Qy	AACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTC 2938	ni, K.
qa		Ajfittle construction and a sequence of the carboxyterminal nonhelical cross link region a Peference number: A43048
Qy	2939 CACTCCCTCTACTCTCTTAGGACTGGGCTGATGAAGGCAC 2980	A; Molecule type: protein
qq	1228 HisGlyPheProGlyValGlnGlyPro	
Οy	2981 IGCCCAAAAITICCCCTACCCCCAACTITCCCCTACCTTCCCCACCACCTCCA 3040	C; Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hyd C; Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) ar
qq	GlySerProGlyProAla	the alpha 1(I) chain or
οy	3041 CAACCC 3046	C;Comment: The complete chain contains 1052 residues. C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homolo
qa	1253 AsnPro 1254	C, Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trime F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
RESULT	29	F;1/Modified site: pyrrolidone carboxylic acid (6111) *status experimentat
CGBO1S CO1lag	en alpha 1(1) chain - bovine (tentative sequence) (fragments)	ent scores: 7.65e-12 Length:
C; Spec	16s: De printgenius taurus (cattle) 24. Abra - 1884 #seminare regision 31-Den-1963 #text change 31-Mar-2000	321.00 Matches: 31.12% Conservative:
C; Acce	ssion: A91193; A91229; A91387; A91211; A91201; A91200; A43048; A02853	Best Local Similarity: 26.69% Mismatches: 269
R;Raut Eur. J		1 Gaps:
A;Titl A;Refe	III Call and	$US-09-759-143-110 (1-3410) \times CGBO1S (1-779)$
A; Acce A; Mole	A; Accession: A91193 A; Molecule type: protein	Qy 2365 GTTAAGGGGCTTAGAGATGGGAAACCAGGTGAGTTTATTCA 2321
A; Kesi A; Expe	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	lyHisArgGlyPheSerGlyLeu
A;Note R;Fiet	: the epsilon carbon of Lys-9, by homology with the rat alpha 1(1) chain, is conve .zek, P.P.; Kuehn, K.	Qy 2320 GCTCCCAAAAACCCTTCTCTAGGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGC 2261
Eur. J	. Biochem. 52, 77-82, 1975 e: The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide	Db 119 GlyProAlaGlyProLys124
A;Refe A:Acce	rence number: A91229; MUID:76022320; PMID:1164916 ssion: A91229	OY 2260 CIGGGTAATCCACCIGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGC 2207
A; Mole A; Resi	A:Molecule type: protein A:Residues: 20-145 <fie></fie>	
A; Expe A; Note	rimental source: skin :: Lys-103 is hydroxylated and binds glucosylgalactose	QY 2206 CICCCTGTATAAGTCCAGACTGAAACCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGA 2147
R, Fiet FEBS I		Db 144 LeuProGlyPheProGlyProLysGlyAlaAlaGlyGluProGly 158
A; Tit.	e: The covalent structure of collagen: amino acid sequence of alphal-CB3 Ifom call	

ò	2146 GACTGGGGAGAGGGACGCACCCCACCCCAGOTGTGCACCTAACCAACTAA 2000	-
qq	LysalaGlyGluArgGlyValProGlyProProGlyAlaValGlyProAlaGlyLys	Db 411 oProGlyProlleGly
δy	2089 GCAGCACAGGGGAGAGAGAGAGATTACTTTGGCAGCAAAAAGGGGGGGG	QY 1146 AAGGTCATGAGTGCA
QQ	178 AspGlyGluAlaGlyAlaGlyPro186	Db 427 gGlySerAlaGlyPro
δλ		Oy 1086 GGCATGCGGCAGCACA
qq	187ProGlyProAlaGlyProAlaGlyGluArgGlyGluGlnGlyProAlaGly 203	
ογ	1987	Qy 1032 AAAGCCAAGCGGGCCC
qq	204 SerProGlyPheGlnGlyLeuProGlyProAlaGlyProProGlyGluAlaGlyLys 222	Db 459ProProGlyPro
ογ	1948 TTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAATACTACCTGTGTAGCAAAGTA 1889	Qy 972 TCTGCTGGCTCGGTGG
qά	222 222	Db 477 -ProAlaGlyArgPro
Οy		Qy 912 CAGGTGAGGAAGATGA
qq	223 ProGlyGluGlnGlyValProGlyAspLeuGlyAlaPro235	Db 491
Οy	1832 TGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGGAGGAAGG 1776	Qy 869CCTGGGTGC
qo		Db 505 aGlyAlaProGlyThr
. Qy	1775 CACTATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGGCCCGGAACCACCCTG-GCCTCG 1717	QY 848 -CCAGGGCACTGGTGT
qq	:::	Db 525 uProGly
Qy	1716 GIGGGCTCACCCACCACCACACGIACGGAGACATCACAGGCAGAGGCCCCGCAG 1663	QY 795 CCAAGACTGATCATGA
qa		Db 538 oGlyPro
οy		Oy 735 AAGAGGTCAGAGGA
Ωp	285 SerGlnGlyAlaProGlyLeuGlnGlyMetProGlyGluArgGlyAlaAlaGlyLeuPro 304	552
٥y	1626 GCACCCACGTCCATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGC 1579	QY 677GCAGCCCACGC
qu		Db 571 oGlyGluSerGlyArg
ολ	1578 AGGAAGCTGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATT 1521	QY 624 CACAGCCTGCTA
qq	:::	Db 587 yArgAspGlySerPro
ογ	1520	OY 564 AAGGACAGTGCCCAGA
qq	343 oGlyAspLysGlyGluAlaGlyProSerGlyProAlaGlyThrArgGlyAlaProGlyAs 363	Db 607 oGlyProPro
Οy	1491 TAGAGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGG 1432	504 GCTGAGCC
qq	363 pArgGlyGluPro371	611
0y	1431 GCGGCTGAAGCTGTCACCACGGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCACA 1372	Qy . 444 GTCA
qq	372	Db 624 sSerGlyAspArgGly
· δ	1371 GGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATGGCTGCACCAGCGGG 1312	Qy 399 ACATAGGTGATGCCTG
qq	373 aGly	644 yAlaArgGlyPr
Qy	1311 TCCATGACCAGAGAGAGAGAGGAGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCC 1252	356
qa	380 yAlaAspGlyGlnProGly	664
δλ	1251 ATCGGAACGCCTTCATCATGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACG 1192	
đ	391 oʻlyAspAlaGlyAlaLysGlyAspAlaGlyProProGlyProAlaGlyProAlaGlyPr 411	684
ογ	1191 CCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTG 1147	Qy . 277CCAGGGGGTAC

0	11 oPr	 ProGlyProIleGlyAsnValGly	 yAlaProGlyPro		 LysGlyAlaAr	427
·.	1146 AAG	STCATGAGTGCCATCCAGCTG	GCTCAGC	AAGAGCCGG	CGCAGGGTGCGG	1087
0	427 gGl	roGlyAl	aThrGlyPhePro		G]	440
~ 0	1086 GGC	ATGCGGCAGCACAGCT aalagivargvalgivarg	GGTGCAGCCGG	GGTGCAGCCGGGAAGCAGGGCGCCCCAGGTT	SSS	0 1
			To Table To	yashatadiyridi	ProGLY	
. 0	45	occanoscosceles de la company	:AGCAGTGGGGC	3ACAAGGAGGGGG sGlyProArgGly(SCGACAGCCCT 	973
~.	2 T	CTGCTGGCTCGGTGGCCCAGCGCTGCTCCTCAGCCACCAGCAGTGTGGCTGCTAC	CTGCCTCCTCA	SCCACCAGCAGTG1	C)	913
^	- 7	oAlaGlyArgProGlyGluVal	GlyProProGl	ProPro		490
	912 CAG	AGGTGAGGAAGATGAGGTGAGCCCAAAGAGGCACTCCT	GGCCAAAGAGGG :::::: 	CACTCCT		870
	- 69	CCTGGGTGCCCAGGT	TO THE TOTAL TOTAL	AGGGGG-	TUOTACTOR	
	505 aGly	 AlaProGlyThrProGlyPr	GlnGlyIleAl		lValGlyLe	~
	848 -CC/	-ccaggcacrggrgrcccagrcaa	AGTCAATGGCAGGCAGGA	.596	racccaggcagccc	0 0
	5 6	SGLY SGACTGATCATGAAGGCATAGA	GINALGGL)	GLUARGGLYPNer	GlyLeuPr	538
_	38	061yProSetGlyGluPro61yLvsGlnPro	SerGlyGluPro		Sergival	7.50
	735 AAG	AGGTCAGAGAGAGGCCTCCA	GTGGAGTGAAGC	ACACCTGGCCACA	AGTCCA	, i
	552 aser	::: rGlyGluArgGlyProProGlyProMetGlyProProGlyLeuAlaGlyPro	GlyProMetGl _y	 ProProGlyLeuA	Pr	571
	7	AGCCCCACGCCC	AGGATGAGCAGTGCCAGCTCCAGGGGCC	CCAGGGGCCT	99 -	625
	0	yGluSerGlyArgGluGly	Ala	ProGlyAlaGluG	261	587
	624 CACP 587 yArg	'ACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGA 	GCCCTTGGGATGAGAAGAGG 	GAAAGAGGCTCAG GluThrGlyProA	CCC PF	565
	564 AAGG	AAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTG	GGGGGGGCCAT	AGCGTCCACGCCA		505
-	607 ogly	yPropro				610
	504 GCTG	GCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACT	CCAGGCCCAGCA	CTGGACCAATGCCCAGCACCAT	O	445
	1 7	TW. 10	FIGGLYFIOVAL	4.75	> 1	624
	5 5	31yAspArgGl	-TGAACTICICCICIACCCCCACITCCAGC 	CTT CCAGCAGC ::: IleGlyProvalGl	AGAGGCGGC yProAlaGl	400
	399 ACATA	AGGTGATGCCT	ACACCTCCAGGC	CAAAGG	3	22
	644 yAla	ArgGlyProAlaGlyProGlnC	3lyProArgGly	>-	hrG1,y***** 6	64
	56		CAGCAAGAGCT	.gg.	GCCGCAGC	
	4 *GLY	***ArgGLy	ArgGlyPheSer	GlyLeuGlnGlyP	roProGlyPr 6	84
	312 AGGC 684 oPro	GGCTCACCCACAGCCTCTGGACCATAGTGGG GlySerProGlyGluGlnGlyPro-SerGlyAl	CCATAGTGGG	aSerGlyProAla	GlyProArgG 70	78
•	772	-ccaggggggggggggggggggggggggggggggggggg	SGCCGTTCAGG	GGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCG	CTTCGTCTCG 2	23

		CCCAGTGAG		1870 GCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCAT 1811 	1810 AAACAGGGATGGGGCCACCTGGGACAGCAGGAGGCACTATCCAGGATGGCGAGGT- 1755 11	1754CCAGGCAGAGAGCCCCGGCCCGGAACCACCCTGGCCTCGGTGGGCTC 1709	1708 ACCCACCACCACCACGAGAGACATCACAGGCAGAGGCCCGGAGAGGGGGGGG		1612 ATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAG 1562	1561 GCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTT 1502		erProGlyGluAsnGlySerProGlyProMetGlyProArg-GlyLeu		1381 GGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTG 1322	1321 CACCAGCGGTCCATGACCAGAGAGACCAGGGAGATGGCGCACTGCAGGAACAGCC- 1263	ccaggcrgcccarccgaacgccrrcararargrgrcrccgggccrcggrgcccgg	366 lyphebroglyAlabroglyAlaLysGlyGluAlaGlyProThrGlyAlaArgGlyProG 386		GAAGGTCATGAG	403
;	ලී රු සි	, vo q	oy do	Qy Db	Qy	QY	Oy	, YO	Qy	QY	qo ö	G Q	Qy Dp	QY	Qy	QY QY	qa ,	da —	ō,	gg Vo
Db 704 lyProProGlySerAlaGlySerProGlyLySASpGlyLeuA 718	Qy 222 GCTCTGCTCCAGAAGCTGCGGCCTCTTGCTGCCGCCAACTGCCTAGGAATCAGC 163	Qy 162 CAGGCGCCCATTCTGCCAGCCTTTGGTGCGGTCCAGCTCTCAGCCC 113	. o	ge 16-Jul-1999	A, Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and A, Reference number: A41182; MUID:91358489; PMID:1885613 A, Accession: B41182 A, Accession: B41182 A, Status: preliminary: not compared with conceptual translation	carboxyl	matrix; g <vwc> logy <fcc< td=""><td>7.65e-12 Length: 31.00 Matches: 30.67% Conservative:</td><td>Mismatches: Indels: Gaps:</td><td></td><td>Qy 2557 GGCCACATCCTGATAAAGGTAAGAGGGGGGTGGATCAGCAAAAAGACAGTGCTGTGGGC 2498 </td><td>OY 2497 TGAGGGACCTGGTTCTTGTGTGTTGCCCCTCAGGACTCTTCCCCTACAATAAGTC 2441 ::: ::: ph 48 TweDrogarGerCysArtTleCvsValCysAspfhrGlyAspValLeUCysAspSple 67</td><td>2440 ATAIGTICAAATCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGTACAT </td><td>2380 TAAACGAAGCTGCAGGTTAAGGGGCTTAGAGATGGGAAACCAGGTGACTTATTTCA</td><td>CCTTCTCTAGGTGTGTCT</td><td>88</td><td>Oy 2260 CIGGGTAATCCACCTGCAGAGTCCCCGCATTCAGTGGATGGA</td><td>2200 GIATAAGICCAGACTGAAACCCCTTGGAAGGCCTCCAGTCAGGCAGCCTAGACACTGG</td><td>Db 104</td><td>Db 112 ArgaspileileGlyProArgGlyProProGlyProGlnGlyPro 126 Qy 2080 GGTGGCAGCAGAGCCACATACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAG 2021</td></fcc<></vwc>	7.65e-12 Length: 31.00 Matches: 30.67% Conservative:	Mismatches: Indels: Gaps:		Qy 2557 GGCCACATCCTGATAAAGGTAAGAGGGGGGTGGATCAGCAAAAAGACAGTGCTGTGGGC 2498	OY 2497 TGAGGGACCTGGTTCTTGTGTGTTGCCCCTCAGGACTCTTCCCCTACAATAAGTC 2441 ::: ::: ph 48 TweDrogarGerCysArtTleCvsValCysAspfhrGlyAspValLeUCysAspSple 67	2440 ATAIGTICAAATCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGTACAT	2380 TAAACGAAGCTGCAGGTTAAGGGGCTTAGAGATGGGAAACCAGGTGACTTATTTCA	CCTTCTCTAGGTGTGTCT	88	Oy 2260 CIGGGTAATCCACCTGCAGAGTCCCCGCATTCAGTGGATGGA	2200 GIATAAGICCAGACTGAAACCCCTTGGAAGGCCTCCAGTCAGGCAGCCTAGACACTGG	Db 104	Db 112 ArgaspileileGlyProArgGlyProProGlyProGlnGlyPro 126 Qy 2080 GGTGGCAGCAGAGCCACATACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAG 2021

Db	417 lyAlaLysGlySerAlaGlyAlaProGlyIleAlaGlyAlaProGlyPheProGlyP 436		
ογ	1027 CAAGCGGGCCCGGCATGGACAGCAGTGGGCGACA	Qy .	2
QQ	31yProLeuGlyProLysGlyGlnA 45	qa	7
· Yo		Qy 1	-
QQ		Dp 40	~
QY	ACGCAGGTGAG	0y 1	
qo	471 lyGluThrGlyProAlaGlyProGlnGlyAlaPro	Dp 4	~
οy	904 GAAGATGAGGGTGAGCAAAGAGGCACT	Qy	
Db)8 qa	~
٥y	873 873	Qγ	
qq	503 leGlyProProGlyGluArgGlyAlaProGlyAsnArgGlyPheProGlyGlnAspGlyL 523	. Db da	
٥y	872CCTCCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGGTGTCCCAGTCAAT 824	RESULT 31 S48789	
qq	523 eualaGlyProLysGlyAlaProGlyGluArgGlyProSerGlyLeuAlaGlyProLysG 543	sucrose tran C;Species: N	= -
λα	823 GGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGAC 770	C;Date: 27- C;Accession	
e G	543 lyAlaAsnGlyAspProGlyArgProGlyGluProGlyLeuProGlyAlaArgGlyLeuT 563	R;Buerkle, submitted t	\sim \circ
λά	769 AGAGTAGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGGCGCGTCCAG 710	A; Reference A; Accession	
අ	563 hrGlyArgProGlyAspAlaGlyProGlnGlyLysValGlyProSerGlyAlaProG 582	A;Status: p A;Molecule	<u>-</u>
λά	709 TGGAGTGAAGCACCCGGCCACAGAAGTCCAGCAGCCCCACGC	A; Residues: A; Cross-ref	····
ąc	582 lyGluAspGlyArgProGlyProProGlyProGlyAlaArgGlyGlnProGlyValM 602	C;Superfami	—
27	FGAGCA	Alignment Sc Pred. No.:	U
ą	602 etGlyPheProGlyProLysGlyAlaAsnGlyGluProGlyLysAlaGly- 618	Score: Percent Simi	•
λζ	613 TGCTAGCCAGCCGGCCCTTGGGATGAGAGGCTCAGCAGGATGCCCAAGGA 560	Best Local S Query Match:	01
qc	619GluLysGlyLeuAlaGlyAlaProGlyLeuArgG 630	DB:	
λ.	559 CAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGA 500	US-09-759-14	4
q	:: 630 lyLeuProGlyLysAspGlyG 637	0y 27	7
٨		qa	-
q	GlyGluArgGlyGluGlnG	0у 33	3
λλ	460 AATGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGGGGG 401	qq	~
ą		Qy 39	6
 .	AAGGTTAG	qq	4
ą		Qy 45	2
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ą	rqGlyGluArqGlyP 70	Qy 51	_
<u>~</u>		Db 8	ന
ą		Qy 57	^
<u>۲</u>	265 GGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCT 206	Db 10	0
ą		0у 63	m

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05 GCGGCCTCTCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTCTGC 146
                       45 CAGCCCTTTGGT------113
                                                                                                   82 AspGlyGlyArgGlyLeuThrGlyProlleGly-ProProGlyProAlaGlyAlaAsnGl 801
                                                                                                                                                                                                                                                       8 CCCACTATGGTCCAGAGGCTGTGGGGTGAGCCGCCTGCTGCGGGCACCGGAAAGCCCAGGTC 337
                                                                                                                                                  12 ------ATGCTCAACACCTGCTGCTGGGGGCACCTCAGTGG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 TTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTAT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAAGATTCATGACCATGGTGCTGGGC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 ATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CGTGGACGCTATGGCCGCCGCCCGTTCATCTGGGCATGTTGGGCATCCTGGGCT 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 GGACACGTCTCATCACTCAGATCCTGGC------CGAGGCGCGCGCGCGTGTCACC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 SerSerArgPheGlyArgArgArgGlyPheileAlaAlaGlyAlaAlaLeuValThrile 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGCCCGGATCCC--- 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ProLeuProLysSerLysLeuTrp------LysIle 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::: ||| ::: :::|||::: |||||| ::: :::
8 LeuThrProTyrValGlnLeuLeuGlyIleProHisLysPheAlaSerPheIleTrpLeu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nsport protein - common tobacco
Nicotiana tabacum (common tobacco)
Jan-1995 #sequence_revision 27-Jan-1995 #text_change 26-May-2000
N.Y.Z.; Frommer, W.B.
or the EMBL Data Library, October 1994
: number: S48787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507
126
87
207
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   type: mRNA
1-507 <BUED.
erreces: EMBL:X82276; NID:g575350; PID:g575351
ly: common tobacco sucrose transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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319.50
41.04%
24.28%
4.98%
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Similarity:
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21 oGly 822
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A; Cross-references: GB:S63190; NID:9234368; PIDN:AAB19627.1; PID:9234369
A; Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIP:63192)
C; Superfamily: collagen alpha I(I) chain; fibrillar collagen carboxyl-terminal homolo C; Keywords: alternative splicing; colled coll; extracellular matrix; glycoprotein; tr F; I191-1419/Domain: fibrillar collagen carboxyl-terminal homology <PCC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carti
                                                                                                                                                                                                                                                                                                 exon structure,
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M65161
R;Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.
Development 111, 945-953, 1991
A;Title: Expression of the mouse alpha 1(II) collagen gene is not restricted to
A;Reference number: A44885; MUID:91347939; PMID:1879363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1954 GGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGC 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1894 AAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTG 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1834 GCTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAGGC 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2104 CAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAGCCACATTACTTTGGCAGCAAC 2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2044 AGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGGGGCTGGGA--- 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -------CCCAGTGAGGCAGGCCCTCCACCCCAATGTGCT 1955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89 ProGlyAsnProGlyProAlaGlyProProGlyProProGlyProProGlyLeuSerAla 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GlyAsnPhe-----AlaAla 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
-CIGCICCCACCICCACCGGG 1660
                                                                                                                                               C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
C;Accession: A41182; A44885
                         71 LysGlyGluLysGlyAlaProGlyProArgGly-----ArgAspGlyGluProGlyThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 GlnLysGlyGluProGlyAspIleArgAspIleIleGlyProArgGlyProFroGlyPro
                                                                                                                                                                                                                                                                                                 sedneuce,
                                                                                                                                                                                                                                           Ribersacratta, M.; Toman, D.; de Crombrugghe, B.; Vuorio, E. J. Biol. Chem. 266, 16862-16869, 1991
A;Title: Mouse type II collagen gene. Complete nucleotide sequer A;Reference number: A41182; MUID:91358489; PMID:1885613
A;Stetus: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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  1619 GTGGGTGCTGGAGGCAGTGGC-
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.318.50
.31.66%
.26.75%
5.12%
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A; Residues: 1-1419 <MET>
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Best Local Similarity:
Query Match:
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A; Residues: 1-28 <CHE>
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----CCAGGCAGATGCCCCGGCCCGGAAC 1730

1774 ACTATCCA---GGATGGCGAGGT

RESULT 33 CGHU1E COllagen alpha 1 N;Alternate name	872AGGGGGC 848 872	Qy Db
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Oy 48 -	erytioaraciyeluciuciyLysArgelyAlaargG	}
Db 725 oi		: 음
QY 100 TC	TACGCAGGTGAGGAAGATGAGGTGAGCAGAGGCGAAGGCAACT	γ̈́ο
Db 706 G		QQ
Qy 130 G		٥y
Dp 989 C	379 lyProLeuGlyProLysGlyGlnAlaGlyGluProGlyIleAlaGlyPheLysGlyAspG 399	qq
Qy 169 A		٥y
Db 666 A		q
Qy 229 C		٥y
Db 647 L		qq
Qy 286 C		οy
Db 627 a		g
Qy 316 C	1171 CACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACGTCAGC 1112	οy
Db 607 1		QQ
Qy 364 G		οy
Db 597 1		QQ
Qy 424 C		٥y
Db 581 r	283GlyProAlaGlyProProGlyP 290	οp
Oy 467 -		δy
Dp 265 -		οp
Qy 523 T		δλ
. Db 554 e		QQ
Qy 577 C	ACCACGGCCAC	δy
Db 543 s		QQ
QY 637 C	GTGTAGGGCAG	δ
Db 526 1		g
Qy 673 C	1585 GCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCG 1526	λ̈́
Db 506 y		qq
Qy 733 G	1636 ACTGCCTCCACCACCACGTGTCCATTAGGGAAGGGAGCTCCAGGCTTAGG 1586	ογ
	::: 188 uAlaGlyLysProGlyLysSerGlyGluArgGlyLeuProGlyProGlnGlyAlaArgGl 208	QQ
Qy 793 #	1672 GGCCCCGCAGAGCGCGGGTGGAGGTGGGAGCAGGCC 1637	δÿ
Db 467		Dp
Qy 847 C		٥y
	150 roGlyProGlnGlyPheGlnGlyAsnProGlyGluProGlyGluProGlyValSerG 169	qq

ΟY	847	TCCCAGTCAATGGCAGGCAGGA
Db	467	
Qy	793	AAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGAA 734
QQ	487	lyLeuProGlyalaArgGlyLeuThrGlyArgProGlyAspAlaGlyProGlnGlyL 506
0y	733	AGGTCAGA :
QQ		ysValGlyProSerGlyAlaProGlyGluAspGlyArgProGlyProProGlyProGlnG 526
Qy	673	CCCCACGC
qq	526	lyAlaArgGlyGlnProGlyValMetGlyPheProGlyProLysGlyAlaA 543
Οy	637	CCTGGGATCCGGGCACAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCT 578
qa	543	snGlyGluProGlyLysAlaGlyGluLysGlyLysG
Qy	577	CAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCG 524
qq	554	euAlaGlyAlaProGlyLeuArgGlyLeuDro
٥y	523	TCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGGCCCAGGCCCAGCA 468
qq	565	
Ωy	467	CTGGACCAATGCCCAGCACCATGAACTTCTCCTCTAC 425
qa	581	roAlaGlyGluArgGlyGluGlnGlyAlaProGlyProSerGlyPheG 597
λχ	424	CCCCATTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGCGGCCAAACACACCTCCAG 365
qq	597	<u> —</u> д
λχ	364	GCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCC 317
qc	607	
λγ	316	CAGCAGGCGCCTCACCCCACACCTCGGCAC
qc	627	alGlyProArgGlyGluArgGlyPheProGlyGluArgGlySerProGlyAlaGlnGly- 646
2y	286	CATAGTGGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGGTT 230
q	647	LeuGlnGlyProArgGlyLeuProGlyThrAspGlyProLysGlyAla 665
27	229	CGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGG 170
qc	999	1,4
λy	169	AATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCC 131
q	989	rgGly
27	130	
q	902	ysAspGlyGlyArgGlyLeuThrG
λλ	100	GCTGCTGTGGGGCACCTCATCAC
q	725	oproGlyproAlaGlyAlaAsnGlyGluLysGlyGluValGlyProProGlyProSerGl 745
λλ	48	CGAGGCGCGGCTGTCACCCGGA 25
q	745	ySerThrGlyAlaArgGlyAlaProGly 754
ESULT 33 GHU1E Ollagen a	llpha e na	ESULT 33 CHUIE Ollagen alpha 1(XI) chain precursor – human i.Alternate names: procollagen alpha 1(XI) chain

2954 AGAGTAGAGGGAGTGGAACTAGGACCAGGCTGGCCCAACAGAACAGGAGGGTGTTA	2744 516 2696 536 2639 . 555	GIGGLYPTOPTOGLYPTOTHTGENERGY	2390 630 2366	Qy 2312 AAACCCTTCTFA GGTGTGTCTCAACTAGGAGCTAACCTGTTAACCCTGAGCCTGGG 2230	Qy 2162 GTCAGGCAGCCCTA
C:Species: Homo sapiens (man) C;Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 08-May-1998 C;Accession: A35239; A31795 R;Yoshioka, H.; Ramirez, F. J. Biol. Chem. 265, 642-6424. A;Reference number: A35239; MUID:9020294; PMID:1690726 A;Reference number: A35239; MUID:9020294; PMID:1690726 A;Residues: 1-558 <	A, Accession: A31795 A; Molecule type: DNA, mRNA A; Molecule type: DNA, mRNA A; Cross-references: GB:J04177 A; Note: parts of this sequence were determined by protein sequencing C; Comment: Prollines and lysines at the third position of the tripeptide repeating unit (ed and subsequently 0-glycosylated. C; Genetics: A; Gene: GDB:COLINA; COLLG A; Gene: GDB:L20595; OMIM:120280 A; Map position: Lp21-lp21 A; Introns: 561/3; 579/3; 597/3; 615/3; 638/3; 666/3; 681/3	A; Noce: The list of introns is incompleted A; Noce: The list of introns is incompleted 3(XI) chain (see PIR:CGHUGC), initially linked by disulfide bonds among their carboxyl- med with desmosine cross-links made from lysine and allysine residues C; Function: A; Description: structural component of extracellular fibrous polymer associated with cell A; Note: may play a role in controlling the lateral growth of collagen lifibrils C; Superfamlly: collagen alpha 1(V) chain; fibrilar collagen carboxyl-terminal homology C; Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproli F; 37-540/Domain: PRP-like #status predicted <parp> F; 37-511/Domain: amino-terminal propeptide #status predicted <prp> F; 512-1565/Product: collagen alpha 1(XI) chain #status predicted <amt> F; 512-1555/Product: collagen alpha 1(XI) chain #status predicted <amt> F; 512-1565/Product collagen alpha 1(XI) chain #status predicted <amt></amt></amt></amt></prp></parp>	F;1543-1565/Region: carboxyl-terminal nonhelical telopeptide F;156-1806/Domain: carboxyl-terminal propeptide *status predicted <ctp> F;1583-1805/Domain: fibrillar collapsoryl-terminal homology <fcc> F;61-243.182-236/Disulfide bonds: *status predicted F;505/Modified site: allysine (Lys) *status predicted F;612,1452/Modified site: 5-hydroxylysine (Lys) *status predicted F;612,1452/Binding site: carbohydrate (Lys) (covalent) *status predicted Alignment Scores:</fcc></ctp>	ed. No.: 1.54e-11 Length: 1806 cre: 316.00 Match: 315 cre: 31.07% Concerts: 315 st Local Similarity: 26.03% Mismatches: 413 sry Match: 1 Gaps: 71 co9-759-143-110 (1-3410) x CGHUIE (1-1806) 3101 ACAAAGGCTTGGGAAACCGCACTTTGTGCTTCTGGT	Db 409 ThrasplieThrGluThrSerileAshGlyAlaTyFGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLySGlyGluLyGlyGluLyGlyGluLyGlyMetLeuvalGluL

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£	:::	qa	1044 ysGlyGlyGlu
łò	AAATGGGGGCCCAGCCGGGAGCCCC	Qy	1126 GCTGCACAGCT
? සි	erLysGlyGluLy	qa	::: 1055 roValGlySer
Qy	GAGCGGGGAGCTGGGACCC	. 0y	1066 GTGCAGCCGGG
qa	 796 19AspArgGlyGluValGlyGlnIleGlyProArgGly***AspGlyProGluGlyProL 816	qa	1069 lyProlleGly
VO	TTCTACGCTGAGTATTTGGCC	Qy	1006 GCAGTGGGGCG
đ		qa	1089 ysGlyAlaPro
δ	ATGGCGACCAGAC	Qy	946 TGCCTCCTCAG
qa	ysLeuG	qa	1102
Qy	rgac,	δλ	886 GCCAAAGAGGC
qq	838 lyValProGlyLeuProGlyTyrProGlyArgGln	q _Q	1108 1у
ογ	1819 GGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAGGCACTATCCAGGATGG- 1761	δλ	829 GTCAATGGCAG
q	850	qa	1119
ογ	1760 1731	δλ	769 AGAGTAGGCCT
q	 861 roGlyAlaAsnGlyGluLySGLyAlaArgGlyValAlaGlyLysProGlyProArgGlyG 881	qa	1131 leGlyGluPro
Οy	1730CCACCCTGGCCTCGGTGGGCTCACCCACCACGTACGGAGACATCACA 1679	δλ	709 TGGAGTGAAGC
qq		ପ୍ଧ	1150Gly
οy		Qy	649 CAGCTCCAGGG
qq		qα	1163 lealaglygly
Qy	1618 GTGTCCATTAGGGAAGGAAGCTCCAGGCTTAGGCCTGGCAGGAAGCTGGTCATCAGGCT 1559	δδ	589 GAGAAAGAGGC
QQ	918 gGlyproGlnGlyproGlnGlyproValGlyPheProGlyProLys 933	QQ	
Qy	GTGTCC	Qy	529 ATAGCGTCCAC
QQ		qq	1190 PheProGlyPro
Oy	1498 CCGGTGGTAGAGGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCC 1439	δλ	469 CACTGGACCAA
QΩ		qa	1206 roGlyGluLys
Οy	1438 GCTGAGGGGGCTGAAGCTGTCACCACGGCCACTGTGGGACAGGCATGTGGCACCGGC 1379	ογ	421 CACTTCCAGCA(
qq		qa	1224 roglyproarg
Oy	1378 AGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCAC 1319	QY	361 AAAGGTTAGCA
q		qa	1244
δλ		δδ	301 CCACAGCCTCTC
qq		qa	1257 roGlyGluAlaC
δλ		Qy	244 ACTCCAGAACTC
qq		qa	1277GluArg
Qy	1204 AGCTCTGGGCACGCCTGGTACA1776	óy	187 TGCCGC
qq	 1024 lyLeuArgGlyPheProGlyGluArgClyLeuProGlyAlaGlnGlyAlaProGlyLeuL 1044	ପ୍ଧ	-
٥y	1175CGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCA 1127	δλ.	147 -GCCAGCCCTT1
		qa l	1314 oGlyAspProGl

1044	ysGlyGlyGluGlyProGlnGlyPro	r.
1126	GCTGCACAGCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCACCTG 106 :::	67
1066	GTGCAGCCGGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATGGACA 100	39
1006	GCAGTGGGGCGACAAGGAGGGGCGACAGCCCTTCTGCTGGCTG	7 11
946	TGCCTCCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGATGI	
œ Ö	GCCAAAGAGGCACTCCTCGGGTGCCCAGGTAGGGGCCAGGGCAGGG	
829	GTCAATGGCAGGCAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGAC 770	
769	AGAGTAGGC 1 1eGlyGluP	0 0
709	TGG	
649	CA le	_ =
589	GAGAAAGAGGCTCAGCAGGATGCCCAAGATGAAGGCCGGCGGCGGCCGCCGCCGCCGCCGCCGCCGCCGC	
529	ATAGCGTCCACGCCAGTGGTCACTGGCTGAGCGAGCGGGACACAGACCAGGCCAAA	
469	CACTGGACCAATGCCCAGCACCATG	
421		
361	AAAGGTTAGCAGGTAGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCGCTCAC 302 ::	
301	CCACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGGC 245	
244	ACTCCAGAACTGCTTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGC 188	4
1295	TGCCGC	4
147	-GCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGTGGG 89	თ

88 GCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGCCGA	Qy 320 CACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACC :::	c 358 526
Db 1329 pGlyValGlyGlyAspLySGlyGluAspClyAspProClyGlnProClyFroFroGlyFr 1349	OY 359 TITGGCCTGGAGTGTGTTTGGCCGCAGCATCACCTATGTGCCGCCTCTGCTGCTGGAAAA	
oscielyclualaclyproproclyproproclyLysargclyproproclyAlaala	527GlyProLysGlyAspArgGlyGlyThrCysAlaPheCysAla:	H 541
RESULT 34	Oy 419 GTCGGGGTAGAGCAGAAGTTCATGATCATGGTCCTGGGCATTGGTCAGTGGTGGCTTGGCTGGC	
	478	
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 13-Aug-1999 C;Accession: S16366	559 lnGlyGluArgGlyLeuProGlyIleProGlyAlaThrGlyAlaProGlyAspAsp	 GlyL 579
the nonellow VIII the	Oy 482 TGTGTCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCGGGGGGGG	36 541
lpna-z(iv) coilagen and	Db 579 euProGlyAlaProGlyArgProGlyProProGlyProProGlyG	yG 594
A; MCCess101: 510300 A; MOlecule , Type: mRNA A; Docidation 1172 / TET	QY 542 CCCTTCATCTGGGCACTGTCCTTGGGCATCCTGTGAGCCTCTTTCTCATCCCAAGGGCC ::	
A; Residues: 1-103 CDE, A. A. A. A. C. A. C.	Db 594 lnAspGlyLeuProGlyLeuProGlyGlnLysGlyGluProThr	-G 609
C; venetics: A; Introns: 229/3; 266/3; 305/3; 360/3; 424/1; 489/1; 548/1; 656/3; 790/1; 891/1; 963/1;	Qy 602 GGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATC	rc 661
C; Superramily: collagen alpha 1(1V) chain C; Keywords: alternative splicing; basement membrane; cell binding; coiled coil; disulfid	ThrLeuArgProGlyPro	ep 629
F.1-2A/Domain: signal sequence #status predicted <515/7 F:27-13/S/Product: collagen alpha 2(IV) chain #status predicted <mat> F:27-42/Domain: non-collagenous NH1 #status predicted <nh1></nh1></mat>		CC 718 647
	070	
F;1530-1763/Domain: carboxyl-terminal nonhelical, NC1 #status predicted <nc1> F;1530-1638/Domain: repeat NC1 #status predicted <nc11></nc11></nc1>	Oy /19 CIGCICICIGACCICITICGGGA CCCGGACCACGG ICGCCAGCCIACLICIGAC	
F;1639-1763/Domain: repeat NCI *status predicted <nc.12> F;31,34,39,41,536,539/Disulfide bonds: interchain *status predicted p.136,739,7134,730,739/Disulfide bonds: interchain *status predicted p.136,739,739,739,739,739,739,739,739,739,739</nc.12>	773	
ď		og 684
ent Scores: 2.5e-11	OY 833 GACACCAGTGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGC	6C 886
ve:	Db 684 lyTyrGlyGlnProGlyMetProGlyLeuProGlyMetLysGlyAspAlaGlyI	uP 703
		CA 946
US-09-759-143-110 (1-3410) x S16366 (1-1763)	/US IOGIY beut todiy beut to	
ATCTGAG		
404 GlyProGlyLeuProGlyLeuProGlyLeuGluGlyLeuProGlyProLysGlyGlu	E	1062
Oy 62 TGATGAGACGTGTCCCCACTGAGGGCCCCCACGGGCAGGTGTGAGCATGGG 115 11	roGlyLeuProGlyProLysGlyGluAlaGlyPheProGlyA	
116 CTGAGAAGCTGGACCGGCACCAA	Qy 1063GCACCAGCTGCTGCCGCATGCCCCG	-6 1090
Db 440 LeualaGlyProProGlyAlaLySGlyGluProGly-ProArgGlyValAspGl 457	1097	
164 CTGATTCCTAGGCAGTTGGCGGCAGCAAGGAGGCCGCAGCTTCTGGAGCAGAGCC :::	773	Æ
457 yGlnSerIleProGlyLeuProGlyLysAspGlyArgProGlyLeuAspGlyLeuProGl	Qy 1156TTACACGGATTTCGTGGCGAGGGCTGTACCAGGC	sec 1192
UY 2.44 GAGAGGAAGGAAGTITIGAAGTGCCITTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO	laGlyLy	.yG 809
264 CCCTACCCCCTGGCCCACTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGG		TT 1246
Db 497 yLeuProGlyProProGlyPro-ArgGlyProGln	DO 809 INFROGLYLEUKTOGLYFLOLEYSCHYGLUFLOGLYFLOGGLIMINGTHIGHTOTTOGLIFFOLDER CO. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7. 7.	TG 1291

qa	Qy	qq	λo d	an .	oy	Q C	οy	q ₀	Oy	qa	0y	අු	Qy	qa	δλ	qa	Οy	Db	QY	qa		qa	δδ	අු	δλ	qQ	δy	qq		o QQ	δy	qa	RESULT A54849	collage N;Alter	C;Speci C;Date: C;Acces
	13		_	869 ProGlyLeuAlaGlyAlaProGlyPheProGlyAlaLysGlyGluProGlyLeu-ProGl 888	1403 AGIG	888 yLeuProGlyLysGluGlyProGlnGlyProProGlyGlnProGlyAlaProGl 906	1442 TTCACCTTCTCAGCCTGCAGATCCTGCCCTA	906 yPheProGlyGin-LysGlyAspGluGlyLeuProGlyLeuProGlyValSerGlyMetL 926	GAA	926 ysGlyAspThrGlyLeuProGlyValProGlyLeuAlaGlyProProGlyGlnProGlyP 946	1523 TACCGAGGGACACTGGA	946 hePro-dlyGlnLysGlyBlnProGlyPheProGlyValAlaGlyAlaLysGlyGlu 964	1559 AGCCTGATGACCAGCTTCCTGCCAGGCCCTAAAGCCTGGAGCTCCCTTCCCTAATGGACAC 1618	965AlaGlyLeuProGlyLeuProGlyAlaProGlyGlnLysGlyGlu 979	ACCTCCACCGCGCTCTGC	980 GlnGlyLeuAlaGlyLeuProGlyIleProGlyMetLysGlyAlaProGly 996	1679 TGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGC1722	997	1723CANGGGTGGTTCCGGGCCGGGCATCTGCCTGGCTCGCCATCCTGGA 1770	1010 ProGlyValLysGlyAspArgClyPheAsnGlyLeuProGlyGluLysGlyGluProGly 1029	1771 TAGTGCCTT	1030 ProAlaAlaArgAspGlyGluLysGlyGluProGlyLeuProGlyGlnPro 1046	1810 TATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGG 1869	1047GlyLeuArgGlyProGlnGlyProProGlyLeuProGlyLeu 1060	1870 CCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGC 1929	1061 ProGly 1062	1930 CAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT	1063LeuLysGlyAspGluGlyGlnProGlyTyrGlyAlaProGlyLeu-MetGlyGluLy 1081	1990 CCAGCTCCCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTGC 2049	1081 sGlyLeuPro1090	2050 TGCCAAAGTAATGTGGCTCTCTGTGCTGCTGCTGCTGAGGTGCGTAGCTGCACAG 2109	1090 1090	2110 CTGGGGGCTGGGGCGTCCCTCTCCCCCAGTCTCTAGGGCTGCCTGACT 2163	1091GlyArgProGlyAlaPro-GlyProLysGlyLeuAspGlyAlaProGlyP 1107	2164 GGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGAGGCCAGAAGGGCTCCATG 2223
QQ	Qy	qq	Qy	d d	οy	qq	ογ	QQ	οy	QΩ	οy	qa	οy	qq	δ	g	Qγ	QQ	δy	qq	δλ	qq	Οy	qq	ογ	q	οy	qq	δy	QQ	δλ	qa	δ	q	δŏ

QQ	1107	heProGlyLeuLysGlyGluAlaGlyLeuProGlyAlaProG 1121
Qy	2224	CACTGGAATGCGGGGACTCTGCAGGTGACCCCAGGCTCAGGGTTAACAGCTAGCCTC 2283
QQ	1121	
QY Db	2284	CTAGTTGAGACACCACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTT 234
٥y	2344	
qq	1152	
Οy	2404	CTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAG 245
Db	1159	roGlylleArgGlyGluLysGlyAspAlaGlyLeuProGlyLeuProGlyGluArgG 117
οy	2460	AGTCCTGAG
QQ	1178	lyLeuAspGlyLeuProGlyGlnLysGlyGluAlaGlyPhePro 1192
Οy	2512	CTCTTACCTTTATCAGGATGTGG
qq	1193	GlyAlaProGlyLeuProGlyProValGlyProLysG 1205
οy	2572	TTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAT
qo	1205	
δλ	2632	GGAATCCATTGCTAGCTTTTCTGTGTTGGTGTATATTTGGGTAGGTGGGGGGATCCC 2691
qo	1217	lll
λζ	2692	
QC C	1228	
λy	2706	CCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTCTCTGGGGTCTG 2763
qc	1248	euProGlyLeuProGlyMetLysGlyGluAlaGlyLeuProGlyLeuProGlyGlyGlyGluAlaGlyLeuProGlyLeuProGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG
λy	2764	GCCCCCCAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCC 2823
q	1266	
λγ.	2824	AAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGT 2868
q	1286	AspGlyLeuProGlyL
λλ	2869	2874
q	1306	 GlyAlaAlaGlyIleLysGlyGluProGlyLeuProGlyIleProGlyAlaLysGlyGlu 1325
λλ	2875	ī
q	1326	ProGlyLeuSerGlyIleProGlyLysArgGlyAsnAspGlyIleProGlyLysProGly 1345
λi	2917	CCAGCCTGGTTCCCCCCACTTCCA
٠. و	1346	ProAlaGlyLeuProGlyLeuProGlyMetLysGlyGluSerGlyLeúProGlyProGln 1365
λ	2956	TCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCC 3012
ð	1366	GlyProAlaGlyLeuProGlyLeuProGlyLeuLysGlyGluProGlyLeuPro 1383
ESULT	35	

Collagen alpha l(VII) chain precursor - human N.Alternate names: procollagen alpha l(VII) chain C.Species: Homo sapiens (man) C.Species: 04-Nov-1994 #sequence_revision 04-Nov-1994 #text_change 20-Sep-1999 C.Accession: A54849; PH0844; S16316; 156328; A30296; 184686

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2.5e-11
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31.26$
27.37$
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
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A; Residues: 2395-2871, 'S', 2873-2944 <RE2>
A; Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
A; Cross-references: GB:L06862; NID:9388713; PIDN:AAA89196.1; PID:9388714
B; Christiano, A.M.; Rynaenen, M.; Uitto, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 3549-3553, 1994
A; Title: Dominant dystrophic epidermolysis bullosa: identification of a Gly --> Ser subs
A; Reference number: A55255; MUID:94224777; PMID:8170945
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: GDB:COL7A1; EBR1; EBD1; EBA; A;Cross-references: GDB:128750; OMIN:120120
A;Cross-references: GDB:128750; OMIN:120120
A;Map position: 3921.3-3921.3
A;Note: GdFects in this gene can result in dominant and recessive dystrophic epidermolys A;Note: there are 118 introns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Description: structural component of extracellular polymer associated with anchoring for Superfamily: unassigned collagens; animal Kunitz-type proteinase inhibitor homology; for Experiments: colled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolif;; 116/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: keratinocyte
R; Gammon, W.R.; Abernethy, M.L.; Padilla, K.M.; Prisayanh, P.S.; Cook, M.E.; Wright, J.;
J. Invest. Dermatol. 99, 691-696, 1992
A; Title: Noncollagenous (NCI) domain of collagen VII resembles multidomain adhesion prot A; Reference number: 156328; WUID:93107742; PMID:1469284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: EFR' 372-517,'DV,'520-540,'W','542-1255 <RES>
A;Cross-references: GB:S51236; NID:3262308; PIDN:AAB24637.1; PID:9262309
B;Seltzer, J.L.; Eisen, A.Z.; Bauer, E.A.; Morris, N.P.; Glanville, R.W.; Burgeson, R.E.
A; Blol. Chem. 264, 3822-3826, 1989
A;Title: Cleavage of type VII collagen by interstitial collagenase and type IV collagena
A;Reference number: A30296; MUID:89139437; PMID:2537292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Modecule type: protein
A; Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'
A; Residues: 'A',1240-1246,'G',1248-1250,'XE',1253-1255,'Q',1257,'E';2032,'C',2034-2041;'
A; Note: two reported peptides cannot be reliably located
R; Greenspan, D.S.
Hum. Mol. Genet. 2, 273-278, 1993
Hum. Mol. Genet. 2, 273-278, 1993
A; Title: The carboxyl-terminal half of type VII collagen, including the non-collagenous
A; Reference number: 148103; MUID:93271985; PMID:8499916
A; Accession: 184686
R;Christiano, A.M.; Greenspan, D.S.; Lee, S.; Uitto, J.
J. Biol. Chem. 269, 20256-20262, 1994
A;Title: Cloning of human type VII collagen. Complete primary sequence of the alphal(VII
A;Reference number: A54849; MUID:94327588; PMID:8051117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Parente, M.G.; Chung, L.C.; Ryynaenen, J.; Woodley, D.T.; Wynn, K.C.; Bauer, E.A.; Mat Proc. Natl. Acad. Sci. U.S.A. 88, 6931-6935, 1991
A; Itle: Human type VII collagen: cDNA cloning and chromosomal mapping of the gene. A; Reference number: S16316; MUID: 91334380; PMID: 1871109
A; Accession: S16316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 'EFK',340-475,'RALSTASHSTLCWRATRWHPCNRGSHWTRAACEPCNRPASHRAARAG',524-528,'C',
A; Cross-references: DDBJ:D11152; DDBJ:D13694; NID:g453698; PIDN:BAA02853.1; PID:g453699
A; Experimental source: Keratinocyte
A; Note: the authors translated the codon ACC for residues 394 and 397 as Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit ed and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 815-892, 'E', 894-1439 <PAR>
A;Cross-references: GB:M65158; GB:S49017; NID:9180914; PIDN:AAA96439.1; PID:9180915
                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Mosaidues: 1-294 cCHR>
A; Cross-references: GB:LD2870; NID:9987124; PIDN:AAA75438.1; PID:9987125
A; Cross-references: GB:LD2870; NID:9987124; PIDN:AAA75438.1; PID:9987125
R; Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
B; Janaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
B; Tanaka, T.; Takahashi, K.; Furukawa, F.; Imamura, S.
A; Title: Molecular cloning and characterization of type VII collagen cDNA.
A; Reference number: PHO844; MUID:92231902; PMID:1567409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Complex: type VII collagen is probably a homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A30296
                                                                                                                                                                 A; Accession: A54849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: PH0844
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F.1254-2783/Region: interrupted helical
F.1354-2783/Region: cell attachment (R-G-D) motif
F.1364-1386/Region: cell attachment (R-G-D) motif
F.2553-2555/Region: cell attachment (R-G-D) motif
F.2554-255/Region: cell attachment (R-G-D) motif
F.2554-2595/Region: cell attachment (R-G-D) motif
F.2554-2595/Region: cell attachment (R-G-D) motif
F.2553-2555/Region: cell attachment (R-G-D) motif
F.2554-2595/Region: cell attachment (R-G-D) motif
F.2554-2999/Domain: carboxyl-terminal nonhelical #status predicted
F.2167,2176,2185,2188,2664,2667,2673/Modified site: 4-hydroxyproline (Pro) #status experimental
F.2655,2631/Modified site: carbohydrate (Lys) #status experimental
F.2655,2631/Regioning site: carbohydrate (Lys) (covalent) #status experimental
F.2654,2802,2804/Disulfide bonds: interchain #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2318 TCCCAAAAACCCTTCTCTA----GGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCT 2265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2489 CCTGGTTCTTGTGTTG-------CCCCTCAGGACTCTTCCCCTACAATAAGT 2442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2441 CATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACA 2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1177 IleargGluala-GinalaSerGlyLeuAsnValValMetLeuGlyMetAlaGlyAlaAs 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1236 aSerPheThrThrGlnProArgProGluPro---CysProValTyrCysProLysGly-- 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------GlnLysGlyGluProGlyGl 1261
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F;17-2944/Product: collagen alpha 1(VII) chain #status predicted <MAT>
F;17-1253/Domain: amino-terminal nonhelical #status predicted <NCI>
F;36-201/Domain: ibronectin type A repeat homology <NAI>
F;337-413/Bomain: fibronectin type III repeat homology <FNI>
F;414-502/Domain: fibronectin type III repeat homology <FNI>
F;598-683/Domain: fibronectin type III repeat homology <FNA>
F;598-683/Domain: fibronectin type III repeat homology <FNA>
F;586-731/Domain: fibronectin type III repeat homology <FNA>
F;586-771/Domain: fibronectin type III repeat homology <FNA>
F;686-771/Domain: fibronectin type III repeat homology <FNA>
F;686-712/Domain: fibronectin type III repeat homology <FNA>
F;684-952/Domain: fibronectin type III repeat homology <FNA>
F;684-952/Domain: fibronectin type III repeat homology <FNB>
F;1052-1219/Domain: fibronectin type III repeat homology <FNB>
F;1189-1253/Region: cell attachment (R-G-D) motif
F;1189-1253/Region: cell attachment (R-G-D) motif
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
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2030 AGCCGGCAGCCCATGGGGCTAACAG :: 1297 luargGlyPheProGlyAlaAspG	AGCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGACCCAGTGAGCAGG ::	1974 1315 1914	
1316 ProGlyThrProGlyAla 1913 CAAATACTACTGTGTAGCAAAGTAAA	ProglythrProglyAla	1321	
322		32	
1853 TATAGGCAGTGACAGACTGGCTGAGCT	TATAGGCAGTGACAGAGGTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCA 	1794	
ოთ	CCTGGGACAGGAAGGCACTATCCAGGAFGGCGAGCTCCAGGAGA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	3 7 6	
1745 TGCCCGGCCCGGAACCACCCTGG 	TGCCCGGGCCCGGAACCACCCTGGCCTCGGTGGGCTCACCCACCACCACGTACGG	1689 1383	
1688 AGACATCACAGGCAGAGGCCCC 		1656 1403	
1655 GTGGAGGTGGGAGCAGCCACTGCTC 		1596 1416	
1595 CAGGCTTAGGGCCTGGCAGGAAGCTGG :: 1416 lyGlyIleAlaProGly	GTCATCAGGCTGTCCTCACTGCTAGCACCTCCAG	1536 1421	
1535 TGTCCCCTCGGTATTTGGGCAGGAACA(<pre>rGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG</pre>	1476 1438	
1475 TGTAGGGCAGGATCTGCAGGGCTGAGAI 		1416 1458	
1415 CCACGGCCACACTGTGGGACAGGCATG: ::: 1459 GlyGlnProGlySerProGlyGluGlnC		1362	
1361CCACACTGGCCAAATAGAC :::111 1479 LysGlyAspArgGlyPheProGlyProl		1311	
1310 CCATGACCAGAGAGAGACCAGGAGA 		1251 1509	
1250 TCCGAACGCCTTCATCATAGTGTCTCCC		1191 1529	*
1190 CCTGGTACAGCCCCTCGCCCAGAAATC		1131 1545	
1130 TCCAGCTGCACAGCTCAGCCACGAAGAC	TCCAGCTGCACACCACGAAGAGCCGGCGCAGGGTGCGGGCATGCGGC	1077	
1076 AGCACAGCTGCTGCAGCCGGGGAAGCAC 		1017 1585	
1016 GGCATGGACAGCAGTGGGGCGACAAGGA		957	

Db	1586		1603
Qy	926	GGCCAGCGCTCCTCAG	936
qq	1604		1623
Οy	935	CCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGC	876
Dp	1624	ProGlyProValGlyProArgGlyArgAspGlyGluValGlyGluLysGlyAspGluGly	1643
Qy Db	875	ACTCCTCCTGGGTGCCCAGGTAGG	846
Qy	84		່ ເດ
QQ	1664		1678
ΟŶ	785	TCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGGTCCCGGAAGAGGTCAG	726
Db	1679	5	1698
٥y	725		702
qq	1699	ø	1718
Oy.	701	AGCACACCTGGCCACAGAAGTCCAGGAGGCCCACGC	
QQ	1719		1737
Οy	656	U	597
qq	1738	LeuProGlyAla	1743
٥y	296	TTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCC	552
qa	1744		1760
Qγ	551	AGATGAAGGGCCGGCGGCGATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGA	492
. qa	1761		1769
οy	491	F4 -	432
qq	1770		1781
ργ	431		372
qq	1782	GlyLeuAspGlyLysProGlyAlaalaGly	1794
γ̈́ς	371		318
qc	1795	ProksnělykalaklaciyLyskilatik ProksnělykalaklaciyLyskalaciykspPročiyArgAspčiyLeuPročiyLeuArg	1814
27	317		278
qo	1815	_	1834
λά	277		231
q	1834		1854
λy	230		171
qc	1854	y Arglyschyschyschyaspserchyalaserchyargchuchyargaspchyproby	1874
λλ	170	GAATCAGCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCC	114
q	1874		1894
λλ	113	CATGCTCAACACCTGCTGCTGTGGGGCACCCTCAGTGGGGACACGTCTCATCACTCAG :	57

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A; Description: structural component of extracellular fibrous polymer associated with A; Note: may play a role in controlling the lateral growth of collagen I fibrils C; Superfamily: colled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxypr F; 1-26/Domain: signal sequence #status predicted <51G>F; 27-1250/Product: collagen alpha 2(V) chain #status predicted <AMT>F; 27-1250/Product: collagen alpha 2(V) chain #status predicted <AMT>F; 27-193/Domain: amino-terminal propeptide (uncleaved) #status predicted <NMP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;109-186/Region: helical
F;109-186/Region: helical
F;109-186/Region: helical
F;109-186/Region: helical
F;109-186/Region: helical
F;109-186/Region: cell attachment (R-G-D) motif
F;101-106/Region: cell attachment (R-G-D) motif
F;101-106/Region: cell attachment (R-G-D) motif
F;103-1126/Region: cell attachment (R-G-D) motif
F;103-1126/Region: cell attachment (R-G-D) motif
F;103-1136/Region: cell attachment (R-G-D) motif
F;103-1136/Rodified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;104/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;290,293,296,608,614,1004,1007,1013,1028,1034/Modified site: 3-hydroxylysine (Lys) #status seperimental
F;290,1397/Binding site: 5-hydroxylysine (Lys) #status experimental
F;1250-1251/Cleavage site: Glu-Asp (procollagen C-endopeptidase) #status predicted
F;1293,1299,1325/Disulfide bonds: #status predicted
F;1293,1299,1325/Disulfide bonds: #status predicted
F;133-1494,1402-1447/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 2q31-2q31
A; Introns: 33/1; 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 114
C; Complex: type v collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHUIV),
alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among
ength, is formed with desmosine cross-links made from lysine and allysine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA A; Restaudes: 1449-1463, Ex,1465-1495, AA <TSI>A; Restaudes: 1449-1463, Ex,1465-1495, AA <TSI>A; Restaudes: 1449-1463, Ex,1465-1495, AB Control of the such of the such of the codon GAA for residue 1460 as Gln, and GAG for restaudent: prolines and lyshines at the third position of the tripeptide repeating unit are 5-hydroxylated and subsequently 0-glycosylated.

C; Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
                                                                                                                                                                                                           R;Tsipouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeld, C.S.; Weil, D.; Ramirez, F. Genomics 3, 275-277, 1988
A;Title: Genetic distance of two fibrillar collagen loci, COL3Al and COL5A2, located A;Reference number: A30017; WUID:89138450; PMID:3224983
A;Recession: A30017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AGCCGCGCCTCGG-----CCAGGA 55
                                      A; Molecule type: mRNA
A; Realdues: 1227-1417, 'T',1419-1437,'S',1439-1496 <MYE>
A; Cross-references: GB:M11718; NID:9180912; PIDN:AAA52058.1; PID:9180913
A; Experimental source: normal fibroblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;27-108/Region: nonhelical
F;40-99/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GDB:119064; OMIM:120190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-759-143-110 (1-3410) x CGHU2V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212.00
312.00
30.80%
26.46%
4.86%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
A; Accession: A25374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB:COL5A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Function:
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A; Residues: 1003-1034 (RES)
A; Cross-references: GB:M11135; NID:g179693; PIDN:AAA51857.1; PID:g179694
A; Note: part of this sequence were determined by protein sequencing
R; Myers, J.C.; Loidl, H.R.; Seyer, J.M.; Dion, A.S.
B; Biol. Chem. 260, 11216-11222, 1985
A; Title: Complete primary structure of the human alpha-2 type V procollagen COOH-termina
A; Reference number: A25374; MUID:85289337; PMID:2411731
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A;Residues: 288-291, P', 293-294, X', 296-297;606; X', 608-617 <MOR>
A;Residues: 288-291, P', 293-294, X', 296-297;606; X', 608-617 <MOR>
K;Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
Nucleic Acids Res. 15, 113-198, 1987
Nucleic Acids Res. 15, 113-198, 1987
A;Title: The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrill
A;Reference number: A25874; MUID:87146331; PMID:3029669
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A;Note: part of this sequence were determined by protein sequencing
R;Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
A;Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm
A;Reference number: 159025; MUID:85216505; PMID:3858826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 31 -Ual-1999 #sequence_revision 28 -Ual-1995 #text_change 31-Dec-2000
C; Accession: A31427; A54555; S43643; A25874; I55239; I59025; A25374; A30017
R; Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
Biol. Chem. 264, 2735-2738, 1989
A; Title. Amino-terminal propeptide of human pro-alpha2(V) collagen conforms to the struct A; Reference number: A31427; WUID:89123368; PMID:2914927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:MS8529; NID:g180834; PIDN:AAC41699.1; PID:g553235
R;Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Ber Eur. J. Blochem. 221, 987-995, 1994
A;Title: Diversity in the processing events at the N-terminus of type-V collagen. A;Reference number: $43642; MUID:94237164; PMID:8181482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Homology between alpha2(V) and alpha1(III) collagen promoters and evidence for A;Reference number: A54555; MUID:92314691; PMID:1820205 A;Accession: A54555
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                                                                                                                                            1894 rovalGlyProProGlyGlnGlyPheProGlyValProGlyGlyThrGlyProLySGlyA 1914
                                                                                       -CGAGGGGGGGGGC 36
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A, Residues: 398-1496 <WEI>
A, Cross-references: GB:X04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
A, Experimental source: rhabdomyosarcoma cell line
R, Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
J. Biol. Chem. 260, 5533-5541, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB:J04478; NID:g179697; PIDN:AAA51859.1; PID:g179698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
Gene Expr. 1, 29-39, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha 2(V) chain precursor - human
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                                                                                                                                                                                                                                                                                                                                                            1934 lyGluProGlySer 1938
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                                                                                                                                                                                                                                                                          35 TGTCACCCGGAGCC 22
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A; Residues: 1002-1226 <RE2>
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A; Residues: 1-32 <GRE>
                                                                                  56 ATCCTGGC
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242	2 ProGlyAsspProGlyProMetGlyProIleGlySerArgGlyProGluGlyProProGly	261	
56	TCTGAGTGATGAGACGTGTCCCCACTGAGG	85	
262		281	
98		124	
282	2 GlySerProGlyAlaArgGlyPheProGlyAlaProGlyLeuProGlyLeuLysGly	300	
125		145	
301	HisArgGlyHisLysGlyLeuGluGlyProLysGlyGluValGlyAlaProGlySerLys	320	
146	5	181	
176		340	
182	2 GCGGCAGCAAGGAGAGAGAGCCGCAGCTTCTGGACCAGAGCGAACGAA	241	
242		257	
360	::: :::) yMetProGlyLysProGlyProMetGlyProLeuGlyIleProGlySerSerGlyPhePr	380	
257		257	
380) oGlyAsnProGlyMetLysGlyGluAlaGlyProThrGlyAlaArgGlyProGluGlyPr	400	
258		29.2	
400		420	
293	AGGCTGTGGGTGGGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTG	340	
341		400	
401		460	
456	 GlySerThrGlyProGlnGlyAsnSerGlyLeuProGlyAspProGlyPheL	473	
461	GGTCCAGTGCTGGGCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCG- 	519 493	
520		537	
493	roProGlyGluGlyLysArgGlyProArgGlyAspProGlyThrLeuGlyProProG	513	
538	CCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTT	586	
587		646 552	
647		703	
552		570	
704	ACTCCACTGGAGGCCTGGT	742	
743		790	
590	roglygluAspGlyArgProGlyProProGlys	601	

Qy	791	CTTGGGGGCTGCCTGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCC 85
qq	601	
Qy	851	CCCTA
QQ	616	roLysGlySerAsnGlyAspProGlyLysProGlyGluAla4GlyAsnP 632
Qy	896	CTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGC 955
QQ	632	roGlyValProGlyGlnArgGlyAlaProGlyLysAspGlyLysValGlyP 649
Qy	926	CCCAC
qq	649	rissary proprogly proprogly Leu Arggly Gluding Jy Pro 667
ΟY	992	TTGTCGCCCCACTGCTGTCCATGCCGGCCCGCTTGCCGAACCTGGGCGCCCTG 1051
qq	899	GlnGlyHisProG 678
Οy	1052	CTTCCCCGGCTGCACCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTG 1111
qa	678	lyProProGlyProProGly
QY	1112	TGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGT
Dp	685	
Qy	1172	GGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACAC 1231
qq	069	
οy	1232	TATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCCATC 1285
QQ	707	
٥y	1286	-
Db	724	euProGlyGluLysGlyMetalaGlyGlyHisGlyProAspGly738
Qy	1337	TGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGG
Db	739	
٥y	1397	CTTCTCAGCC 14
Db	744	lyProSerGlyThrProGlyAspThr752
Qy	1457	CTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACGGGAGAAGCAGGTGTTCCTG 1516
qa	753	GlyProProGlyLeuGlnGlyMetProGlyGluArgGlyIleAlaGlyThrProG 771
Qy	1517	
qq	771	
Qy	1574	TTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTAATGGACAC 1618
Db	790	AsnaspGlyalaGlyGlyLeuProGlyProLeuGlyProProGlyProAlaGlyLeu 808
Qy	1619	GTGGGTGCTGGAGGCAGT 1654
qq	809	.:: LeuGlyGluLysGlyGluProGlyProArgGlyLeuValGlyProProGlySerArgGly 828
٥y	1655	CCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTG 1699
QQ	829	AsnProGlySerArgGlyGluAsnGlyProThrGlyAlaValGlyPheAlaGlyProGln 848
Οy	1700	
Dh.	849	G vSerAsnG vG nProG vVa I.vsG vG nProG vG u-Pro-G vG nIvsG vA 868

Db 189	912	qq
Qy 1928 CCAAGICGCICIT	1889 TACTITGCTACACAGGTAGTATITGACAAGAGCGACTIGGCCAAATACTCAGCGTAGAAA 1948	Qy
 Db 173 ProGlyLeuProC	901 lyProPro 912	qq
ογ 1966	1829 CTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATT 1888	δλ
Db 153 GlySerThrGln	884ProHisGlyProHisGlyValProGlyLeuLysGlyGlyArgGlyThrGlnG 901	q
Qy 2017 CATGGGGCTAACA	1781 CTGCTGTCCCAGGTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAG 1828	Qy
Db 147	867 ysGlyAspAlaGlySerProGlyProGlnGlyLeuAlaGlySerProGly 883	qa
Qy . 2077 GGCAGCAGAGAG		δy
::: Db 130GlnAlaGly	848 ProGlnGlySerAspGlyGlnProGlyValLysGlyGluProGlyGlu-Pro-GlyGlnL 867	qa
Qy 2137 GAGAGGAGAGGG	1700	Qy
Db 118GlnLysGly	ArgGlyAsnProGlySerArgGlyGluAsnGlyProThrGlyA	g
Qy 2197 TAAGTCCAGACT	1655CCGCGCTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGTG 1699	οy
 Db 102 ThrileGluPro	808 GlyLeuLeuGlyAlaProGlyGluProGlyProArgGlyLeuValGlyProProGlySer 827	QO
Qy 2257 GGTAATCCACCT	1613 GGACACGTGGGTGCTGGAGGCAGT	οy
 Db 82 GlyProGlyLeu	789 AlaGlyAsnAspGlyAlaArgGlyLeuProGlyProLeuGlyProProGlyProAla 807	QQ
Qy 2311 AACCCTTCTCTA	1571 AGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTAAT 1612	Qy
QY 2308 CAGGITAAGGGG ::::: Db 62 GlnLeuArgArg	770 hrProGly-ProLysGlyAspArgGlyGlyIleGlyGluLysGlyAlaGluGlyThr 788	qa
-09-759-143-	mmccmccocoxxxxmxccccccccccccccccccccccc	3 8
	1451 TCAGCCCTGCAGATCCTGCCTACACACGGGCTCCCTACCACCGGGAGAAGCAGGTG 1510	oy 1
Percent Similarity: 30 Best Local Similarity: 26	743 snProGlyProThrGlyThrIleGlyAspThr 753	ą
	1391 TGCCTGTCCACAGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTC 1450	οy
Alignment Scores:	740 ProLysGly 743	qa
A; Note: sequence extracted C; Superfamily: unassigned	1331 GGCACTCGAGCAGTCTATTTGGCCAGTGTGGGCAGCTTTCCCTGTGGCTGCCGGTGCCACA 1390	δy
A; Cross-references: GB:S63 A; Experimental source: ep1	723 hrGlyLeuProGlyGluLySGlyMetalaGlyGlyHisGlyProAspGly 739	qq
A; Molecule type: nucleic a A; Residues: 1-920 <lii></lii>	1280 GCCATCTCCCTGGTCTTCTCTCGTCATGGACCGGCTGGTCCAGCGATTC 1330	δλ
A; Accession: A45748 A; Status: preliminary	708ArgGlyGluArgGlyGluAsnProGlyGluArgGlyGluProGlyIler 723	qq
A;Title: cDNA cloning and A;Reference number: A45748	1226 AGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGC 1279	Οy
R;Li, K.; Christiano, A.M. Genomics 16, 733-739, 1993	689 ysAlaGlyAspGlnGlyValProGlyGluProGlyAlaValGlyProLeuGlyPro- 707	qa
C;Date: 16-Feb-1994 #seque C;Accession: A45748	1166 TTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGG 1225	О
collagen alpha 1(VII) chai C;Species: Mus musculus (h	686	qa
RESULT 38 A45748	1106 TICGIGGCIGAGCIGIGGAGCIGGATGGCACCATGACCTICACGCTGTTTACACGGAT 1165	Qy
Db 928 GlyProAlaGly	677 euProGlyProProGlyProProGly	qq
Qy 2009 AGCCCCATGGGG	CIG	δ
Db 913		qq
QY 1949 ACTICCAGCACA	986 CCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGC 1045	Qy

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chromosomal mapping of the mouse type VII collagen gene (Co
                                                                                                                                                                                                                                                                                          ; Copeland, N.G.; Gilbert, D.J.; Chu, M.L.; Jenkins, N.A.;
TTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCCTGTT 2008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTG 2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGTA 2198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3AAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGA 2138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAATGTGCTGGAAGTTT------TCTACGCTGAGTATTTGG 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCA--- 1872
                                GlnThrGlyPro---CysAlaValHisCysProLysGly------ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| |||||| ::
ProProGlyProProGlyLeuProGlyArgThrGlyAlaPro----- 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GlyProGlnGlyProPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||
|3lyValProGlySerProGlyIleLysGlySerThr------ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||| ||||
-----GlyArgProGlyProArg 194
                                                                                                                                                                                                            .n - mouse (fragment)
louse mouse)
since_revision 18-Nov-1994 #text_change 20-Sep-1999
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dermal keratinocyte
from NCBI backbone (NCBIN:135000, NCBIP:135001)
                                                                                      CTGCCGGGC----TGGCCGCCA 2038
                                                                                                           |||||||
|GluProGlyLysGluGlyProPro 939
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Matches:
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1871	GGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACCTGGACCATGGAGCCCA	1812	
1811	TAAACAGGGATGGGCCACCTGGGACAGGAAGGCAC	1773	
215	IleThrGlyGlyGlyGlyPhoollyPheProGlyLySlySclyAspProGlyProSerGly	234	
235	richedigescheitzengerengen in hillilli	254	
1715	1006CTCACCCACCACCACGTACGGAGACATCACAGGCAGGGGCCCGCAGAGCGCGGGGGGGG	1656	
254	oGlyIleSerValLysGlyAspLysGlyAspArgGlyGluArgGly-ProProGlyProG	274	
1655	GTGGAGGTGGGAGCAGGCCACTGCCTCCAGCAC	1623	
1622	INTEGRIFY CONTROL OF THE CONTROL OF	1599	
294		314	
1598	CTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCAC	1551	
314	::: ::: :::	334	
1550	TGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGT	1491	
334	lyMetThrGlyProLysGlyAspArgGlyLeu-ThrGlyThrProGlyGluProGlyVal	353	
1490	AGAGGGAGGCAGTGTAGGGCAGGAACGTGAGGGCTGAGAAGGTGAACCCGGTGAGGG ::::	1431	
304	Lyselyslu	336	
1430	CGGCTGAAGCTGTCACCACGGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCACAG	1371	
357		361	
1370	GGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGT	1311	
362	ProvalGly	364	
1310	CCATGACCAGAGAGAGACCAGGGAGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCA 11	1251	
1350	シンスペンシンの単語はアペン語というとはいってはないというというとはいまえてはないないとなって アー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・	191	
370	CONTRACTOR CON	389	
1190	CCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA	1131	
390		406	
1130	TCCAGGTGCACACGTCAGGCACGAGGGGGGGGGGGGGGG	1071	
407		426	
. 1070	GCTGGTGCAGCCGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATG	1011	
427	SerGlySerLysGlyGluGlnGlyAlaProGlyLeuAlaLeuProGlyAspProGlyPro	446	
1010	GACAGCAGTGGGGGGACAAGGAGGGGCCGACAGCCCTTCTGCTGGTGGGTG	954	
447	LysGlyAspProGlyAspArgGlyProlleGlyLeuThrGlyArgAlaGlyPro	464	
953	3	930	
465	ThrGlyAspSerGlyProProGlyGluLySGlyGluProGlyArgProGlySerProGly	484	
929	GCAGTGTGGTTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGAGGCACTCCT	870	

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Cylagen alpha 1(I) chain - rat (tentative sequence) (fragments)
Cyspecies: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: 13.-U1-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
C;Accession: A90559; A90552; A92029; A90353; A90566; A90357; A90362; A90379; A91209;
R;Bornstein, P.
Biochemistry 8, 63-71, 1969
A;Title: Comparative sequence studies of rat skin and tendon collagen. II. The absence A;Reference number: A90559; MUD:69155173; PMID:5777344
A;Contents: CNBrO and CNBr1
A;Molecule type: protein
A;Rosidues: 1-19 <B01>
A;Molecule type: protein
A;Rosidues: 1-19 <B01>
A;Sperimental source: tendon
A;Rote: sequences from skin and tendon appear to be identical
A;Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during
B;Cangenistry 6, 788-795, 1967
A;Title: The amino acid sequence of peptides from the cross-linking region of rat ski
A;Roterne number: A90552; MUID:67162268; PMID:5337886
A;Contents: CNBr1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 GGC------CAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGGTTTCCGGTGCC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           618
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                                                                                                                                                                                                                    525 ArgGlyProVal-----GlyGluLysGlyAspGlnGlyAspProGlyGlu 539
                                                                                                                                                                                                                                                                                               999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 ProGlyGlnGluGlyProArgGlyProLysGlyAspProGlyProProGlyValSerGly 599
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505 GlyGluProGlyLeuProGlyLysAlaGlyGluArgGlyLeuArgGlyAlaProGlyPro 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 AspArgGlyProProGlyLeuAspGly------ArgSerGlyLeu
                                                                      -- GGGCCAGGGCAC
                                                                                                                                                                                                                                                                    779 AGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGACA
                                                                                                                                                                                                                                                                                                                                                                   719 -----GGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                560 ProProGlyProProGlyArgLeuValAspAlaGlyIleGluSerArgAspLysGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                               665 CCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCC
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|640 AspGlyLysProGlyAlaProGly-----
                                                                           -----CCTGGGTGCCCAGGTAGG-----
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CGRT1S
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A.Note: the composition of peptides comprising residues 1-9 and 1-19 confirms the seq A.Note: the composition of peptides 651-671 above) probably corresponds to positions 1032-1 c.Comment: Prolines and lysines at the third position of the tripeptide repeating unled and subsequently 0-glycosylated.
C.Comment: The order of the nine CNBr peptides in the alpha 1(1) chain of rat skin co c.Comment: The complete chain contains 1052 residues.
C.Comment: The complete chain (1) chain; fibrillar collagen carboxyl-terminal homolo C.Keywords: blocked amino end; colled coll; extracellular matrix; glycoprotein; hydro F:1/Modified site: allysine (Lys) #status experimental
F:103.424,547/Midding site: carbohydrate (Lys) (covalent) #status experimental
F:103/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
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Matches:
Conservative:
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310.00
33.33%
28.63%
4.98%
                                              A,Molecule type: protein
A,Residues: 651-671 <ST2>
A,Experimental source: skin
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A;Molecule type: protein
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A:Reference number: A90566; MUID:70085124; PMID:5411206
A:Contents: CNBr5
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R; Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
R; Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
A; Title: Structural and immunogenic properties of a major antigenic determinant in neutr
A; Reference number: A91209; MUID:74011954; PMID:4126850
A; Contents: CNBr6
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Blochemistry 13, 2946-2953, 1974
A;Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino A; Reference number: A90379; MUID:74271984; PMID:4356532
A; Contents: CNBr3
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                                                                                                                                                                                                               collagen.
                                                                                                              R.Bornstein, P. 4. 2572-2574, 1967
J. Biol. Chem. 242, 2572-2574, 1967
A:Title: The incomplete hydroxylation of individual prolyl residues in A;Reference number: A92029; MUID:67165368; PMID:4290711
A;Contents: CNBr2
                                                                                                                                                                                                                                                                                                                                                           A Molecule type: protein
A;Residues: 20-55 <B02>
A;Experimental source: skin and tendon
B;Butler, W T.; profds, S.L.
Biochemistry 10, 2076-2081, 1971
A;Title: Chemical studies on the cyanogen bromide peptides of A;Reference number: A90353; MUID:71263178; PMID:4327399
A;Contents: CNBY
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ERS Lett. 26, 61-65, 1972
A;Title: Non-hell-61 regions in rat collagen alphal-chain.
A;Reference number: A91385; MJID:73049495; PMID:4636751
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Balian, G.; Click, E.M.; Bornstein, P.
Lochemistry 10, 4470-4478, 1971
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A;Residues: 56-102 <BUI>
A;Experimental source: skin
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A; Residues: 239-418 <BA2>
A; Experimental source: skin
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A; Residues: 568-651 <ST1>
A; Experimental source: skin
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A; Residues: 103-139 <BU2>
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A; Molecule type: protein A; Residues: 5-19 <KAN>
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QY 2044 AGAAACTGGCGGCCAGC	641 GGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAGA 582	Qy
	698 ACACCTGGCCACAGAAGTCCAGCACCCCAGGATGAGCAGTGCCAGTCCA 642	Qy Db
QY 2104 CAGCTACGCACCTCAGC	. Iy SerProGlyPheGlnGlyLeuProGlyProAlaGlyProProGlyGluAlaGly	đ
110		οy
US-09-759-143-110 (1-3410) x A4	//b Caragacagagraggccrggcgaagraggcccgggrcccggaagaggraggcagagagag	oy Op
Query Match: 4.97% DB: 2	roGlyProProGlyAlaValGlyProAlaGlyLySASpGlyGluAla	g .
Percent Similarity: 32.52% Best Local Similarity: 27.41%	SATCATGAAGG 7	Oy
Alignment Scores: 3.8e-11 Pred. No.: 309.50		7 A
F;1263-1492/Domain: fibrillar o	GCACTCCT	ò
C; Keywords: coiled coil; extract F; 37-96/Domain: von Willebrand 1	941 CCTCAGCCACCACCAGTGTGGCTGCTACCAGGTGAGGAGGAGGTGAGGGTGAGGAGCAGGCCAA 022 409 Pro	රු සි
A) Note: this sequence is presented they replace; the appropriate		đ
A; Residues: 1-1492 <sua> A; Cross-references: GB:M63596</sua>		Qy
A,Accession: A40333 A,Status: nucleic acid sequence A.Wolecule type: mRNA	aLysGlyLeuThrGlySerProGlySerProdlyProAsp	7 점
A;Title: Expression of two nona.	田が大きだいまたからの日本でいっています。 「「「「「「「」」」「「」」「「」」」」「「」」「」」「「」」「」」「「」」「」「	ł
C;Accession: A40333 R;Su, Mw.; Suzuki, H.R.; Biekel T Call Biol 115 565-575 199	1109 CGAAGACCGGCGCAGGGGGCATGCGGCAGCAGCAGCTGGTGCAGCGGGAAGCA 1050	å å
C;Species: Xenopus laevis (Afric	359 GlySerPro 361	qq
RESULT 40 A40333 A40333	1169 CGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACGCTCAGCCA 1110	
631		<u>3</u> 8
Qy 248 AGGCACTCCAGAACTGCT	319 ProGlyProProGlyGluArgGlyGlyFroGlySerArgGlyFreFroGlyAlaAspGly 338 1000 ememonogenenenenenenenenenenenenenenenenenen	8 8
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29 524 GICCACGCGGGGGCACCACGGGGGGCACCACGGGGGGGACACGGGGGG	1475 TGTAGGGCAGGATCTGCAGGCTGAGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTGTCA 1416	Qy
524	11111	QQ
581	1535 TGTCCCCTCGGTATTTGGGGAGGAACACCTGCTTCTCCCGGTGGGAGGGA	Qy
506		qq
	1589 PAGGGCCTGGCAGGAAGCTGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAG 1536	òò

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allelic type II procollagen genes during Xenopus laevis
ID:92011898; PMID:1918153
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.yserProGlyLys***GlyLeu***GlyLeu------ 612
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ican clawed frog)
revision 16-Sep-1992 #text_change 16-Jul-1999
AAGGACAGTG----CCCAGATGAAGGGCCGGCGGCGCCATAGC
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364 alGlyproAlaGlyPheProGlyAlaProGlySerLysGlyGluAlaGlyP 384 1228 TGCGGGCCGGGTCAGCTCTGGGCACGCCTGGTCACCTCGCCCAC 1169 1228 TGCGGGCCCGGGTCAGCTCTGGGCACGCCTGGTACAGCCCTCGCCCAC 1169 134 roThrGlyAlaArgGlyProGluGlyProArgGlyGluSerGlyThrProG 404 1168 GAAATCGTGTAAAACAGCTGTAAGGTCATGAGTGCACTCCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTCAGCTGAAGCTGTAAACAGCTGTAAACAGCTGTAAACAGCTGAAGGTCATGAGTGTAAACAGCTGAAGGTGTAAACAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGAAGCTGGTGAAGCTGGTGAAGCTGGTGGGGGAAGCAG 1109 1108 GAAGGCCGGCGGGGGGATGCGGCGCACACACGTGGGGGAAGCAG 1149 1108 GAAGGCCGGCGGGGGGATGCGGCGCACACACGCGGGAAGCAG 1149 1109 GAAGGCCGGCGGGGGATGCGGCGCACACGCGGGAAGCAG 1149 1108 GAAGGCCGGCAGGGGGGCATGCGCGCACACACGGGGGAAGCAG 1149 1109 GAAGGCCGGCAGGGGGCATGCGCGCACACACGGGGAAGCAG 1149 1100 GAAGGCCGCAGGATCCGGCACACACGCGGCACACACACGGGGAAGCAG 1149 1101	Qy	GGCGCACTGCAGGAACAGCCCCAAGGCTGCCCATCCGAACGCCTTCATCATAGTG	Qy	412 CAGCAGAGGCGCCACAT
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Qy	904	-ACTCCTC 86
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٥y	868	CTGGGTGCCCAGGTAGGGGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGGCAG 815
Db	532	ysGlyAlaProGlyGlyBroLysGlyGlyAsnGlyA 552
oy.	814	GAGGTAGCCCAGGCAGCCCCCAAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTG 758
QQ	552	 uProGlyLeuProGlyA
Qy	757	GCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAG 722
QQ	572	
Οÿ	721	CAGGGCCTCCAGTGGAGTGAAGCACACGTGGCCACAGAAGTCCAGCAGCCCCACGC 666
Db	592	roGlyProProGlyProGlnGlyAlaArgGlyG 603
Qy	665	
Db	603	
٥y	625	GCACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCC 566
Db	620	
Óγ	565	CAAGGACAGTGCCCAGATGAAGGGCGGGGGGGGGCGATAGCGTCCACGCCAGTG 512
Dp	631	roGlyLeuArgGlyLeuProGlyLysAspGlyGluThrGlyAlaGlnG 647
Qy	511	GTCACTGGCTGAGCCTAGGAGCGGGACACAGA
. qa	647	
	469	CACIGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAG 413
Db	299	erGlyPheGlnGlyLeuProGlyPro
Qy	412	CCTGC
qa	929	SlyGluGlyGlyLys
Qy	367	CAGGCCAAAGGTTAGCAGGTTGACCAGGAAGAGCTGGGCTTTCCGGTGCCGCAGCA 312
Db	685	roGlyAspGlnGlyValProGlyGluAlaGlyAlaAlaGlyLeuValGlyProA 703
Qy	311	T
Db	703	rgGlyGluArgGlyPheProGlyGluArgGly-SerSerGlyProGlnGlyLeuGlnGly 722
Οy	262	TCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGC221
Db	723	SerArgGlyLeuProGlyThrProGlyThrAspGlyProLysGly 737
Qy	220	TCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCT 173
Db	738	AlaThrGlvProSerGlvProAsnGlvAlaGlnGlvDroProGlvIenGlvGlvMatoro 757

122 yGlyLeuLeuGlyAspThrAlaAspAsnLySThrMetAlaIleValAlaPheValIleGl 142 667 CGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCTGCTCT 726 112		
90		
Oy 172 AGGAATCAGCCAGCCCATTTCTGCAGCCTTTGGT	SULT 41 4339 crose-proton transport protein - carrot Alternate names: sucrose/H+ symporter protein Species: Daucus carota (carrot) Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 # Accession: T1433 Shakya, R.: Sturm, A. ant Physiol. 118, 1473-1480, 1998 Title: Characterization of source- and sink-specif Reference number: 217991; MUID:99063785; PMID:9847 Accession: T44339 Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-501 - SMBA. Cross-references: EMBA. Experimental source: cultivar Namtaise: leaf Genetics: Superfamily: common tobacco sucrose transport prot	Alignment Scores: A. 08e-11 Length: 501 Score: 309.00: Matches: 131 Best Local Similarity: 37.44 Conservative: 94 Best Local Similarity: 37.44 Conservative: 94 Best Local Similarity: 37.44 Conservative: 94 Best Local Similarity: 4.61% Mismatches: 159 Busty Match: 2.1.80% Mismatches: 159 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Mismatches: 2.1.80% Mismatches: 16 Busty Mismatches: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 16 Busty Match: 2.1.80% Mismatches: 2.

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Matches:
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                                                                                                                                      A; Molecule type: mRNA
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DB:
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A; Residues: 1-1670 < MAR>
A; Across = references: GB: MBNO31; NID:9577563; PID:9577564
A; Cross = references: GB: MBNO31; NID:9577563; PID:9577564
A; Experimental source: kidney
B; Turner, N.; Mason, P.J.; Brown, R.; Fox, M.; Povey, S.; Rees, A.; Pusey, C.D.
J. Clin. Invest. 89, 592-601, 1992
A; Title: Molecular cloning of the human Goodpasture antigen demonstrates it to be the all A; Reference number: A43928; MUID:92147878; PMID:1737849
A; Accessation: A43928
A; Molecule type: mRNA
A; Residues: 1331-1524, 1',1526-1670 < TUR>
A; Residues: 1331-1524, 1',1526-1670 < TUR>
A; Residues: Ferences: GB: MB1379
A; Experimental source: Kidney
B; Outlones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
J. Biol. Chem. 267, 13780-19784, 1992
A; Title: Exon/intron structure of the human alpha 3(IV) gene encompassing the Goodpastur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oliagen alpha 3(IV) chain precursor, long splice form - human
N'Alternate names: Goodpasture antigen; procollagen alpha 3(IV) chain long splice form
C'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Date: 28-Oct-1994 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C'Accession: A54763; A43928; A44043; A45971; A39786
R'Mariyama, M.; Leinonen, A.; Mochizuki, T.; Tryggvason, K.; Reeders, S.T.
A'Title: Complete primary structure of the human alpha3(IV) collagen chain. Coexpression
A'Reference number: A54763; MUID:94364994; PMID:8083201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1427-1444 <BER>
A;Note: sequence extracted from NCBI backbone (NCBIP:133363); sequence incorrectly ident
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Reference number: A44043; MUID:93015826; PMID:1400291
A. Reference number: A44043; MUID:93015826; PMID:1400291
A. Reference number: A44043; MUID:93015826; PMID:1400291
A. Molecule type: DNA; MRNA
A. Residues: 1386-1670 <QUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI>A. COUI
A. Note: sequence extracted from NCBI backbone (NCBIP:115597)
B. Quinones, S.; Bernal, D.; Garcia-Sogo, M.; Elena, S.F.; Saus, J.
A. Reference number: A44738; MUID:94274734; PMID:8006044
A. Contents: annotation; erratum; correction to intronic sequence in A44043
A. Contents: annotation; erratum; correction to intronic sequence in A44043
A. Fille: The human mRNA encoding the Goodpasture antigen is alternatively spliced.
A. Reference number: A45971; MUID:93280184; PMID:8505332
1678 CTGTGATGTCTCCGTACGTGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTG---GTTCC 1734
                                                                                                                               ------GGCCGGGCATCTGCCTGGACCTCGC 1761
                                                                                                                                                                                                                                                  1762 CATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCAT 1821
                                                                                                                                                                                                                                                                                                                                                                               ----AGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGC 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1867 AGGCCTGGGTCTGCTTTACTTTGCTACAGGTAGTATTTGACAAGAGCGACTT 1926
                                                       399 eSerAlaLeuIleValPheAlaIleLeuGlyIleProLeuAlaIleThrTyrSerValPr 419
                                                                                                                                                                                    419 oTyrAlaLeuValSerThrArgIleGluSerLeuGlyLeuGlyGlnGlyLeuSerMetGl 439
                                                                                                                                                                                                                                                                                          459 pAspGlnLeuPheGlyGlyAsnSerProAlaPheValValAlaAlaLeuSerAlaPh 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown
                                                                                                                         1735 G-----
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C;Superfamily: collagen alpha 1(IV) chain
C;Superfamily: collagen alpha 1(IV) chain
C;Superfamily: collagen alpha 1(IV) chain
C;Superfamily: collagen alpha 1(IV) chain
C;Superfamily: collagen alpha 1(IV) chain
C;Superfamily: collagen alpha 1(IV) chain
E;1-28 Domain: signal sequence #status predicted <SIG>
F;29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MA
F;29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MA
F;29-1670/Product: collagen alpha 3(IV) chain, long splice form #status predicted <MA
F;39-198/Region: cell attachment (R-G-D) motif
F;39-198/Region: cell attachment (R-G-D) motif
F;136-1308/Region: cell attachment (R-G-D) motif
F;144-1156/Region: cell attachment (R-G-D) motif
F;143-143/Region: cell attachment (R-G-D) motif
F;143-143/Region: cell attachment (R-G-D) motif
F;143-165/Domain: carboxyl-terminal nonhalical, NCl <NCl>
F;143-165/Domain: collagen IV carboxyl-terminal repeat <CT2>
F;31,33,39,41,125,422,476,479,682,722,809,1837/Disulfide bonds: interchain #status predicted
F;1460-1548,1493-1551/Disulfide bonds: (or 1460-1551, 1493-1548) #status predicted
F;150-1511,1616-1652/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted
F;1570-1662,1604-1665/Disulfide bonds: (or 1570-1665, 1604-1662) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:128351; OMIM:120070
A;Map position: 2q36-2q37
A;Introns: 1385/1; 1418/1; 1488/1; 1585/3; 1643/2 #status incomplete
A;Introns: 1385/1; 1418/1; 1488/1; 1547/2; 1585/3; 1643/2 #status incomplete
A;Note: the alpha 3(IV) and alpha 4(IV) chain genes are encoded on opposite strands w
C;Complex: This minor type IV collagen is thought to form a heterotrimer of two alpha
mong trimer aminor terminal domains (with disulfide and desmosine cross-links), dimeril
er associations in the interrupted helical domain (with disulfide and desmosine cross
                                                                                                                                                                                                                                                                                              A;Residues: 1453-1593,'A',1595-1670 <MOR>
A;Cross-references: GB:S55790, NID:g234418; PIDN:AAB19637.1; PID:g234419
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unied and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Comment: In Goodpasture's syndrome, an autoimmune response develops against an epit
R;Morrison, K.E.; Mariyama, M.; Yang-Feng, T.L.; Reeders, S.T.
Am. J. Hum. Genet. 49, 545-554, 1991
A;Title: Sequence and localization of a partial cDNA encoding the human alpha3 chain
A;Reference number: A39786; MUID:91353570; PMID:1882840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3011 GGAAAGTTGGGGGTAGGGGAAATTTTGGGCAGTGCCTTCATCAGCCCCAGTCCTAGAGAGA 2952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1930 GGGAACCAGGCTGGGCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAGACCTGAAGCC 2871
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Mismatches:
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	604 rodiyserProdiyprohiadiyprohiadiyproficiyTyrdiyprodluglg6 623 1021 GGCCCGCATGGACAGCAGT
	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
1910 GGGATGAGTACTAGGGGTTAGGCCATTTTGGGGGGCCGAGCCCCAGGGGGTTAGGGCTAGGGCCCAGGCCCAGGGGGCAGGGCCCAGGGGCCAGGGGCCAGGGCCCAGGGGGCGCAGGGCCCAGGGGGCGCAGGGGGCGCAGGGGGG	325 uAspGlylleLysGlyGlnLysGlyAspIleGlyProProGlyPheArgGLyPro 1961 ATGTGCTGGAAGTTTTCTACGCTGAGTATTTGCCCAAGTCGTTTGTCAATACTACCT 344

C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 07-May-1999
C;Accession: A02862; A38001; A38002; A38004; A38005; S71946
B;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K. Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino acid seq A;Reference number: A02862; MUID:80026026; PMID:488906

A; Molecule type: protein A; Residues: 243-422 CDEW1> R; Bentz, H.; Fietzek, P.P.; Kuehn, K. Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979 A; Title: The covalent structure of calf skin type III collagen. III. The amino acid s A; Reference number: A38002; MUID:80026028; PMID:488908

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A Molecule type: protein A; Residues: 1-242 FFIED-R:Dewes, H.; Fietzek, P.P.; Kuehn, K. Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979 A; Title: The covalent structure of calf skin type III collagen. II. The amino acid A; Reference number: A38001; MUID:80026027; PMID:488907 A; Molecule type: protein
A; Readdues: 423-571 (2018)
A; Readdues: 423-571 (2018)
B; Lang, H.; Glanville, R.W.; Fletzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A; Title: The covalent structure of calf skin type III collagen. IV. The amino acid se
A; Reference number: A38003; MUID:80026029; PMID:488909
A; Accession: A38003

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A;Accession: A;8004
A;Rolcaule type: protein
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B;Residues: 94

collagen. V. The amino acid seq

A Molecule type: protein
A; Residues: 572-808 < LAN>
R; Dewes, H.; Fietzek, P.P.; Kuehn, K.
HOppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A; Title: The covalent structure of calf skin type III c
A; Reference number: A38004; MUD:80026030; PMID:488910

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٥y	796 CCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCG 744
DÞ	735 ro
Qy Db	743 GGTCCCGGAAGAGGTCAGAGCA 720 746 alalaMetProGlyPlroGlyThrProGlyPheProGlyGluArgGlyAsnSerGlyG 766
. qq	719GGGCCTCCAGTGGAGTGAAGCACACCAGAA 683
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pp	786 lyLeuAspGlyProArgGlyAspProGlyGlnProGlyProProGlyGluGlnGlyP 805
. qq	628 CGGGCACAGCAGCCTGCTAGCCAGCCGCTTGGGATGAGAAAGAGGCTCAGCAGGAT 569
λΌ	GCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCGTTAGCGTCCAAGGCCCAAGGGCCGAGGGC
qa	euProGlyLeuAsnGlyLeuLysGlyGlnGlnGlyA
٥y	508 ACTGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAG 452
qq	831 rgArgGlyLysThrGlyProLysGlyAspProGlyIleProGlyLeuAspArgSerGlyP 851
oy .	451 CACCATGGTCATGAACTTCTCCTCTACCCCACTTCCAGCAGAGGGGGGGCACATAGGT 392
qa	851 heProGlyGluThrGlySerProGlyIleProGlyHisGlnGlyGluMetGly 868
0y	391 GAIGCTGCGCCAAACACTCCAGSCCAAAGGTIAG 353
QQ	LeuGlyGlnArgGlyTyrProGlyAsnProGly
Oy Db	352 CAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGCGCTCACCCACACGCT 293
'n	CTGGACCATAGTGGGCCAGGGGGGTTAGGGCTCAGGGGGGCCGTTCAGGCAATCCAGGAA
- qa	
٥y	
qq	920 ile
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٥y	115 CCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGA 56
Db	942 ProGly-ProSerGluIleSerHisValIleGlyAspLysGlyGl 956
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A; Kesiluges: 948 luly 4 Ablus
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F; 107/Binding site: carbohydrate (Lys) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1049
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QY 263 GCCTACC	ACCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGGGGGTGAGC 307	7 8	
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OY 308 CGCCT	CGCCTGCTGCGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACC 358	· 8	
Db 243 lyPro	lyProAlaGlyIleProGlyAlaProGlyLeuIleGlyAlaArgGlyProProGlyProP 263	^o	
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Qy 473 GG	GGCCTGGTCTGTGCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTAT 529	ÿ £	
Db 297 lyserProG	ProGlylleAla 302	3 8	
. QY 530 GGCCG	GGCCGCCGCCCGTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTC 589	S	
303	GlyProLysGlyGluAspGlyLysAspGlySerProGlyGluProGlyAlaA 320	3 3	
Qy 590 ATCC	590 ATCCCAAGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGGATCCCAGGCCCCTGGAGCTG 649	δ i	
. Db 320 snGly	:: snGlyLeuProGlyAlaAlaGlyGluArgGlyValProGlyPheArgGlyProAlaGlyA 340	g (
Qy 650 GCACT	GCACTGCTCATCCTCGG	λο i	156Z CTGATGACCAGCTTCCTGCCAG
Db 340 laAsn	 aAsnGlyLeuProGlyGluLysGlyProProGlyAspArgGlyGlyProGlyProAlaG 360	gg ———	
оу 667	CTTC	Oy	
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QY 722 CTCTC	ອວວວ	ολ	1658 GCGCTCTGCGGGGCCTCTGCCT
111 Db 378 lyLeu	 11	qq .	
Qy 782 ATGAT	ATGATCAGTCTTGGGGGCTGCCTGGCTACCTCCTGCCTGC	à €	1/18 G
Db 391	AsnGlyLysProGlyProProGly	3 8	
		<u></u>	1 4 0 1 GCC 1 GGACC 1 C 7 C

ą	407	
λy	887	CTGCT
qo	425	ıı roGlyProLysGlyAsnAspGlyAlaProGlyLysAsnGlyGluArgGlyGlyProGlyG 445
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ą	445	lyProGlyProGlnGlyProAlaGlyLySASnGlyGluThrGlyProGlnGlyProProG 465
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ąc	590	roGlySerSerGlyValAspGlyAla
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qo	599	
λζ	ıñ (GCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTTACCACCGGGAGAAGCAGGTGTTC 15
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QQ	684	Gly-AlaAlaGlyProAlaGlyGlySerGlyPro
λά	1718	G
e e	869	oGlyProGlnGlyValLysGlyGluArgGly
λχ	1748	TGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGCTCCCA

TCTGC TCTGC AGCGA G1yAs G1	1799	CCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTG 1858	
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Qy	2765 CCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCA 2824
2 (oorgetoning from the following f
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Oy	ACGGUTTCCUTAACCACCCCTCTTCTTGGCCCAGCTTGGTTCCCCCCCACTTCCACTCC 29
QQ	1000HisproGlyProlleGlyPro-ProGlyProArgGlyAsnArgGly 1014
δλ	CTAGGACTGGCTGATGAAGGCAC
qq	
Qy	3005 ACTITCCCTACCCCCAACTITCCCCACCACCACACACCCTGT 3049
QQ	1029 GlyProProGlyProProGlyAlaProGlyProCys 1040
RESUL B4033 colla C;Spe C:Dat	RESULT 44 B40333 collagen alpha 1(II) chain precursor - African clawed frog C;Species: Xenopus laevis (African clawed frog) C;Species: Xenopus precursor - African clawed frog) C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999
C; Acc R; Su,	.; Ramirez, F.
A;Tit	11.1 BIO1. 115, 263-275, 1991. 12.1 BIO1. 115, 263-275, 1991. 13.1 Procollagen genes during Xenopus laevis erence number: A40333; MUID: 92011898; PMID: 1918153
A; Acc A; Sta	ession: B40333 ession: Yes preliminary
A; Res A; Cro	
C; Sup C; Key F; 37 - F; 125	; Superioning: Collegen alpha 1(1) Tomain; ilbrillar Collagen carboxyl-terminal homolo ; Superioning: colled coil: extracellular matrix; glycoprotein; trimer; triple helix ; 37-96/Domain: von Willebrand factor type C repeat homology <wg>; 1258-1486/Domain: fibrillar collagen carboxyl-terminal homology <fc></fc></wg>
Align Pred.	
Score Percer Best I Query DB:	308.00 Matches: 277 33.50% Conservative: 54 arity: 28.04% Mismatches: 362 1 Gaps: 1 Gaps: 61
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QY	24
QQ	
Qy	2449 AAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAA 2390
QQ	155 155
QY	2389 GAGCTACATTAAACGAAGCTGCAGGTTAAGGGGCCTTAGAGATGGGAAACCAGGTGACTGA 2330
QQ	156 161 ArgAspGlyGlubroGly 161
٥y	2329 GTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTCTCTCAACTAGGAGGCTAGCTGTTA 2270
QQ	162ThrProGlyAsnProGly
δλ	2269 ACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGGAGCCCTTCT 2210

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Qy	AGIGCCAICCAGCTGCACA 1
Db	Glybeurn 363
Qy	0
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Qy	1058 GGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGCCCGGCATG 1011
Db	aArgGlyGlnProGlyVal 60
δλ	~
Dp	ıLysGly 62
Qy	94
qq	yserGln 64
Qy	AGCAGGC 88
qq	65
Qy	GGGGGCCAGGGCACTGGTGCCC 83:
QQ	ProproGly
οy	
qa	67
Qy	72
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Qy	CCCIGCTAGCCAGCCGCCCTIGGGAIGAGAAAGAGGCICAGCAGGAIGCCCA 56
QQ	ProPro 74
Qy	51
qa	GlyAsp 76
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349 CCTGCTAACC: ::: 38 aSerileAla/ 409 GCTGCTGGAAC: ::: 58 rileGlnLeui 469 GCTGGCCTGG :::: 78 eSerGlyMet; 529 TGGCGCGCG 529 TGGCGCGCGC 529 TGGCGCGCGC 529 TGGCGCGCGC 529 TGGCGCCGCC 529 TGGCGCCGCC 520 TGGCGCCGCC 520 TGGCCCCGCC 520 TGGCCCCGCC 520 TGGCCCCCGCC 520 TGCCCCCCGCC 520 TGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	118 ulle	805 GGCCTAG	955 CCCCACGAGCCAGCAGAAGGCTGTCGGCCCCTTGTCGCCCCACTGCTGTCCATG 1014 252 erProprodindlyAspLys	1131 TGGCACTCATCACCGTGTTTTACACGGATTTCGTGGGGGGGG	
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14	1449 TCTCAGCCTGCAGATCCTG	478
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Ħ	1595GGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTG 16	1637
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publication No. US2002018259641

SEMERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: Compounds FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REPREBENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880

CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338

SOFTWARE: FastSEQ for Windows Version 3.0

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                          1904 GTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGCG 1942
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Vinals de Bassols, Carlota
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Publication No. US20020183251A1
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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Wantanabe, Yoshihiro
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Wang, Aijun
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                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
                                                                                                  3.32e-151
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                                                                    ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
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APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Bkelky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa de Bassols, Carlota
APPLICANT: Foy, Teresa Cary R.
APPLICANT: Foy, Teresa CAMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SED ID NOS: 982
SOFTWARRE: FastSEQ for Windows Version 3.0
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Mismatches:
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Vedvick, Thomas S
Carter, Darrick
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APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Oarter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samel X.
APPLICANT: Li, Samel X.
APPLICANT: Hepler, William T.
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APPLICANT: Or INVENTION: Compositions and METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
                                                                 Sequence 113, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                                                                                              Harlocker, Susan L.
Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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US-09-895-814-113
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                                                                                                                                                                                                 Sequence 113, Application US/10010940

Fublication No. US20030088062a1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker Susan Louise

APPLICANT: Harlocker Susan Louise

APPLICANT: Harlocker Susan Louise

APPLICANT: Harlocker Susan Louise

APPLICANT: Read's Cary

APPLICANT: Read's Cary

APPLICANT: Retter, Mark

APPLICANT: Retter, Mark

APPLICANT: Retter, Mark

APPLICANT: Retter, Mark

APPLICANT: Solk, John

APPLICANT: Solk, John

APPLICANT: Solk, John

TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE

CURRENT APPLICATION NUMBER: US/10/010,940

CURRENT FILING DATE: 2001-12-05

SOFTWARE: EastSEQ for Windows Version 3.0

SEQ ID NO 113

LENGTH: 553

TUDENGTH: 553

TUDENGTH: 553
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Gaps:
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Mismatches:
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                                                 210121.428C3
                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
                                                REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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                                                                                                                             LENGTH: 553 amino acids TYPE: amino acid
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                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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6300 Columbia Center, 701 Fifth Avenue
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Patent No. US20020081580A1
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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Dβ	221	aLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerPr	
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qq	241	CysProCysArgAl	
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Dp	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340	
Qy	1304	TATTTGGCCAGTGTGGC	
Пр	341	LMetAspArgLeuValGlnArgPheGl	
Qy	1364	CTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT 14	
qq	361	laAlaGlyAlaThrCysLeuS	
Qγ	1424	CCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGC	
qq	381	erAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400	
ογ	1484	רז	
Db	401	erLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 4.	
οy	1544	CTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCC	
qa	421		
Οy	1604	GGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCT	
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Qγ	1724	GGGTGGTTCCGGGGCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCT	
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οy	1844	SGTGTCTGCCGCAGGCCTGGTCGCCATTTACTTTGCTACACA	
Db	521	hralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 5	
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Sequence 113, Application US/09822827 Patent No. US20020081680A1 GENERAL INFORMATION:

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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210.11.534.11
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT APPLICATION NUMBER: US/09/822,827
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
LENGTH: 553
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                       CACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCCGGCTCTTCGTGGCTGAGCTGTGC
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APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
ITTLE OF INVENTION: METHODS FOR THEIR USE
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                                                                                                  Length:
Matches:
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Indels:
CURRENT APPLICATION NUMBER: US/09/115,453B
                          3.0
       CURRENT FILLING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version
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2861.00
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                                                              ; ORGANISM: Homo sapien
US-09-115-453-113
                                                                                                                    Percent Similarity:
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                                              LENGTH: 553
                                    SEQ ID NO 113
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Tang, Yuqiu
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
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                                             APPLICANT: Skeiky Allun
APPLICANT: Skeiky Yalun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: ORPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEO ID NOS: 992
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Matches:
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                                     Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
MCNeill, Patricia D.
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 Thomas
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                                                                                            COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER 21.534C1
AspLysSerAspLeuAlaLysTyrSerAla 1079
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Matches:
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GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 746
                                                                               AGGGTGGTTCCGGGGCCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
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284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG 343
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: For INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: OMBOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121, 534625, 793
CURRENT FILLER DATE: 2001-06-29
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                             Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
Wang, Aljun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                              APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                             Harlocker, Susan L.
Jiang, Yuqiu
Kalos, Michael D.
US20020192763A1
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              GENERAL INFORMATION:
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Sequence 974, Application US/09895793

Db 21 ValAsnLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40	Oy 404 CCTCTGCTGCAAGTGGGGGTAGAAGAAGAAGACATCATGACCATGGTGCTGGGCATTGGT 463	Qy 464 CCAGTGCTGGTCTGTGTCCCGGTCCTAGGCTCAGTGACACTGGCGTGGA 523	Oy 524 CGCTATGGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGGTGAGCCTC 583	Qy 584 TITCTCATCCCAAGGGCCGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCTG 643	Qy 644 GAGCTGGCACTGCTCGGCGTGGGGCTGGACTTCTGTGGCCAGGTGTGCTTC 703	Qy 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 763	OY 764 TACTCTGTCTATGCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	Oy 824 ATTGACTGGGACACCAGTGCCCCTACCTGGGCACCCAGAGGAGTGCCTCTT 883	Oy 884 GGCCTGCTCACCTCATCTTCACCTGCGTAGCAGCCACACTGGTGGCTGGGGGG 943	Oy 944 GCAGCGCTGGGCCCACCGAGCGAGAGAGGGTGTCGGCCCCTCCTTGTCGCCCCAC 1003	Oy 1004 TGCTGTCCATGCCGGCCCCTTGCCTTTCCGGAACTGGCGCCCTGCTTCCCGGCTG 1063	Qy 1064 CACCAGCTGTGCTGCCTGCGCCCGGCTCTTCGTGGCTGAGCTGTGC 1123	Qy 1124 AGCTGGATGGCACTCATGACCTGTTTTACACGGATTTCGTGGGCGAGGGCTG 1183	Qy 1184 TACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGGAGACACTATGATGAAGGC 1243	ESULT 17 S-10-012-896- Sequence 708 Publication GENERAL INFC APPLICANT:	APPLICAN APPLICAN	; APPLICANT: Kalos, Michael D. ; APPLICANT: Retter, Marc W.	APPLICAN APPLICAN APPLICAN
Db 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140	Oy 704 ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 763	Oy 764 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCGTGCCTGCC	Oy 824 ATTGACTGGGACACCAGTGCCCTGCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 883	Oy 884 GGCCTGCTCACCTCATCTTCCTCACGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943	Qy 944 GCAGCGCTGGGCCCACCGAGCAGCAGCAGCAGCGCTGCTCCTTGTCGCCCCAC 1003 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 1004 TGCTGTCCATGCCGGGCCCGCTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1063	Qy 1064 CACCAGCTGTGCTGCCGTAGCCCGGCCTGCGCCGGCTCTTCGTGGCTGTGCTGTGC 1123	Oy 1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGTG 1183	Oy 1184 TACCAGGCCTGCCCAGAGCTGAGCCGGCACCGAGGCCCGGAGACACTATGATGAAGGC 1243	RESULT 16 US-09-822-827-974 ; Sequence 974, Application US/09822827 · Datort No resolutional on 1	GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	FILE REFERENCE: 210121.534CI ; CURRENT APPLICATION NUMBER: US/09/822,827 ; CURRENT FILING DATE: 2001-03-28	; NOMBER OF SEQ ID NOS: 982 ; SOFTWARRE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 974 ; LENGTH: 359) TIPE: FRI) ORGANISM: Homo sapiens US-09-822-8274	Alignment Scores: 1.35e-86 Length: 359 Score: 5core: 1696.00 Matches: 320 Fercent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 10 Gaps: 0 BB:	US-09-759-143-110 (1-3410) x US-09-822-827-974 (1-359)	Oy 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG 343	Qy 344 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCG 403

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Alignment Scores:
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LENGTH: 371
TYPE: PRT
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                                                                                                                           APPLICANT: Fanger, Gary R.
APPLICANT: Wantenabe, Yoshihiro
APPLICANT: Mantenabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427027
CURRENT APPLICATION UNBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
SUMBER OF SEQ ID NOS: 1011
SOFTWARE: FasLSEQ for Windows Version 3.0
SEQ ID NO 708
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Mismatches:
Indels:
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Matches:
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                         Henderson, Robert A.
Hural, John
                                  Skeiky, Yasir A.W.
Hepler, William T.
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Carter, Darrick
Li, Samuel X.
                        Wang, Aijun
                                                                                                                    Foy, Teresa
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US-10-012-896-708
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Best Local Similarity:
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                     CAGCTGTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGC 1126
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT REPLICATION NUMBER: US/09/895,793
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTESEQ for Windows Version 3.0
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 708, Application US/09895793; Publication No. US20020192763A1; GENERAL INFORMATION:
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Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
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315 aValSerGly 318
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Wang, Aijun
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US-09-895-793-708
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US-09-895-793-708
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|LeuLeu------AlaGlyIleGlyPro 35
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                                                                                           US-09-759-143-110 (1-3410) x US-09-895-793-708 (1-371)
 Length:
Matches:
Conservative:
Mismatches:
                                                   Indels:
2.57e-71
1420.50
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Query Match:
               Score:
Percent Similarity:
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                                                                          APPLICANT: AL JangCnun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.4.27226
CURRENT FELLICATION NUMBER: US/09/895,814
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Mismatches:
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Matches:
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               Sequence 708, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                 APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Ralos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
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1420.50
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US-09-895-814-708
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LENGTH: 371
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                                          CCACTGGAGGCCCTGCTCTGTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTAC
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                                                                                                                                                                                                                                                                                                                   COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 708, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Skeiky, Yasir A.W.
Hepler, William
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Vedvick, Thomas S
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                                         FastSEQ for Windows Version 3.0
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001.01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 3.(
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1420.50
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ORGANISM: Homo sapiens
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APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REPERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 708
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; Patent No. US20020081680A1
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CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
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Patent No. US20020051977A1
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Ralos, Michael D.
Fanger, Gary R.
Fetter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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McNeill, Patricia D.
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SOFTWARE: FastSEQ for
SEQ ID NO 708
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APPLICANT: Xu, Jia
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                   ; ORGANISM: Homo sapiens
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LENGTH: 371
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Hepler, William T.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Hepler, William T.
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Conservative:
  DIAGNOSIS OF PROSTATE CANCER
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Indels:
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TITLE OF INVENTION: DIAGNOSIS OF PROSTATE FILER REPERBENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 852
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; ORGANISM: Homo sapiens
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Query Match:
DB:
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TYPE: PRT
CORGANISM: Homo sapiens
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 852
LENGTH: 400
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Hepler, William T.
Henderson, Robert A.
Hural, John
MCNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                        Sequence 852, Application US/09895814; Publication No. US20020193296A1; GENERAL INFORMATION:
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Halos, Michael D.
APPLICANT: Retler, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carler, Marc W.
APPLICANT: Carler, Marc W.
APPLICANT: Carler, Day, Craig H.
APPLICANT: Carler, Darrick
APPLICANT: Carler, Darrick
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Wang, Aijun
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207 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 226
                                                                                                                                 716 GCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTAT
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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FERERAL INFORMATION: APPLICANT: XU, Jiangchun
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Ketter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, John A.
APPLICANT: Jay Craig H.
APPLICANT: Carter, Thomas.S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
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Skeiky, Yasir A.W.
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Dillon, Davin C.
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                                           APPLICANT: Reluction, NOBELL A.
APPLICANT: Reluction, March W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Carly H.
APPLICANT: Oby, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Garter, Darrick
APPLICANT: However, Milliam
APPLICANT: Hepler, William
APPLICANT: Houghton, Maymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: 2001-02-09
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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                                  Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
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Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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McNeill, Patricia D.
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Kalos, Michael D.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
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Matches:
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Patent No. US20020081680A1
GENERAL INFORMATION:
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                        247 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1011
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Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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Hepler, William T.
Henderson, Robert A.
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Wantanabe, Yoshihiro
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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188
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                                                                                                            Conservative:
Mismatches:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Kalos, Michael
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Retter, Mark
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Day, Craig
                        ; ORGANISM: Homo sapiens
US-10-012-896-1011
                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                    Alignment Scores:
LENGTH: 355
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APPLICANT:
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             TYPE: PRT
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1493 CACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGT 1552
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
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Conservative:
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FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Version 3.0
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Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
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McNeill, Patricia D.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Hepler, William T.
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Query Match:
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US-10-010-940-571
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LENGTH: 84
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.53462 CURRENT APPLICATION NUMBER: US/09/895,793 CURRENT FILING DATE: 2001-06-29
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Mismatches:
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Matches:
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SED ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 706
LENGTH: 123
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Jiang, Yuqiu
Kalos, Michael D.
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Skeiky, Yasir A.W.
Hepler, William T.
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Vedvick, Thomas S.
Carter, Darrick
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Stolk, John A.
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                                                                                                    ) ORGANISM: Homo saplens US-10-012-896-706
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REPERENCE: 21012.1.427C26
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 9900
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
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SOFTWARE: FastSEQ for Windows Version 3.0
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Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
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McNeill, Patricia D.
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Vedvick, Thomas S.
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Hepler, William T.
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Stolk, John A.
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                                                               ORGANISM: Homo sapiens
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                                                                                                                                 Pred. No.:
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1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCC 1429
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APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Rotter, John A.
APPLICANT: Ody, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Sameel
APPLICANT: Hapler, William
APPLICANT: Hapler, William
APPLICANT: Hapler, William
APPLICANT: Hapler, William
APPLICANT: Moneill, Patricia D.
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
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US-09-780-669-706
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT APPLICATION WHERE: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
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Patent No. US2002002248A1
GENERAL INFORMATION:
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Jiang, Yuqui.
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Vedvick, Thomas S.
Carter, Darrick
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                 ) ORGANISM: Homo sapiens
US-09-895-814-706
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1250 ATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGTCATG 1309
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Pettent No. US20020081680A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE FEELS FEELSEQ for Windows Version 3.0
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Mismatches:
Indels:
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Sequence 103, Application US/10096986
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426.00
97.83%
94.57%
6.64%
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
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TITLE OF INVENTION: No. US20030083464Alel Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2347 GGGAAACCAGGTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAA 2288
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                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr Hobbach Test Albritton & Herbert LLP
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: I ELOPY ULSA.

COMPUTER: I ELOPY ULSA.

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/096,986

FILING DATE: 12 Amar-2002

CLASSIFICATION: CURNOWN

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/44,791

FILING DATE: 22-No. US2003008446A1-1999

APPLICATION NUMBER: US 08/482,085

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/175,155

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/053,049

FILING DATE: 29-DEC-1993

APPLICATION NUMBER: US 08/053,049

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US 08/053,049

FILING DATE: 29-OCT-1987

APPLICATION NUMBER: US 06/927,258

FILING DATE: US 06/927,258
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263
32
327
218
57
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REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-759-143-110 (1-3410) x US-10-096-986-103 (1-837)
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Conservative:
Mismatches:
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                                      APPLICANT: Ferrari, Franco A.
Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-398-3249 INFORMATION FOR SEQ ID NO: 103:
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                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
Publication No. US20030083464A1
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 117
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356.50
35.16%
31.35%
5.73%
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                        GENERAL INFORMATION:
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	2227 AGTGCATGGAGCCCTTCTGGCCTGCTATAAGTCCAGACTGAAACCCCCTTGGAAGGC 2168 14 LeuproGlySerproGlyAlaProGlyThrProGlyProGlnGly 88			101 ProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyP 116	2047 AACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGAGCTGGGA 1988 11	CCCAGTGAGGCAGGCCCTCCACCATGTGCTGGAAGTTTTCTACGCTGAGTATTGGC		CAAGTCGCTCTTGTCAAATACTACGTGTGTAGCAAAGTAAATGGC	GLYPTOGLNG1YLGURIO			169GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaP 186	1768 CAGGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGC 1721	roglyThrProglyProglnGlyLeuProglySerProglyAlaProglyThrFroglyF	1720 CTCGGTGGCTCACCCACCACACACACAGAGACATCACAGGCAG 16/4	TOGINGLY LEUKTOGLYSELYIOOLYAHAKIOOLY INLYLUGALYELOGINGLY LEUKLOO	AGGCCCCGCAAAGCGCGGGGGTGAAAGTTGGAAGAAGCCACCACTACCTCCAGGAACAACTGCCTCCAACAACACCACGTGTTCTCTCTTCTTCTTCTTCTTCTTCTTCTTTTCTTTTTT	IYSEFFIOGIYAIAFTOGIYTIIR FLOGIYFIOGINGIY LEGETTOGIYSEFFIOGIYALGE	1613 CATTAGGGAAGGAAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554	上し出していまして、「「「「「「「」」」」。 「「」」」」 「「」」」」 「「」」」」 「「」」」」 「「」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「「」」」 「」」 「「」」」 「「」」 「「」」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「」」 「「」」」 「「」」 「」」 「「」」 「」」 「「」」 「「」」 「」」 「「」」 「「」」 「」」 「「」」 「「」」 「「」」 「」」 「「」」 「「」」 「」」 「「」」 「「」」 「」」 「「」」 「「」」 「「」」 「「」」 「」」 「「」」 「「」」 「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「」」 「」」 「「」」 「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「「」」 「」」 「「」 「「」 「「」」 「「」 「「」 「「」 「」		CCCGGTGGTAGAGGGAGG	279 ProGlyProGlyLeuProGlySerProGlyAla-ProGlyThrPr 294	CGGTGAGGGCGGCTGAAGCTGTCACCACGCCACCACTGTGGGACAGGCATGTGGCACC	oglyproglnGlyLeuProglySerProglyAlaProglyThrPr	-GGCAGCCACAGGGAAAGCIGCCACACIGGCCAAAIAGACIGCIGGAGIGCCGAAICGCI	oGlyProGlnGlyLeuProGlySerPro	1322 GCACCAGCGGTCCATGACCAGAGAGAGACAGGAGATGGCGCACTGCAGGAGATA 1200		
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SCT----GGTGCAGCCGGGGAAGCAGGCCCCCAGGTTCCGGAAAGCCAAGCGGG--- 1020 ATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCC 1179 CTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGC---- 1125 ----TGCACACGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCACA 1071 CATAGGTGATGCCTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339 AGAGCTGGGGCTTTCCGGT---GCCGCAGCAGCGGCTCACCCACAGCCTCTGGACCATAG 282 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr-Pr 639 TGGGCCAGGCGGG---TAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225 ||||||| |SerProGlyAhlaProGlyThrProGlpToGlyLeuProGlySerProGly----- 529 AGGACAGTG---CCCAGATGAAGGGCCGGCGGCGCCATAGCGTCCACGCCAGTGGTCAC 507 TGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA 447 TGGTCATGAACTTCTCCTCTACCCCCA------CTTCCAGCAGCAGAGGCGGCA 399 CCCCAAGACTGATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGT 741 AGTCCAGCAGCCCCACGCCCAGGATGAGCAGTGCCAGGGGCCTGGGGATCCGGGC 624 ACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCA 564 CCGGCATGGACAGCAGTGGGGCGACAAGGAGGGGGGCCGACAGCCCTTCTGCTGGTCGG 960 GGGGCCCAGCGCTGCCT --- CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGA 903 GATGAGGGTGAGCCAAAGAGGCACTCCT------CCTGGGTGCCCA 858 --- CCCGGAAGAGACAGAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACACTGGCCACAGA 684 lyAlaProGlyThrProGlyProGlnGly------LeubroGlySerProGly 394 lyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 359 roglySerProGlyAlaProGlyThrProGlyPro---GlnGlyLeuProGlySerPro 378

229 AsnGlyAspAspGlyGluAle	106 Db	693 Qy 1927	60 Db 264 MetLysGlyPhisArgGlyPheSerGlyLeuAspGlyAlaLys 712 Qy 1867 TGCGGCAGACACCATATAGGCAGACACAACA	284	Qy 1807 CAGGGATGGGGCCACCTGGGACAGCAGGAGGCACTATCCAGGATGGCGAG	Qy 1756	Db 317 lyProAlaGlyAsnAspGlyAsnAspGlyAlaThrGlyAlaAlaGlyProGlyProT Produced by Plants, Me Qy 1717 GGTGGGTCACCACCACCACCACCACCACCACCACCACCACCACCAC	Db 337 hrGlyProAlaGlyProProGlyPheProGlyAlaValGlyAl	QY 1679 AGGCAGAGGCCCCGCAGAGCGCGGGTGGAGCAGGCAGCAGCCAGGCCAACAGGCCAACAGGCCAACAA	357	OY 1634 TGCCTCCAGCACCCACGTCCATTAGGGAGGGGGCTCCAGGCTTAGGGC DD 374 1yProPro61yProAlaG1yAlaAlaG1yAproFloG1yAlaAspG1yAspG1yAlaAspG1yAspG1yAlaAlaG1yAspG1yAlaAlaG1yAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yAlaAspG1yG1yG1yAlaAspG1yG1yG1yAlaAspG1yG1yAlaAspG1yG1yAlaAspG1yG1yAlaAspG1yG1yG1yAlaAspG1yG1yG1yAlaAspG1yG1yG1yG1yAlaAspG1yG1yG1yAlaAspG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG1yG	1583	DD 394 rodlyAlaLys-GlyAlaAsnGlyAlaProGly Oy 1523 ATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTACAGGGAGGCCAGTGTGTAAGGCAGG	Db 405 ill		2300 Oy 1403		2183 Qy 1289 GGGAGA Db 471 AlaArd	182 2123 QY 1241	189 Db 491	AGAGCCA 2063 QY 1199 TGGCACGCCTGGTACAGCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCA 11111	2003 QY 1139	
CGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAG ::	GCCAGGCGCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCTCATCTCA-	uProGlySerProGlyAlaProGlyThrProGlyProGlnGly-LeuProGlySerP	remoustrated and the state of t	CAGATCCTGGCCGAGGCGCGCGCTGTCACCCGGAGCC 22	nrProGlyProGlnGlyLeuProGlySerProGlyAla 725	Sequence 21, Application US/10216705 Publication No. US/20030096973A1 Publication No. US/20030096973A1	A. lagens and Derived Proteins	heir Uses	CURRENT FILING DATE: 2002-09 PRIOR APPLICATION NUMBER: US 09/331,347	FALON FILING DATE: 1999-08-17 NUMBER OF SEQ ID NOS: 22 SORTWARE: PatentIn vos: 23		ORGANISM: Homo sapiens 0-216-705-21	8.41e-12 Length: 347.00 Matches:	Percent Similarity: 32.42% Conservative: 42 Best Local Similarity: 28.02% Mismatches: 330 Ouery Match: 315	Gaps:	CAGCTCCCAAAAACCCT	GGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA	GAGTCCCCGCATTCCAGTGCATGGAGCCTTCTCGCCTCCCTGTATAAGTCCAGACTGAA	setintslysiyileservalproGlybrometGly	 	CCCCAGCCCCCAGCTGCAGCTACGCACCTCAGCACAGGGTGGCAGCAGAGAGCCA 	CATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGGCTAACAG	::::::

q	524GlyGluAlaGlyArgProGlyGluAlaGlyLeuProGlyAlaLysGlyLeuThrGly 542	
٥٥	1031 AAGCCAAGCGGGCCCGGCATGGACAGCAGTGGGGGGGGAAAGGAGGGGGCCCAAAGCAAAGAAAAAAAA	
7 A		864
		QY 188 CIGCCGCC
Š.		Db 879 aAlaGlyA
qa		Qy 128 TCCAGCTTG
Οy	929GCAGTGTGGCTG 918	
qa	572 GlyAlaArgGlyGlnAlaGLyValMetGlyPheProGlyProLysGlyAlaAla 589	7.4
δy	917 CTACGCAGGTGAGGATGAGGGTGAGCAGCCCAAAGAGGCACTCCTCCTGGG 864	610
qq	590GlyGluProGlyLysAlaGlyGluArgGlyValProGlyProProGly 605	216
Qy	863 TGCCCAGGTAGG 852	
qq	 606 AlaValGIyProAlaGIyLySASpGIyGLWAlaGIyAlaGlnGIyProProGIyProAla 625	932
δλ	851 GGGCCAGGGCACTGGTGCCCAGTCAATGGCAGGCAGGA	RESULT 39 US-10-060-036-159
qq	 626 GlyProAlaGlyGluArgGlyGluGlnGlyProAlaGlySerProGlyPheGlnGlyLeu 645	; Sequence 159, Applic ; Publication No. US20
οy	812 GGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGC 756	
Db		
Oy	755 GACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCAGGGCCTCCAGTGGAG 705	; APPLICANT: Persing ; APPLICANT: Hepler,
qa		
δλ	704 TGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCACGCATGAGCAGTGCCA 648	
qa		; CURRENT APPLICATION ; CURRENT FILING DATE
δλ	6476TTCCAGGGGCCTGGGATCCGGCACAGCACC 615	SOFTWARE: FASTSEQ f
qa		; SEQ ID NO 159 ; LENGTH: 1464
Qy	614 CTGCTAGCCAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCCAAGGACAGTG 555	; ORGANISM: Homo sap
qa	::: :::	
Οy	554 CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTA 495	Alignment Scores: Pred. No.:
1 4		Score:
QCI	ProLysGlyaspargGlyaspalaGlyProLysGlyAlaaspGlyselFlO	Best Local Similarity:
Ολ	CTGGAC	Query Match: DB:
qa	758 GlyLysAspGlyValArgGlyLeuThrGlyProIleGlyProProGlyPróAla 775	US-09-759-143-110 (1-3
Οy	461 CAATGCCCA 453	Qy 2353 AGAGATGG
Ор	776 GlyAlaProGlyAspLysGlyGluSerGlyProSerGlyProAlaGlyProThrGlyAla 795	
Qy	452GCACCATGGTCATGAACTTCTCCTCTACCCCACTTCCAGCAGAGGGGGCA 399	2299
d d	796 ArgGlyAlaProGlyAspArgGlyGluProGlyProProGlyProAlaGlyPheAlaGly 815	
Qy	398 CATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCA 351	101
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දි සි	GlyPro-AlaGlyProProGlyProIleGlyAsnValGlyAlaProGlyAlaLySGlyAl	Qy 2122 CCCAGCC

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GAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCT-----TCTCTA 2300
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                                                       AACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGG 129
                                                                              gvalGlyProProGlyProSerGlyAsnAlaGlyProProGlyProProGl 899
                 GCTTCGTCTCGGCTCTGCT-----CCAGAAGCTGCGGCCTCTCCTTC 189
                                                                                                                 CICAGCCCAIGCICAACACCIGCIGCIGIGGG-----GCACCICAGIGGGG 75
                                                                                                                                                                            SATCACTCAGATCCTGGCCGA-----G 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPOSITIONS AND METHODS FOR THE THERAPY
AND DIAGNOSIS OF PANCREATIC CANCER
1121.56
NUMBER: US/10/060,036
S. 2002-01-30
S: 4560
or Windows Version 4.0
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Michael J.
g, David H.
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λλ	2062		
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λy	2002	AGCGGGGAGCTGGGA1967	
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λ	1966	CGCTGA	
ą	249	ProGlnGlyAlaArgGlyLeuProGlyThrAlaGlyLeuProGly 263	
λ̈́α	1927	CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCC 1868	
მ	264	MetLysGlyHisArgGlyPheSerGlyLeuAspGlyAlaLysGlyAspAlaGlyProAla 283	
۲	1867	TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808	
ą	284	GlyProLysGlyGluProGlySerProGlyGluAsnGlyAlaProGly 299	
ر م م	300	CAGGGATGGGGCCACCTGGGACAGCAGGAAGGCACTATCCAGGATGGCGAG 1757	
٨	1756		
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<u>γ</u>	1679	GGGAGCAGG	
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× 4	1634	TGCCTCCAGCACCACGTGTCCATTAGGGAGGGAGCTCCAGGCTTAGGGC 1584	
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ъ ō	1583 394	CTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTGGGT 1524	
۸	1523	ATTTGGGCAGGAACACCTGCTTCTCCGGTGGTAGAGGAGGCCAGTGTAGGGCAGGA 1464	
۾	405		
Y	1463	TCT6CAGGCCTGAGAGGTGAACCCGGTGAGGCGGCTGTCACCACGCCACAC 1404	
Q	420	Pro-GlnGlyProGlyGlyProLysGlyAsnSerGlyGluProGlyAl 438	
٨		TGTGGGACAGGCATGTGGCACCGGCACACAGGGAAAGCTGCCACACTGGCCAAATAGA 1344	
Q	438	aProGlySerLysGlyAspThrGly-AlaLysGlyGluProGlyPro 453	
>-	1343	CTGCTCGAGTGCCGATCGCTGCACGGCGGTCCATGACCAGAGAGAAGACCA 1290	
Ω	454	Val-GlyValGlnGlyProProGlyProAlaGlyGluGluGlyLySArgGly 470	
>-		GGGAGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGC 1242	
Δ		AlaArgGlyGluProGlyProThrGlyLeuProGlyProProGlyGluArgGlyGlyPro 490	
>-			
Ω		GlySerArgGlyPheProGlyAlaAspGlyValAlaGlyProLysGlyProAlaGlyGlu 510	
× -c	1199	TGGGCACGCCCTGGTACAGCCCCTCGCCCACGAATCCGTGTAAAACAGCGTGAAGGTCA 1140	
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1139	TGCACAGCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGC 10	080
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~	ACAGCTGGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGA 10	32
524	::: aLysGlyLeuThrGly 54	2
1031	AAGCCAAGGGGCCGGCATGGACAGCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTT 97	
543	SerProGlySerProGlyProAspGly55	9
971	CTGCTGGCTCGGTGGGGCCCAGCGCTGCCTCCTCAGCCACCA 93	0
557		
929		89
572	GlyAlaArgGlyGlnAlaGlyValMetGlyPheProGlyProLysGlyAlaAla 58	6
\vdash	CTACGCAGGTGAGGAAGATGAGGTGAGCAGAGAGGCACTCCTCCTGGG 86	4
290	GlyGluProGlyLysAlaGlyGluArgGlyValProGlyProProGly 60	2
863	TGCCCAGGT-1	2
909	AlaValGlyProAlaGlyLysAspGlyGluAlaGlyAlaGlnGlyProProGlyProAla 62	Ñ
851	GGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGGA	m
626	GlyproAlaGlyGluArgGlyGluGlnGlyProAlaGlySerProGlyPheGlnGlyLeu 64	Ŋ
\vdash	GGTAGCCCAGGCCCCCAAGACTGATGAAGGCATAGACAGAGTAGGCTGGC 75	ڥ
4	ProGlyProAlaGlyProProGlyGluAlaGlyLysProGlyGluGlnGlyValProGly 66	Ŋ
755	GACAGTGGTCCGGGTCCCGGAAGAGCTCAGAGAGCAGGCCTCCAGTGGAG 70	ñ
99	AspLeuGlyAlaProClyProSerGlyAlaArgGlyGluArgGlyPheProGl	4
704	NGCAGCCCCACGCCCAGGATGAGCAGTGCCA 64	8
685	ArgGlyValGlnGlyProProGlyProAlaGlyProArgGlyAlaAsnGlyAlaProG	4
647	GCTCCAGGGCCTGGGATCCGGG	2
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614	CTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTG 555	
723	AlaProGlyLeuGlnGlyMetProGlyGluArgGlyAlaAlaGlyLeuProGly 740	0
554	CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGACGCCTA 495	2
741	ProfyselyAspArgdlyAspAlaGlyProLysGlyAlaAspGlySerPro 757	7
494	GGAGCGGGACACAGA	7
758	sAspGlyValArgGlyLeuThrGlyProlleGlyPr	S
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APPLICANT: Schiegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Chen, Yan
APPLICANT: Kametkar, Shubhangi
APPLICANT: Kametkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION: OF CERVICAL CANCER
TITLE OF INVENTION: 0F CERVICAL CANCER
TITLE OF INVENTION: 06 CERVICAL CANCER
TITLE OF INVENTION WUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-01-11-14
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                                                                        242 TCCAGAACTGCTTCGTCTCGGCTCTGCT-----CCAGAAGCTGCGGGCCTCTCCTCCTTG 189
                                                                                                                                                                      188 CTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGG 129
                                                                                                                                                                                                                                                       ----GlyGlyLysGlyProArg-GlyG 912
GGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGCGCCTCACACCACAGCCTCT 291
                           844
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                  290 GGACCATAGTGGGCCA------GGCGGGTAGGGCTCAGGGGGCCGTTCAGGCAC
                                                                                                                                      864 a------ArgGlySerAlaGlyProProGlyAlaThrGlyPheProGlyAl
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                                                                                                                                                                                                                                                                                     74 ACACGTCTCATCACTCAGATCCTGGCCGA-----G
                                                                                                                                                                                         2353 AGAGATGGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCT--
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                          899 yProAlaGlyLysGlu-------
                                                                                                                                                                                                                                                                                                                                                                          932 lyGluLysGlySerProGlyAla 939
                                                                                                                                                                                                                                                                                                                                               GCGCGCGCTGTCACCCGGAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/10171311 Publication No. US20030087270A1 GENERAL INFORMATION:
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LENGTH: 1464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1807 CAGGGATGGGGCCA-----CCTGGGACAGCAGGAAGGCACTATCCAGGATGGCGAG 1757
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                                                                                                                                                                                    2242 GAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGTATAAGTCCAGACTGAA 2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2062 CATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGGCTAACAGG 2003
                                                                2299 GGTGTGTCTCAACTAGGAGGCTAGCTGTTA---ACCCTGAGCCTGGGTAATCCACCTGCA 2243
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131 ArgAspGlylleProGlyGlnProGlyLeuProGlyProProGlyProProGlyProPro 150
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190 ProGlyProProGlyAlaPro---GlyProGlnGlyPheGlnGlyProProGlyGluPro
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                                                                                                                          151 GlyProProGlyLeuGlyGlyAsnPheAlaProGlnLeuSerTyrGlyTyrAspGluLys
                                                                                                                                                                                                                                                                                                            2182 ACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAGAGGGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 GlyProLysGlyGluProGlySerProGly------GluAsnGlyAlaProGly
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Oy 461 Db 776 Oy 452	Db 796 ArgGlyalaProGlyaspargGlyGluProGly Qy 398 CATAGGTGATGCCTGCGGCCAAACACCTCCA Db 816ProPro	. 0y 350 Db 827 Qy 290		Db 864 aArgGlySerAlaGlyPro Qy 188 CTGCCGCCAACTGCCTAGGAATCAGCCAGGGGG :::::: Db 879 aAlaGlyArgValGlyProProGlyProSerGl	Oy 128 TCCAGCTTCTCAGCCCATGCTCAACACCTGCTG	74	Qy 44 GCGCGCGCTGTCACCCGGAGCC: 22	RESULT 41 US-10-096-986-103 ; Sequence 103, Application US/10096986 ; Publication No. US20030083464A1	GENERAL INFORMATION: APPLICANT: Ferrari, Franco A. Richardson, Charles Chambers, James	Causey, Stuart Pollock, Thomas J. Cappello, Joseph Crissman, John W.	; TITLE OF INVENTION: NO. US2003008346; ; NUMBER OF SEQUENCES: 117 ; CORRESPONDENCE ADDRESS:	ADDRESSEE: Flehr Hohbach Test Albi STREET: Four Embarcadero Center, S CITY: San Francisco STATE: Callifornia	COUNTRY: US ZIP: 9411 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	COMPUTER: IBM PC compatible COPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/096,986
1289 GGGAGATGGCGGACTGCAGGACAGCCCCAGGCTGCCCATCCGAACGC 1242		AGGGTGCGGGGCATGC	CGGGGAAGCAGGCGCCCAGGT CGlyGluAlaGlyLeuProGlyAla GGACAGCAGGGGGGCAAGAGG	543 SerProdlySerProdlyProAspGlyLysThrGlyProPro 556 971 CTGCTGGCTCGGGCCCAGGC	GlyAlaArgGlyGlnAlaGlyValMetGlvPheProGlyProLysGlyGlaAla	CTACGCAGGTGAGGAAGATGAGGAGGCAGCAAGAGGCACTCTCCTGGG 86	863 TGCCCAGGT-+AGG 852 606 AlaValGlyProAlaGlyLysAspGlyGluAlaGlyAlaGlnGlyProProGlyProAla 625		812GGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGACAGTAGGCCTGGC 756	755 GACAGTGGTCCGGGTCCCGGAÄGAGGTCAGAGGCCGCCTCCAGTGGAG 705	704 TGAAGCACACCTGGCCACAGAAGTCCAGCACGCCCAGGATGAGCAGTGCCA 648	647	614 CTGCTAGCCAGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCAAGGACAGTG 555 :: ::	554 CCCAGATGAAGGGCCGGCGGCGATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTA 495
oy oy	do Qy Oy	oy da	oy Oy	ob Oy	δδ .	oy Oy	oy ga	Qy	oy Db	Qy	Oy Dp	Qy	Qy Db	Oy Dp

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.1el Peptides Comprising Repetitive
ds and DNA Sequences Encoding the Same
ACCCCCACTTCCAGCAGCAGGGGGC 399
                                                                                                                                                                                                                                                                                                                                                               CCATTTCTGCCAGCCCTTTGGTGCCGG 129
                                                                             SerGlyProAlaGlyProThrGlyAla 795
                                                                                                                                                                                                        GCCAGCAGGGGCTCACCACAGCTCT 291
                                                                                                                                                                                                                                                                                                                                                                                                                GGC-----CAAAGGTTAGCA 351
                                                                                                                                                                         |||||
|GlyAlaAspGlyGlnProGlyAlaLys 826
                                                                                                                                                                                                                                                           GTAGGGCTCAGGGGGCCGTTCAGGCAC 243
                                                                                                                                                                                                                                                                            -CCAGAAGCTGCGGCCTCTCCTCCTTG 189
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|OProGlyAlaThrGlyPheProGlyAl 879
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yAsnAlaGlyProProGlyProProGl 899
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Suite 3400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCT-- 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 GCCG---CCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 GGTGCCCCACAGCAGCAGGTGTTG-----AGCATGGGCTGAGAAGCTGGACCGGCACCA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 AAGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGCGGCAGCAAGGAGGA 197
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                                                                                                                                                                                                                                NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                    APPLICATION NUMBER: US 08/482,085
APPLICATION NUMBER: US 08/482,085
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CT-1987
APPLICATION NUMBER: US 07/114,518
FILING DATE: 29-CT-1987
FILING DATE: 29-CT-1987
FILING DATE: 04-NOV-1986
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
FILING DATE: 12-Mar-2002
CARSSIFICATION: «UNKNOWN»
PAPLICATION DATA:
APPLICATION NUMBER: US/09/444,791
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-10-096-986-103
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 837 amino acids
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 103: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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323.00
30.52%
26.29%
5.03%
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Best Local Similarity:
Query Match:
DB:
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1482 CCTCCCTCTACCACCGGGAGAGCAGGTGTTCCTGCCCAA-----ATACCGAGGGGACA 1535
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                                                                                                                                                                                                                                              182 rProGlyAlaProGlyThrProGlyProGlnGlyLeu-----ProGlySerProGlyAl 200
                                                                                                                                                                                                                                                                                                708 CACTGGAGGCCCTGCTCTGACCTCTTCCGGGA---CCCGGA---CCACTGTCGCCAGG 761
                                                                                                                                                                                                                                                                                                                                 -----GlyAlaProGlyThrPro-----GlyProGl 162
                                                                                                                                                                                                648 IGGCACIGCICAICCIGGGCGIGGGCTGCTGCAGACIICIGIGGCCAGGTGCTICACIC 707
537 GCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822 CCATTGACTGGGACACCAGTGCCCTGGCCCC-----CTACCTGGGCACCCAGGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 ------ProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro------
                                                                                                597 GGGCCGGCTGGCTAGCAGGGCTGCT----GTGCCCGGATCCCAGGCC---CCTGGAGC
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14.9 authority control contr	Q .:0	roGlyAlaProGlyThr	0v 2607 APHTEATHTEATHTEATHEATH
419 General Particul Productive Control (1998) 1915	δō		
165 GARTACACCACCACCACCACCACCACCACCACCACCACCACCA	ф	euProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProG	
166 TETECOTYANGE CONTROL C	. Qy	GCAGTGGCCTGCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATG	2
1666 TCTCCCCACCACCACCACCACCACCACCACCACCACCACC	qq		949
136 FORGET OF CONTROL 196 19	δy		
1746 TOTALGGACCTOGGACTOGGACTOGGACTOCTOGGACTOGCACCC 1805 04 TOTALGGACCTOGGACTOGGACTOGCACCCC 1805 05 TOTALGGACCTOGGACTOGGACTOGCACCCCCC 1805 05 TOTALGGACCTOGGACTOGCACCCCCCCCCCCCCCCCCCCCCCCC	qa		
1806 TOTAL MARCH 1815 1816	Qy		
1906 FOTTAMAGGGGGTCAGGCAGTCAGCAGTCAGTCAGTAGTATTG 1917 1916 FOTTAMAGGGGGTCAGGCGGGGTGAGTAGTATTG 1918 ACAGGGGGGTCGGGTCGCCATTAGTTGGTCACCAGGTAGTATTG 1919 ACAGGGGGGTCGGGTCGCCATTAGTTGGTCACCAGGTAGTATTG 1914 ACAGGGGGGTCGGGTCGCCATTAGTTGGGGGGGG 1914 ACAGGGGGGTCGGGTCGCCATTAGTTGGGGGGGG 1914 ACAGGGGGGTCGGTCGCCAGTTGGGGGGGGG 1914 ACAGGGGGGTCGGTCGCCAGTTGGGGGGGGG 1914 ACAGGGGGGTCGGGGGGCTGGTGGGGGGGG 1914 ACAGGGGGGTCGGGGGGCTGGTGGGGGGGGG 1914 ACAGGGGGGTCGGGGGCTGGTGGGGGGGGGG 1914 ACAGGGGGGTCGGGGGCTGGTGGGGGGGGGGG 1914 ACAGGGGGGTCGGGGGCTGGTGGGGGGGGGGGG 1914 ACAGGGGGGGTCGGGGGCTGGTGGGGGGGGGGGG 1914 ACAGGGGGGGTCGGGGGCTGGTGGGGGGGGGGGGGG 1914 ACAGGGGGGGTGGGGGCCTGGTGGGGGGGGGGGGGGGGG	qa		697 yThrProGlyProGlnGly
1854 General Considitation 0	νο.	TGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTATA	
1854 #PGFTGTCTGCCGCAGGCCTGGCTGCTGCTGCTGCTGCTGCGCGGAGGG 1913 919 929	qa		
1914 ACAAGGGGCTCTGGCCAATACTCGGCTGGAGGG	οy		2907 TTCTCTT
1914 ACAACAGCGCACTTGGCGTAGAAACTTCCACCCACTTGGGCTGAGGG 1973 197	qa		727 yThrPro
1974 CCTGCCTGACTGGGGCTGGGCTGGCCGGGCTGGC 233 3024 TTTCCCAGCTGCCAGCTGGCCGGCTGGC 233 3024 TTTCCCAGCTGCTGGGTGGCCGGGCTGGGCTGGGCTGGG	Qy	TGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGG 197	2964 TGGGCTGATGAAGGCA
1974 CCTGGCTCACTGGGGTCCAGCTCCTGTTAGCCCCATGGGGCTGCCGGCCTGC 1111 1	qa	:::	747 nGly
1111	δŏ	CCTGCCTCACTGGGTCCCAGTTCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	
2034 GECCAGTTTCTGTTGCTGCCAAAGTAATGTGCCTCTCTCTCT	ପୁ	Venifical vestigation and a second control of the second control o	763
2014 GGCGAGTTTGGTGCTGCCAAAGTAATGTGGCCTCTGCTGCCCCCTGTGG 2093 573 IO	} ;	from rootyserricelyna FricelyinrProcifyrocinglyLeuProcifyserP	C A TILL 4.2
573 ro	δō	CGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGCTGAG	US-09-919-497-56
2094 GTGCGTAGCTGCACAGGGGGCTCCCTCTCCTCCTCCTCTAGGG 2153 [111] [11] [11] [11] [11] [11] [11] [1	ପ୍ର	ro	; Sequence 56, Application US/0991; Patent No. US20020106662A1
574 iyala-ProglyrhiProglyrhoglogloglogloglogloglogloglogloglogloglo	δλ	GTGCGTAGCTGCACAGGTGGGGGCTGCCTCTCTCTCTCTC	<pre>; GENERAL INFORMATION: ; APPLICANT: Mutter, George L.</pre>
2154 CTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGCACTTATACAGGGAGGCCAGAA 2213	qq	lyala-ProglyThrProglyProglnGlyLeuProGlySerProglyAlaProgly	; TITLE OF INVENTION: PROGNOSTIC ; FILE REFERENCE: B0801/7225
1 1 1 1 1 1 1 1 1 1	δλ	CTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAA	; CURRENT APPLICATION NUMBER: US/ ; CURRENT FILING DATE: 2001-07-3
2214 GGGCTCCATGCAGGATGCGGGGACTCTGCAGGT	qa	ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln	; PRIOR APPLICATION NUMBER: US 60 ; PRIOR FILING DATE: 2000-07-31
613 divinit	Qy		; NUMBER OF SEQ ID NOS: 100 ; SOFTWARE: PatentIn version 3.0
2250 GGATTACCCAGGCTCAGGGTTAACAGCTAGCTCTAGTTGAGACACCTAGAGAA 2306 1111111	qa	GlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln	; SEQ ID NO 56 ; LENGTH: 1806
628 GIYLCHELONGON GATTTTGGGAGCTGAATAAACTCAGCTGCTTTCCACTTTCCACTTTACC 2366 3307 GGGTTTTGGGAGCTGAATAAACTCAGCTCCTTTCCACTTTCCACTTTACC 2366 1	οy		o sapien
2307 GGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGATTCCCATCTTAACC 2366 ; DOCAM	qa		; FEATURE: ; NAME/KEY: UNSURE
643 GIVLEUPROGIYSEPPROGIYA-THR-PROGIVPR 656	٥y		
3367 TGCAGCTTCGTTTAATGTAGCTCTTGCATGGAGTGAACACTCCTCCATG 2426 05-09-919	qa		
656 oGlnGly	ογ	AATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATG	OTHER INFORMATION: Xaa = 09-919-497-56
2427 GGATTTGAACATATGACTTATTTGTAGGGGAAGGGCGAACACACAC	QQ	oGlnGly	gnment Sco
659	οy	GGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAACACAAGAACC	. No.: 4.38e
2487 AGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCTCTTACCTTTATC 2546	qq	:::	
666 oGlyThrProGlyProGlnGly	Οy		
2547 AGGATGTGGTTGGTTCGTTGTTGCTATCACACACACACAC	Db		US-09-759-143-110 (1-3410) x (13-09-
TO THE TOTAL OF TH	Oy	2547 AGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGACACAGGCATTTAAATATTTA 2606	00 01 01 01 01 01 01 01 01 01 01 01 01 0

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GGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTA 2666
                                                                             CAACAATCAGGTCCCCTGAGATAGCTGGTCATTGG 2726
                                                                                                                                                                                                                                             GCTTCAGGTCTCAACGCTTCCCTAACCACCCTC 2906
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ProGlnGlyLeuProGlySerProGlyAlaProGl 727
                                                                                                                                  TCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAG 2786
                                                                                                                                                                                                                                                                                                   AATGATAATTCCAAATGCTGTTACCCAAGGTTAGG 2846
                                                                                                                                                                                                                                                                                                                                                          VITTCCCCTACCCCCAACTITCCCCTACCCCCAAC 3023
                                                                                                GlyThrProGlyPro------ 686
LeuPro----- 675
                                                                                                                                                            ---GlnGlyLeuProGlySerProGlyAlaProGl 697
                                                                                                                                                                                                                    GlySerProGlyAlaProGlyThrPro----- 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGCTTCTGGT---- 3066
                                                                                                                                                                                                                                                                                                                                                                             FICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 1806
Matches: 315
Conservative: 61
Mismatches: 413
Indels: 71
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697 -Gl ₃	2162 GTC	716 rog]	2148	736 1yL)	2102 GCT			776 erLy		1984 A(1926 AAG	830 lnA		838 LYV		1760	861 roG	1730	881 lnA	1678 GGC	s 668	1618 GTG	918 gGl	1558 GTC			948 roc 1438 GGT		1378 AGC	977 Glu	1318 CAG	984 rgC
qa	Qy	qq	QY	QQ	Qy	QΩ	δλ	a i	Ş 2	G ò	r da	QY	qa	δλ	a :	3 f	λO	da da	Qy	Dp	QY	qa	Qy	qa	Qy	qa	Oy.	an o	전	QY	qq	Qy	qa —
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Y 332 GIGGCTGAC		•,
-09-759-143	1257 roGlyGluAlaGly-AsnProGlyProProGlyGluAlaGlyValGlyGlyGlyGlyBroLysGly 1276	qq
	AGTGGG	Oy
Best Local Similarity: Query Match:	1244SerValGlySerValGlyGluLysGlyGluLysGlyGluP 1257	qa
Score: Percent Similarity:	361 AAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGCGGCTCAC 302	Qy
Alignment Scores: Pred. No.:	roGlyProArgGlyProGlnGlyProAsnGlyAlaAspGlyProGlnGlyProProProGly	g qa
US-10-012-896-547	CACTTCCAGCAGCAGCAGCACATAGGTGATGCCTGAGGCGAAACACCACCACCACACCACCACACCACCACCAC	ò
	roGlyGluLysGlyGluAsnGlyAspValGlyProTroGlyProProGlyProGlyProFile	7 A
	469 CACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCC 422	ογ
, NUMBER OF SEQ ID NO.	1190 PheProGlyProProGlyProlleGlyLeuGlnGlyLeuProGlyProP 1206	qa
CURRENT APPLICATION CURRENT FILING DATE	CACTGGCTGAGCCTAGGAGCGGGACACAGAC	δ
; TITLE OF INVENTION: ; FILE REFERENCE: 210	1172ProArgGly-GinGlnGlyMetPheGlyGlnLysGlyAspGluGlyAlaArgGly 1189	qq
; APPLICANT: Meagher ; TITLE OF INVENTION:	589 GAGAAAGACGCTCAGCAGGATGCCCAAGGGCACAGATGAAGGGCCGGCGGCGGCC 530	οy
; APPLICANT: Fanger, ; APPLICANT: Wantana	1163 leAlaGlyGlyAspGlyGluProGly1171	qq
	649 CAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC	ογ
; APPLICANT: McNeill ; APPLICANT: Houghton	1150GlyProProGlyLeuGlnGlyProValGlyAlaProGly1 1163	qa
	709 TGGAGTGAAGCACACGCGCCACAGAAGTCCAGCAGCCCCACGCAGGATGAGCAGTGC 650	δy
; APPLICANT: Skeiky, ; APPLICANT: Hepler,	1131 leGlyGluProGlyGlnLysGlyGerLysGlyGlyLysGlyGluAsnGlyProPro- 1149	qq
	769 AGAGTAGGCCTGGCGACAGTGGTCCGGGATCCGGGAAGAGGTCAGAGAGCAGGGCCTCCAG 710	δ
; APPLICANT: Vedvick ; APPLICANT: Carter,	1119AlaGlySerProGlyGluAspGlyAspLysGlyGluI 1131	qa
	829 GTCAATGGCAGGCAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGAC 770	δλ
; APPLICANT: Kalos, ; APPLICANT: Retter,	1108 ly1118	qa
	r AGG	Qy
; APPLICANT: Dillon, ; APPLICANT: Mitcham	1102GlyargAspGlyValGlnG 1108	qa
; GENERAL INFORMATION: ; APPLICANT: Xu, Jian	946 TGCCTCCTCAGCCACCAGCAGTGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAG 887	Οy
; Sequence 547, Applic ; Publication No. US20	1089 ysGlyAlaProGlyGluLysGlyProGlnGlyProAla- 1101	qa
	1006 GCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGGTGGGTTCGGTGGGGCCCAGCGC 947	Qy
Db 1349 oSerGlyG	1069 lyProIleGlyLeuArgGlyArgProGlnG.yProProGlyProAlaGlyGluL 1089	qq
Oy 45	AAGCCAAGCGGCCCGGCATGGACA	QY
Db 1329 pGlyValG		qa
Qy 88 GCACCTCA	GCGCAGGGTGCGGGGCATGCGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	δ
Db 1314 oGlyAspP	1044 ysGlyGlyGluGlyProGlnGlyPro	qq
Qy 147GCCAGCC	1175CGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCA 1127	٥٧
Db 1295 AlaLysGl	 1024 lyLeuArgGlyPheProGlyGluArgGlyLeuProGlyAlaGlnGlyAlaProGlyLeuL 1044	qq
Qy 187 TGCCGC	1204 AGCTCTGGGCACGCCTGGTACA	δλ
Db 1277G1	::: :::	qq
	1262CCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTC 1205	40

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|GlyGlyAspLysGlyGluAspGlyAspProGlyGlnProGlyProProGlyPr 1349
SAACTGCTTCGTCTCGGCTCTGCT---CCAGAAGCTGCGGCCTCTCCTCCTTGC 188
                                                -----CAACTGCCTAGGAATCAGCCAGGCGCCCATTCT---- 148
                                                                                                 CCTITIGGIGCCGGICCAGCTICTCAGCCCAIGCTCAACACCCIGCTGCTGGG 89
                                                                                                                                                 GluAlaGlyProProGlyProProGlyLysArgGlyProProGlyAlaAla 1368
                                                                                                                                                                                                    year, Carry X. Yoshihiro
gher, Madeleine Joy
Ghor: ComPoSITIONS AND METHODS FOR THE THERAPY AND
10N: DIAGNOSIS OF PROSTATE CANCER
210121.427627
TION NUMBER: US/10/012,896
DATE: 2001-12-10
D NOS: 1011
EQ for Windows Version 3.0
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Matches:
Conservative:
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.on, Raymond L.
s de Bassols, Carlota
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nam, Jennifer L.
ocker, Susan L.
'Yuqiu
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rr, Marc W.
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ir, William T.
irson, Robert A.
John
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ck, Thomas S.
r, Darrick
amuel X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeu 40
1 LeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeu 40
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                                                                                                                                           APPLICANT: Fanger, Gary R. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches:
Conservative:
Mismatches:
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CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 547
LENGTH: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Li, Samuel X.
Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
MCNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                   Sequence 547, Application US/09895793
Publication No. US20020192763A1
                                                                                                                                                                                                             Sequence 54,,
Sequence 54,,
Publication No. Us.,
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
ANT: Jiang, Yuqiu
Valos, Michael D.
Marc W.
                                                                                                                                                                                                                                                                                                                                                                                             Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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US-09-895-793-547
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Best Local Similarity:
Query Match:
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992 TIGICGCCCCACIGCIGICCAIGCCGGGCCCGCTIGGCTITCCGGAACCIGGGCGCCCCIG 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSer
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REPERENCE: 210121.427266
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 547
LENGTH: 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton, Raymond L.
Vinals de Bassols, Carlota
                                Sequence 547, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:
                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Mitchael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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McNeill, Patricia D.
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Best Local Similarity:
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RESULT 45
US-09-895-814-547
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Published_Applications_NA:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 110, App	Sequence 110, App	Sequence 110, App	Sequence 110, App	Sequence 110, App	Sequence 100, App	Sequence 110, App	Sequence 110, App	Sequence 110, App		Sequence 110, App	Sequence 1, Appli	Sequence 704, App	Sequence 704, App	Sequence 704, App	Sequence 704, App	Sequence 704, App	Sequence 704, App	Sequence 703, App
	DI	US-09-232-880-110	US-10-012-896-110	US-09-895-793-110	US-09-895-814-110	US-10-010-940-110	US-09-745-288-100	US-09-759-143-110	US-09-780-669-110	US-09-030-606-110	US-09-822-827-110	US-09-115-453-110	US-09-838-785-1	US-10-012-896-704	US-09-895-793-704	US-09-895-814-704	US-09-759-143-704	US-09-780-669-704	US-09-822-827-704	US-10-012-896-703
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	96.6	75.8	75.8	75.8	75.8	75.8	75.8	64.4
	Score	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3409.6	3292.4	2585.4	2585.4	2585.4	2585.4	2585.4	2585.4	2196.4
	Result No.	7	8	e	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

703, 703, 703, 702, 702, 702, 702, 702, 702, 705, 705, 705, 851, 851, 851, 851,	Sequence 10, Appl Sequence 10, Appl
9 US-09-895-793-703 9 US-09-8914-703 10 US-09-759-143-703 10 US-09-759-143-703 10 US-09-822-827-703 10 US-09-895-703-702 9 US-09-895-793-702 9 US-09-895-793-702 10 US-09-759-143-702 10 US-09-759-143-702 10 US-09-759-143-705 10 US-09-895-793-705 10 US-09-895-793-705 10 US-09-895-793-705 10 US-09-895-793-705 10 US-09-895-793-705 10 US-09-895-793-851 10 US-09-895-814-851 10 US-09-759-143-851 10 US-09-759-143-851 10 US-09-759-143-851 10 US-09-759-143-851	9 US-10-012-896-10 9 US-09-895-793-10
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                                                                                  APPLICANT: Xu, Jiangchun
APPLICANT: Xi, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
GURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FASTERO for Windows Version 3.0
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100.0%; Pred. No. 0;
:ive 0; Mismatches
                               Sequence 110, Application US/09232880; Publication No. US20020182596A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 3410; Conservative
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                      US-09-232-880-110
RESULT 1
US-09-232-880-110
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Qy Dp	301 GGTGAGCCGCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTGAACCTGGTAACCTT 360 	Qy Dp	1381 CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGA
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Qy		O _Y	1501 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGC
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oy Op	7	cy D	1741 GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTT
Qy	7	QV Op	1801 ATCCCTGTTATGGGGTCCATTGTCCAGGTCAGCTGGCCAGTC
Qy	CCAG	QV QD	1861 TGCCGCAGGCCTGGGTCTGGTCGCCATTACTTTGCTAC
Qy Dp		Qy	1921 CGACTTGGCCAAATACTCAGGGTAGAAAACTTCCAGCAC
Qy		QY	1981 CACTGGGTCCCAGCTCCCCGGTCCTGTTAGCCCCTGGG
Qy		QY	2041 TTCTGTTGCCGAAGTAATGTGGGCTCTCTGCTGCCAC
Qγ Db	CCTGCTTCCCCGGCTGCACCAGCTGTCCTGCCG	Qy	2101 GCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCTC
Qy		QV	2161 ACTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATA
oy GD	120	Qy Dp	2221 ATGCACTGGAATGCGGGACTCTGCAGGTGGATTACCCA
yo da	126	oy da	2281 CTCCTAGTTCAGACACACCTAGAGAAGGGTTTTTGGGAG(
Qy Db	132	QV Dp	2341 GTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTT/
oy ,	-	Qy Dp	2401 TTTCTAGGATGAAACACTCCTCCATGGGATTGAACATA:

GTGGCAGCTTTCCCTGTGGCTGC 1380 ACAGCTTCAGCCGCCTCACCGG 1440 ACTGGCCTCCCTTACCACCGGGA 1500 GGAGGTGCTAGCAGTGAGGACAG 1560 GCTCCCTTCCCTAATGGACACGT 1620 GCGCTCTGCGGGGCCTCTGCCTG 1680 CGGCCAGGTGGTTCCGGGCCG 1740 ACATTGGGGTGGAGGCCTGCCT 1980 TTCCTGCTGTCCCAGGTGGCCCC 1800 TCTGTCACTGCCTATATGGTGTC 1860 GGCTGCCGGCTGGCCGCCAGT 2040 ACACAGGTAGTATTTGACAAGAG 1920 SGGCTGCCGGGCTGCCCGCCAGT 2040 ACCCTGTGCTGCTGAGGTGCGTA 2100 CAGGCTCAGGGTTAACAGCTAGC 2280 PATGACTTATTTGTAGGGGAAGA 2460 ACCCTGTGCTGCTGAGGTGCGTA 2100 rcccagrereraggergeerg 2160 GCTGAATAAACTCAGTCACCTG 2340 ACAGGGAGGCCAGAAGGGCTCC 2220 GCTGAATAAACTCAGTCACCTG 2340 TAATGTAGCTCTTGCATGGGAG 2400

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                                        GATCCACCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580
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GTCCTGAGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT
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Sequence 110, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
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                      US-10-012-896-110
RESULT
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240 240 300 300 360

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APPLICANT: Weagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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100.0%; Pred. No. 0;
iive 0; Mismatches
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASLED OF Windows Version 3.0
                                                                                                                                                                                                                                             Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
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McNeill, Patricia D.
                                                                                                                                                                                                   Henderson, Robert A
             Harlocker, Susan L.
Jiang, Yuqiu
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Hepler, William T.
Mitcham, Jennifer
                                         Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
                                                                                        Day, Craig H.
Vedvick, Thomas
Carter, Darrick
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Matches 3410; Conservative
                                                                                                                                                                                                                                                                                                Fanger, Gary R.
                                                                                                                                        Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                     Wang, Aijun
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Oy 721 Db 721	1 GCTCTCTGACCTCTTCCGGGACCCGGACCAGGCCTACTCTGTCTATGCCTT 780	Qy Db	1801 ATCCTGTTTATGGCTCCATTGT
Qy . 781 Db 781	CATGATCAGTCTTGGGGGTGCCTGGGCTACCTCCTGCCTG	oy Op	1861 TGCCGCAGGCCTGGGTCTGGTCGC
Oy 841 Db 841	TGCCTGGCCCCCTACCTGGGCACCCAGAGAGTGCCTCTTGGCCTGCTCACCTCTT	ζζ	1921 CGACTTGGCCAAATACTCAGGGTACTCAGGCTACTACTCAGGCTACTAGGCCAAATACTCAGGCGTACTCAGGCGTACTCAGGCGTACTCAGGCGTACTCAGGCGTACTCAGGCGTAGGTAG
Qy 901 Db 901	CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCAC	QV DP	1981 CACTGGGTCCCAGCTCCCCGCTCCC
Qy 961 Db 961	CGAGCCAGCAGAGAGGCTGTCGCCCCTCCTTGTCGCCCCCACTGCTGTCCATGCCGGGC 1	Qy Db	2041 TTCTGTTGCTGCCAAAGTAATGTG(
Oy 1021 Db 1021	CGCTTGGCTTTCCGGAACCTGGGCCCCTGCTTCCCGGGTGCACCAGCTGTGCTGCCG	da Db	2101 GCTGCACAGCTGGGGCTGGGGCGG
Oy 1081 Db 1081	CATGCCCGCACCCTGCGCCGG	Qy	2161 ACTGGAGGCCTTCCAAGGGGTTTT
Oy 1141 Db 1141	GACCTTCACGCTGTTTTACACGGATTTCGTGGCCGAGGGCTGTACCAGGGC 	Qy	2221 ATGCACTGGAATGCGGGGACTCTG
Qy 1201 Db 1201	AGCTGAGCCGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1	Qy Db	2281 CTCCTAGTTGAGACACACTAGAG.
Oy 1261 Db 1261	GGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGT 132	Qy	2341 GTTTCCCATCTCTAAGCCCCTTAA
Oy 1321 Db 1321	GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 138	Qy	2401 TTTCTAGGATGAAACACTCCTCCA1
Qy 1381 Db 1381	CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGTTTCAGCCGCCCTCACCGG 144	Qy	2461 GTCCTGAGGGCAACACACAGAAC
Oy 1441 Db 1441	GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC	Oy Dp	2521 GATCCACCCCCTCTTACCTTTAI 1111111111111111111111111111111111
Oy 1501 Db 1501	GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGACAG 15	Qy	581 CAGAGACACAGGCATTTAAAI
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Sequence 110, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Jiang, Yuqiu
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McNeill, Patricia D.
Houghton, Raymond L.
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Hepler, William T.
                                                                                                                                                                                          Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Vinals de Bassols, Carlota
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FASTSEQ for Windows Version 3.0
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1561 CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620 1561 CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTAATGGACAGCT 1620	Qy Db	2641 TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGGGGGATCCCCAACAATCA 2700
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APPLICANT: Retter, Marchael D.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS
FILE REFERENCE: 210121.4.27C26
CURRENT APPLICANTON: UNMERE: US/09/895,814
CURRENT FILNG DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SSOFWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
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Qy 2641 TGCTAGCTTTTC Db 2641 TGCTAGCTTTTC Db 2641 TGCTAGCTTTTC Qy 2701 GGTCCCTGAGA Db 2701 GGTCCCTGAGA Qy 2761 CTGGCCCCCAA Db 2761 CTGGCCCCCCAA Db 2761 CTGGCCCCCCAA CTGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2821 2821 2881 2881 2941 3001	9y 3061 GCAGGACCAGAA Db 3061 GCAGGACCAGAA Qy 3121 ATATCTGTGCTT Db 3121 ATATCTGTGCTT . Qy 3181 GAGGTCTTATCT Qy 3241 TAGCGGGTGAA Db 3241 TAGCGGGTGAA Qy 3361 AAATTAAAGGCT Qy 3361 AAATTAAAGGCT Oy 3361 AAATAAAGGCT Oy 3361 AAAAAAAAAAAAA	RESULT 6 0.09-76-228-100 5.96-07-62-288-100 5.8equence 100, Application 6.8ENERAL INFORMATION: 7.8ENERAL INFORMATION: 7.8ENERAL INFORMATION: 7.8ENERAL INFORMATION: 7.8ENERAL INFORMATION: 7.8ENERAL OF INVENTION: 7.8ENERENCE: 210121 7.8ENERENCE: 21
GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG CCTGATGACCACTTCCTGCCAGGCCCTAAGCCTGGAGGTGCTACCGTAATGGACAGG 11111111111111111111111111111111		CACTAGGACCCAGGCCCTGTTAGCCCCATGGGGCTGCGGGCTGCCCCCCCC	234 GTTCCCATCTTAAGCCCTTAACTTCGTTTAATCTAGGGGGGGG
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           TCAACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCA 2940
IGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA 2700
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Red, Steven G.
Xu, Jiangchun
Dillon, Davin C.
VENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
VENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
                                           CCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGCTTCAGGT
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.ICATION NUMBER: US/09/745,288
.NG DATE: 2000-12-19
& ID NOS: 101
*astSEQ for Windows Version 3.0
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20010018058A1
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US-09-745	288-100
Query Ma Best Loc Matches	tch 100.0%; Score 3409.6; DB 10; Length 3410; al Similarity 100.0%; Pred. No. 0; O; Indels 0; Gaps 0;
Qy Dp	1 GGGAACCAGCCAGCGCTGGCTCCGGGTGACAGCCGCGCCCTCGGCCAGGATCTGA 60
Qy	TGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTGAGCATGGGCTGAG 120
Oy Db	121 AAGCTGGACCAACAAAGGGCTGGAAATGGGCGCCTGGTTGCTAGGCAGTT 180
Qy Dp	DB1 GGCGGCAGCAAGAAGAGGCCGCAGCTTCTGGAGCAGACGAAGAAGAAGTTCTG 240
Qy Db	241 GAGTGCCTGAAGGCCCCTGAGCCCTGGCCCTGGCCCACTATGGTCCAGAGGCTGTG 300 1111111111111111111111111111111111
Oy Db	301 GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTT 360 Db
Oy Db	361 TGGCCTGGAGGTGTTTTGGCCGCAGCATCACCTATGTGCCGCTCTGCTGCTGGAAGT 420
Qy Db	421 GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 480
Qy Db	481 CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCTGGCGTGGCCGCTATGGCCGCCGCGG 540
Qy Db	541 GCCCTTCATCTGGGCACTGTTGGGCATCTTGTGTTGTTCTCATCCCAAGGG 600
Qy Dp	601 CGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCTGGAGCTGGCACTGCTCAT 660
Qy	01 CCTGGGGGTGGTGGTGGTTTGTGGGCTGGGGGTTCACTCCACTGGAGGCCCT 720
QV Dp	721 GCTCTCTGACCTCTTCCGGGACCCGGACCAGGCCTACTGTCTGT
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oy op	841 TGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT 900
Qy	901 CTTCCTCACCTGCTGCTGCTGCTGGTGGGAGGAGCGCTGGGCCCCAC 960
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1021	CTGTGCTGCCG 10 	
1081	GGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCAF 1	
1141	ACCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAGGCCGTGCCCAG 12	
1201	GGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 12 	
1261	CATCTCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 13 	
1321	AGECTATTTGGCCAGTGTGCCAGCTTTCCCTGTGGCTGC 13 	
1381	TCCCACAGIGTGGCCGTGGTGACATTCAGGCGCCCCTCACCGG 144	
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1501	CGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAG 	
1561	CCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 162 	
1621	AGEGGCTGCTCCCACCTCCACCCGCCTTGCGGGGCCTCTGCCTG 168	
1681	1	
1741	GGGCATCTGCCTGGACCTCGCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 1800	
1801	ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACGCTATATGGTGTC 1860	
 1861	TGGTCGCCATTTACTTTGCTACACAGGTAGT 	
 1921	GAAAACTTCCAGCACATTGGGGTGGAGGCCTGCT 198	
 1981 1981	CTGGGTCCCGGCTCCCGCTCTGTTAGCCCCATGGGGCTGCCGGCTGCCGCCAGT 204	
 2041	GCCACCCTGTGCTGCTGAGGTGCGTA	

	Oy 3361 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	Sequence 110, Application US/C Patent No. US2002002248A1 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer APPLICANT: Harlocker, Susan APPLICANT: Jiang, Yuqui	APPLICANT: Henderson, Robert APPLICANT: Kalos, Michael D. APPLICANT: Fanger, Gary R. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Day, Craig H. APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Darrick	APPLICANT: "1, SMINGEL APPLICANT: Wang, Aljun APPLICANT: Skeiky, Yasir A.W APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSIT TITLE OF INVENTION: DIAGNOSI FILE REFERENCE: 210121.427C2 CURRENT APPLICATION NUMBER: U CURRENT FILING DATE: 2001-01	; NUMBER OF SEQ ID NOS: 934 ; SCPTWARE: FastSEQ for Window ; SEQ ID NO 110 ; LENGTH: 3410 ; TYPE: DNA ; ORGANISM: HOMO Sapien US-09-759-143-110	Query Match Best Local Similarity 100.08 Best Local Similarity 100.08 Matches 3410; Conservative Oy 1 GGGAACCAGCTGCACGC Db 1 GGGAACCAGCTGCACGC	61 61 121 121	OY 181 GCCGCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
2101 GCTGCACAGCTGGGGCTGGGGCTCCCTCCTCCTCCCCAGTCTCTAGGGCTGCCTG 2160	CTCCTAGTTGAGACACACCTAGAGAGGGTTTTGGGAGCTGATTAACTTGGGCACCTGGTTTTTGGGAGTGCTGATTAACTTGGCCCTG [GATC GATC GATC CAGA CAGA	TGCTAGCTTTTCTGTGTGTGTCTAATATTGGGTAGGGGGGATCCCCAACAATCA 270 [2761 CTGGCCCCCAAAATGCCTAACCCAGACCTTGGAAATTCTACTCATCCCAAATGATAAT 2820	2881 CTCAACGCCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCA 2940	CCCAP CCCAP CCCAP CCCAP CCCAP CCCAP	3121 ATATCTGTGCTTGGGGAATCTCACAGAAACTCAGGAGCACCCCTGCTGAGCTAAGG 3180
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GAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGC	GAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTC 	TGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTC	GGGGGTAGAGGAGAGTTCATGACCATGGTGCTGGGCAT' 	CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGC	1 GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGTGT	1 CGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGC	CCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCCAGTGTCTGTGCCAGGTGTGGCGTGGGCTGGGCTGGTTCTGTGGCCAGTGTGTGT	1 GCTCTGTGACCTCTTCGGGACCCGGACCACTGTCGCC	1 CATGATCAGICTIGGGGGCTGCCTGGGCTACCTCCTGC	1 TGCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCC	1 CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGT	1 CGAGCCAGCAGAGGGCTGTCGGCCCCCTCCTTGTCGCC	1 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCC	1 CATGCCCCGCACCCTGCCCCGGCTCTTCGTGGCTGAGCT	1 GACCTICACGCTGTTTTACACGGATTTCGTGGGCGAG 	01 AGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATC 1	1 GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTC	21 GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTV

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GGTGCCACATGCCTGTCCCACAGTGT 	GTTCACCTTCTCAGCCTGCAGATCCT 	GAAGCAGGTGTTCCTGCCCAAATACCG 	CCTGATGACCAGCTTCCTGCCAGGCCC 	GGGTGCTGGAGGCAGTGGCCTGCTCCC 	TGATETCTCCGTACGTGTGGTGGTGG 	GGGCATCTGCCTGGACCTCGCCATCCT 	ATCCCTGTTTATGGCTCCATTGTCCA 	TGCCGCAGGCCTGGGTCTGGTCGCCA1 	GACTTGGCCAAATACTCAGCGTA	CACTGGGTCCCAGCTCCCGCTCCTGT' 	TCTGTTGCTGCCAAAGTAATGTGG	GCTGCACAGCTGGGGGCTGGGGCGTC 	ACTGGAGGCCTTCCAAGGGGGTTTCA 	ATGCACTGGAATGCGGGGACTCTGCAGG 	CTCCTAGTTGAGACACACCTAGAGAAG 	GTTTCCCATCTCTAAGCCCCTTAACC	TTTCTAGGATGAAACACTCCTCCATG
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GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCT 2520
       GATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580
                                       CAGAGACACAGGCATTTAAATATTTAACTTATTTAATTTAACAAAGTAGAAGGGAATCCAT 2640
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Sequence 110, Application US/09780669
Patent No. US20020051977A1
                                                                                    Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
                                                                  GENERAL INFORMATION:
APPLICANT: Xu, Jian
APPLICANT: Dillon,
RESULT 8
US-09-780-669-110
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APPLICANT: Horbil, Patricla D.
APPLICANT: Houghton, Patricla D.
APPLICANT: Houghton, Rownond L.
TITLE OF INVENTION: DIAGNOSITS OF PROSTATE CANCER
FILE REFERENCE: 210121.477024
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                                                                                                                                                                                                                                                                                                                                                       Similarity 100.0%; Score 3409.6; Similarity 100.0%; Pred. No. 0; 0; Conservative 0; Mismatches
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CURRENT FILING DATE: 2001-02-09
NUMBER OF SEO ID NOS: 943
SOFTWARE: FASTSEQ for Windows Version 3.0
  Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                                        Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                       Skeiky, Yasir A.W.
Hepler, William
                                      Fanger, Gary R.
Retter, Marc W.
                                                              Stolk, John A.
                                                                                                                          Wang, Aijun
                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapien
                                                                                                                Li, Samuel
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SEQ ID NO 110
LENGTH: 3410
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	δŏ		CICICIGACCICITCCGGGACCCGGACCACCCGGCCTACCTTTTTTTTTT	qq	1801
	QQ		TCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTT /8	Qy	1861
	δō		CATGATCAGTCTTGGGGGCTGCCTGGCTACCTCCTGCCTTGACTGGGACACCAG 840	qq	1861
	අූ	_	TIGGGGGCTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAG B	Qy	1921
	δλ	-	GCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT	qa	1921
	qq	841	SACCCTCAT 9	Qy	1981
	Oy		CTTCCTCACCTGCGTAGCACCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCAC 960	qa	1981
	qq		SGCCCCAC	Qy	2041
	δλ		CGAGCCAGCAGAGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCTGCCGGCC 1020	qa	2041
	g		GCAGAAGGGCTGTCGCCCCCTTGTCGCCCCACTGCTGTCCCGGGC 10	Qy	2101
	Oy.		CCGCTTGCCTTTCCGGAACCTGGGCGCCCCTGCTTCCCCGGCTGCACTGTTGCTTGC	qq	2101
	gg		GCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTG	Qy	2161
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	3 ,		, ,	Qy	2221
	δo		GACCTICAGGCTGTTTTALACGGATTTTGTGGGGGGGGGGTGTACAGGGGGTGTGCAGGGGGTGTGTGT	qq	2221
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	δý		AGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260	Dp	2281
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	δλ	1261	320	qa a	2341
	q	1261	1320	Qy	2401
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	qa	1321		Qγ	246]
	ΟŊ	1381	CACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACGG	qa	2461
	qq	1381	CACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACGG 1	Qy	252]
	δy	1441	ITTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC	QQ	252
	qq	1441	GITCACCITCICAGCCCIGCAGAICCIGCCCIACACACIGGCCICCCTCTACCACGGGA 1500	λŌ	2583
	ΟŊ	1501	GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTACCAGTGAGGACAG 1560	g qa	2581
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	οy	1561	CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620	- qa	264]
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	Qy	1621	GGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCTGCGGGGCCTCTGCCTG 1680	qa .	270
	QQ	1621	GGGTGCTGGAGGCAGTGGCCTGCTCCACCTGCGCGCTCTGCGGGGCCTCTGCCTG 1680	, oy	276

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100.0%; Pred. No. 0;
tive 0; Mismatches
                TELEPHONE: (206) 622-4900
TELEPA: (206) 682-6031
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
      TELECOMMUNICATION INFORMATION
                                                             LENGTH: 3410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                        Homo sapiens
                                                                                                                                                                                                 Matches 3410; Conservative
                                                                                                               MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                     linear
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                                                                                                                                                 US-09-030-606-110
                                                                                                  TOPOLOGY:
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Patent No. US2002001580A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
3000
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                                                                                                                                                                                                                                           3241 TAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACA 3300
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                                                                                                                                                                               CCCAACTITCCCCTACCCCCAACTITCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
ROSISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
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FILING DATE: 25-FEB
CLASSIFICATION:
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ST 11 9-115-453-110

Sequence 110, Application US/09115453B
Patent No. US20020090372A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: MEHHODS FOR THEIR USE
FILE REFERENCE: 210121.427C4
CURRENT APPLICATION UNMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14

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3121 ATATCTGTGCTTGGGGAATCTCACAGAAACTCAGGAGCACCCCTGCCTG	RESULT 12 US-09-838-785-1 Sequence 1, Application US/09838785 Patent No. US20020009455A1 GENERAL INFORMATION: APPLICANT: Lau, Ted APPLICANT: Parkes, Debbie APPLICANT: Parkes, Debbie APPLICANT: Schneider, Douglas APPLICANT: Stanbrecher, Douglas APPLICANT: Stanbrecher, Pam T APPLICANT: Wan Heuit, Pam T APPLICANT: Wu, John TITLE OF INVENTION: DNA Encoding a No. US20020009455A1e1 PROST 03 FILE REFERENCE: 51831AUSM1 CURRENT APPLICATION NUMBER: 60/200,065 PRIOR APPLICATION NUMBER: 60/200,065 PRIOR APPLICATION NUMBER: 60/200,065 SOFTWARR: Patentin Ver: 2.0 SEQ ID NO 1 LENGTH: 3320 TYPE: DNA ORGANISM: Homo sapiens FEATURE: FEATURE: FEATURE: FEATURE: NAME KEYS: CDS	DOCATION: (282)(1943) Useron
1981 CACTGGGTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGCTGGCCGCCAGT 2040 2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTGTGCTGCTGCTGCTGCTGCTGGTGGCTGCTG	2341 GTTTCCCATCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 2400 [11111111111111111111111111111111111	2761 CTGGCCCCCAAATGCCTAACCCAGACCTTGGAAATTCTACTCATCCCAAATGATAAT 2761 CTGGCCCCCCAAATGCCTAACCCAGACCTTGGAAATTCTACTCTCCCCAAATGATAAT 2761 CTGGCCCCCCAAATGCCTAACCCAGGACCTTGGAAATTCTACTCCCCCAAATGATAAT 2821 TCCAAATGCTGTTACCCAAGGTTAGGGTGTGAAGGAAGGTAGAGGTGGGGCTTCAGGT 1
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-0 6-6 6-	GGCCGCAGCCATCATATATATATATATATATATATATATA	1	663 TGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGC 722	TGATCAGTCTTGGGGGCTGCCTGGGCTACCTCTGCCTGCC		1023 GCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGTGCACCAGCTGTGCTGCCGCA 1082	1143 CCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAG 1202
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_	1743	GCATCTGCCTGGACCTCGCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCAT 180
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> 0	1863	CCGCAGGCCTGGGTCGGTCGCCATTTACTTTGCTACAGGGTAGTATTTGACAAGAGCG 1922
	~	ACTIGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGCCTGCCT
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	04	CIGITECIGCCAAAGTAATGTGGCTCTCTGCTGCTGCCCTGTGCTGCTGAGGGTGCGTAGC 2102
•	04	TGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCTGTGCTGCTGCTGGTGCGTAGC 210
	2103	TGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCCCCCAGTCTCTAGGGCTGCCTGAC 2162
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	Ä	GGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCAT 2:
	2223	GCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGGTCAGGGTTAACAGCTAGCCT 2282
	2283	CTAGTTGAGACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGT 23
	2281	34
	2343	TICCCAICTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGAGTT 2402
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                                      TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCCAACAATCA
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Sequence 704, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: AU, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
RESULT 13
US-10-012-896-704
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οy	664 GGGCGTGGGGCTGCTGGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCT 723	Oy	1240 1239
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2058 PANICIDGUCTUTGCTGCCACCTGTGCTGAGGTGCCTAGGTGCTGCACAGGTGGGGC 2117 2761 PANICIDGUCTUTGCTGCACCTGTGCTGAGGTGCCTAGGTGCGGGGC 2220 2761 PANICIDGUCTGCTCTCCTCCCCAGTCTCTAGGGTGCCTAGGTGCGGGCC 2220 277 GGGGTTTCAGTCTGCACTTCTCCCCTGTTCTGAGGTGCCTGAGGTCTCCATCCA		3-704 No. US20020192763A1 No. US20020192763A1 Nu. Jiangchun Dillon, Davin C. Mitcham, Davin C. Harlocker, Susan L. Jiang, Yuqiu Kalos, Michael D. Retter, Marc W. Stolk, John A. Day, Craig H. Vedvick, Thomas S. Carter, Darrick Li, Samuel X. Wang, Aljun Skeiky, Yasir A.W. Hepler, William T. Hepler, William T. Hepler, William T. Henderson, Robert	APPLICANT: MCHILL, PARTICIA D. APPLICANT: Windlil, Raymond L. APPLICANT: Vinals de Bassols, Carlota APPLICANT: Vinals de Bassols, Carlota APPLICANT: Fanger, Gary R. TTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TTLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2 CURRENT APPLICATION NUMBER: US/09/895,793 CURRENT FILING DATE: 2001-06-29 NUMBER OF SEQ ID NOS: 982 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 704 LENGTH: 4034 TYPE: DNA OGGANISM: Homo sapiens US-09-895-793-704	Query Match 75.8%; Score 2585.4; DB 9; Length 4034; Best Local Similarity 82.4%; Pred. No. 0; 1 Indels 709; Gaps 3; Qy 4 AACCAGCCTGCACGCTCGCTCCGGCTCCGCCCCCGCCCCGCCAGGATCTGAGTG 63 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
	2058 TAATGTGGCTCTCTGCTGCCACCTGTGCTGAGGTGCGTAGGTGCACAGCTGGGGGGGG	2298 CCTAGAGAGGGTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC	2656 GTTGGTGTTAATTTAACAAAGTAGAAGGGAATCCATTGCTAGTTTTCTGT 2656 GTTGGTGTAATATTTGGTAGGTGGGGGGATCCCCAACAATCAGTCCCTGAGATAG 2116 GTTGTTGTTTTGGTAGGTGGGGGGATCCCCAACAATCAGTCCCCTGAGATAG 2716 GTTGTTCTTTTTTGGTAGGTGGGGGGTCTGCCCCTGAGATAG 2717 CTGGTCATTGGGTACATTGCCAGAATCTTCTTCTCCTCGGGTCTGGCCCCCCAAAT 3420 CTGGTCATTGGGTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCCCCCCAAAT 2776 GCCTAACCCAGAACTTGCTAGTACTATTCCCTGGGGTCTGGCCCCCCAAAT 2776 GCCTAACCCAGAACTTGCTAGTACATACTATCCCAAATTCTAAATTCCAAATTACTAAATTCCAAAATTACTAAATTCCAAAATTACTAAAATTACTAAAATTAAAATTACTAAAATTAAAATTACTAAAATTAAAATTACTAAAATTAAAATTAAAATTAAAATTACTAAAATTAAAATTAAAATTAAAATTAAAATTAAAATTAAAA	2896 AACCACCCTCTTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCCTCTACTCTCTTCT

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qa	14111111111111111111111111111111111111	QQ	1321 TCTCCATCCTGGCCCCGACT
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Ωp	301 GAGCCGCCTGCTGCTGCTGCTGTGTTTGCTGGTCAACCTGCTTTTGT 360	g :	1340
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'n	TCCTAGGCTCAGCCAGTGACCAGTGGACGCTATGGCCGCCCCCCCC	Qy	1240
, qa		QQ	1561 TGTGCCCTCTGCTCCCCCAAC
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^O	-	Qy	1338 GAGCAGTCTATTTGGCCAGTG
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q	1261	AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACTCTCGGGGCTGTGTCTGGGCTGGTGCC 1320
λ		12
Ω	1321	TCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGGGATGGACCCCATCTGCATACA 1380
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д	1441	TAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAA 1500
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	1501	AGTCTAGAGGGAGTGGAGGAGGAGGTTAAAGGCTGGATTTCAGATCTGCCTGGTTCCAGGCGGAG 1560
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۵	1561	TGTGCCCTTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTCAGG 1620
۶,	1240	1239
	1621	CGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCT 1680
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	1681	GTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCGCCTTCAGCAAGG 1740
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۵	1801	GAAAGGGGAAGGGTGCTGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGGTAC 1860
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۵	1861	CTGTGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCC
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۵	1921	CTGATGGCCCCTCTCCCTCTGCAGGGTTGGGAGCCTGCGGGCTGTTCCTGCAGT 1980
>-	1278	GCGCCATCTCCCTGGTCTTCTCTCTGGTCGACGGCTGGTGCAGCGATTCGGCACTC 1337
٠.	1981	GCCATCTCCCTGGTCTTCTCTCTGTCTTGTTCTTGTTCTTGGTCGGCTGGTGG
>-	1338	AGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGC
a	2041	GAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGT 2100
> -	1398	CCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGC
c	2101	CACAGTGGCCGTGG
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Oy 2776 GCCTAACCCAGGACCTTGGA 		Db 3660 TCTAGGACTGGCTGATGAA Qy 3016 CCCCCAACTTTCCCCACAG Db 3720 CCCCCAACTTCCCCACAG Ov 3076 CAAAGTGGGTTTCCCAAGG		3256	OY 5510 TRATATGTTAAAAA 5550 	ESULT 15 S-09-895-8 Sequence Publicati GENERAL I	APPLICANY: AU. Jangbruni APPLICANY: Dillon, Davin C. APPLICANY: Mitcham, Jennifer L. APPLICANY: Harlocker, Susan L. APPLICANY: Jiang, Yuqiu APPLICANY: Kalos, Michael D. APPLICANY: Retter, Marc W.	APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT:	Vinals de Bassols, Foy, Teresa Fanger, Gary R. INVENTION: COMPOSITIC NEWTION: DIAGNOSI ENCE: 210121.427026 PPLICATION NUMBER: UG
1698 IGGIGGIGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGG	CCATTGICCAGCTCAGCCAGCTCAGCTGICTATATGGTGTCTCCGGGGGCTGGGGCTGGGGTC 187 [1581 TGGTCGCATTACTTGCTACACAGGTAGTATTGACAAGAGCGACTT[1998 CCGCTCCTGTTAGCCCCATGGGGCTGCCGGCCCCCAGTTTCTGTTGCTGCCCAAG 2057 [111111111111111111111111111111111111	2118 TGGGGCGTCCCTCCTCCTCCCCAGTCTCTAGGGCTGCCTCACTGCAGGCCTTCCAAG 2177 [1111111111111111111111111111111111	GACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACACA 22	2298 CCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC 2357 [CCCTTAACCTGCAGCTTCGTTTTTTTTTTTTTTTTTTTT	2476 ACACAAGAACCCCCTCAGCCCACAGCACTGTTTTTGCTGATCCACCCCCTCT 2535	3241 TACCTTTATCAGGATGT-GCTGTTGGTCCTTCTGTTGCCATCACAGAGCACAGGGCAT 3299 2596 TTAAATTTAACTTATTTAATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTTTTT	2656 GTTGGTGTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAG 2715 1111111111111111111111111111111111
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                                                                 CCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG
AAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC
                               KGGAAGCTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCT
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NUMBER OF SEQ ID NOS: 990 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 704 LENGTH: 4034 TYPE: DNA ORGANISM: Homo sapiens -09-895-814-704	Query Match 75.8%; Score 2585.4; DB 9; Length 4034; Best Local Similarity 82.4%; Pred. No. 0; Matches 3325; Conservative 0; Mismatches 1; Indels 709; Gaps 3;		П	64 ATGAGACGTGCCCACTGAGGTGCCCCACAGAGCAGTGTTGAGCATGGGCTGAGAAG 123	124	121	184 GGCAGCAAGGAGGAGGCGCAGCTTCTGGAGCAGAGGCGAGGCGAAGCAGTTCTGGAG 243 	244 TGCCTGAACGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGT 303	304 GAGCCGCTGCTGCGCACACAGAAAGCCCAACATAGATCAACATAAAAAACATAAAAAAAA	301 GAGCCGCCTGCTGCGCACCGGAAAGCCCACCTGTTGTTGTTTTTTTGG 36	364 CCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGG 423	424 GGTAGAGAGAGATCATGACCATGGTGCTGGGCCATTGGTCCAGGCCTGGTCTG 48	421	484 TGTCCCGCTCCTAGGCTCAGCCAGTGACCAGGGGGGGCGCTATGGCCGCCGCCGCC 543	544 CTTCATCTGGGCACTGTCGTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGG	341 604		64 GGGCGTGGGGCTGCACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCT	Н	724 CTCTGACCTCTTCCGGGACCCGGACCAGGCCTACTCTGTCTG	84		844 CCTGGCCCCTACCTGGCACCAGGAGGAGTGCCTCTTTGGCCTGGTCACCTCATCTT 903	2 T T C
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αn	1 CTTGGCTTTCCGGAACCT	GCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGC
oy E	1084 GCCCGCACCCTGCGCCGCGCGCGCGCGCGCGCGCGGCGCGCGC	SCICTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGAC 114
G A	144 CHICACCCHCHHHHACAC	SCICTICGIGGCIGAGCIGTGCAGCIGGGATGGCACTCATGAC II
op Op	41 CTTCACGCTGTTTTACAC	SGATTTCGT
δλ	AGCCGGGCACCGAGGC	CCGCAGACACTAT
qq	1201 TGAGCCGGGCACCGAGGC	
οy	1240	1239
Dp	1261 AGGCTGGTGTGGGAGCCG	CCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCC 1320
Qy	1240	1239
qa	1321 TCTCCATCCTGGCCCCGA	ACTICICIGICAGGAAAGIGGGGAIGGACCCCAICIGCAIACA 1380
οy	1240	1239
qa	1381 CGGCTTCTCATGGGTGTG	GGAACATCTCTGCTTTGCGGATTTCAGGAAGGCCTCTGGCTGCTC 1440
Qy	1240	
qa	1441 TAGGAGTCTGATCAGAGTCGT	CGTTGCCCCCAGTTTGACAGAAAGGCGGAGCTTATTCAA 1500
δλ	1240	1239
QO	1501 AGTCTAGAGGGAGTGGAG	AGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAG 1560
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qa	1561 TGTGCCCTCTGCTCCCCC	CTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTCAGG 1620
οy	1240	1239
QΩ	1621 CGTCCTAGAAGCGTCTTGAAGC	AAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCCGCCT 1680
Qy	1240	1239
qa	1681 GTCCTCACAGCTGAGACTG	GTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGG 1740
Qy	1240	1239
QQ	1741 GGCGTTGCCCACATTCTC	GCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA 1800
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Οy	1240	1239
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Qy	1240	GGATGGGCAGCCTGGGGCTGTTCCT
Db	1921 CTGATGGCCCCTCTCCCTC	CTGCAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGT 1980
Qy	1278 GCGCCATCTCCCTGGTCTT	PCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTC 1337

2525	ATTCGGCACTC 20	Qy	2418 TCCTCCATGGGATTTGAACATATG
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FGCAGATCCTG	TGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGC 1517 	ç qa	241
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TGCCAGGCCCT	TARGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTG 1637	QQ a	2656 GTTGGTGTCTAATATTTGGGTAGG
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CCTAGAGAAGG	GTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC 235 	RESULT 1 US-09-75 ; Sequen ; Patent	RESULT 16 US-09-759-143-704 ; Sequence 704, Application US/09 ; Patent No. US2002202248A1
2358 CCCTTAACCT 	CCCTTAACCIGCAGCTICGTITAANGIAGCTCTIGCAIGGGAGTITCIAGGAIGAAACA 2417 	GENERA; GENERA; APPLI	AL INFORMATION: ICANT: Xu, Jiangchun ICANT: Dillon, Davin C.

AGAGTATAATGTTTATGGTGACAAATTAAAGGCTTTC 3315 3479 2835 3779 3135 3839 3195 2655 3359 2715 3419 2775 3539 2895 3599 CACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTA 3015 CACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTA 3719 CCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCA 3075 2475 3180 3240 2595 AGCACCCCTGCCTCAGCTAAGGAGGTCTTATCTCTC CCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCA IGTTGGTCCTTCTGTTGCATCACAGAGACACAGGCAT TTCTACTCATCCCAAATGATAATTCCAAATGCTGTAC AGGTAGAGGCTGGGGCTTCAGGTCTCAACGGCTTCCCT TTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG CAGAATCTTCTCTCTGGGGTCTGGCCCCCCAAAT CAGAATCTTCTCCTGGGGTCTGGCCCCCCAAAT G--ACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAAC GCCCACAGCACTGTTTTTGCTGATCCACCCCCTCT : AACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGT GGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAG SCCCACAGCACTGTCTTTTGCTGATCCACCCCCTCT 143

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                                                                                                                                                                                APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210.11.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ 10 DOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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                                      Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
 Mitcham, Jennifer L.
            Harlocker, Susan L.
Jiang, Yuqui
                                                                                                                                           Li, Samuel
Wang, Aijun
Skeiky, Yasir A.W.
                                                                                        Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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1239		1240	δy
89	1 CGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGGCCT	1621	qq
~		1240	Qy
1620	CCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTC	1561	QQ
1239		4	οy
1560	GTCTAGAGGGAGTGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAG	1501	QQ
1239	0	1240	δλ
1500	AGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTA	4	Dp
1239		1240	ογ
1440	GGCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGC	1381	QQ
1239		124(δ
1380	CTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCA	132]	qq
1239		124(οy
1320	CTGGTGTGGGAGCCGCCCACCAAGACGACACTCGGGGCTGTGTCTGGGCTGGTG	1261	qq
1239		124(δy
1260	1 TGAGCCGGGCACCGAGGCCCGGAGACTATGATGATGAAGGCCTTGGCAGCCAG	120	qq
1239	4 TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGA	120	Qy
20		4	qq
20	TTCACGCTGTTTTACACGGATTTCGTGGGGGGGGGGTGTACCAGGGCGTGCCCAGA	114	٥y
14	1 GCCCGCACCCTGCGCCGGCTCTTCGTGCTGA	80	QQ
-	4 GCCCCGCACCCTGCGCCGCCGCTTTCGTGGAGCTGTAGAGCTGGATGCACTAGA	108	ò
1083	4 CTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCG 	102	OY DD
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1023	4 GCCAGCAGAAAGGGCTGTCGGCCCCTCCTTGTCGCCCCACTGTTGTCCATGCCGGGCCC	96	δλ
960		06	qq
963	4 CCTCACCTGCGTAGCAACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACG	06	δ
006	1 CTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTCCTCATCTT	84	qq
903	4 CCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCT	84	Qy
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720	1 GGCCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT		8
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099		09	QQ

1741 GGCGTTGCCCACATTCTCTGAG 1240	GGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA 1800		
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1861 CTGTGGTTCCGCCTTCTATCT 1240		ζ έ	2 6
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1338 GCCGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	20	Qy	2418 TCCTCCATGGGATTTGAACATATGACTTA
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	SCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCTGC 1517	δy	536
1518 CCAAATACCGAGGGACACTGG		qq	241 T
	SGTGCTAGCAGGAGGACAGCCTGATGACCAGCTTCC 1577	δλ	596
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Db 2581 TGGTCGCCATTTACTTTGCTACACA	TGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACT 2640	a 8	1 900
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Qy 1998 CCGCTCTGTTAGCCCCATGGGC	CCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAG 2057	da da	3780. CAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAG
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Qy 2058 TAATGTGGCTCTCTGCTGCCACC	TAATGTGGCTCTCTGCTGCCGCCCTGTGCTGCAGGTGCGTAGCTGCACACGCTGGGGGC 2117	7 qa	84

3240 TIGTTGCCATCACAGAGACACAGGCAT 2595 2715 2775 3479 3659 ATTCCCTACCCCAACTTTCCCTA 3015 FTTGGAGCTACTGCAGGACCAGAAGCA 3075 AGGGAATCCATTGCTAGCTTTCTGT 2655 AGCCCCCAGAGTATATCTGTGCTTGGG 3135 2940 GTAGGGGAAGAGTCCTGAGGGGCAAC 2475 CCCAACAATCAGGTCCCCTGAGATAG 3419 3GGGCTTCAGGTCTCAACGGCTTCCCT 2895 2177 2297 2357 GTCTTTTTGCTGATCCACCCCCTCT 2535 CCCAACAATCAGGTCCCCTGAGATAG AAGGGTCCATGCACTGGAATGCGGG GTCTTTTGCTGATCCACCCCCTCT TCTCCTGGGGTCTGGCCCCCCAAAAT GGGCTTCAGGTCTCAACGGCTTCCCT GGCTGCCTGACTGGAGGCCTTCCAAG GGCTGCCTGACTGGAGGCCTTCCAAG AGTCACCTGGTTTCCCATCTCTAAGC

241 TGCCTGAACGCCCCCTGAGCCCTACCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGT 300 304 GAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTTGTGTGTAGTTTGGTGTAGTTTGGTGTAGTTTGGTGGTG	364 CCTGGAGGTGTTTGGCCGCAGGATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGG 423 	* 424 GGTAGAGGAGAAGTTCATGACCATGGTGCTGGCCATTGGTCCAGTGCTGGCCTGGTCTG 483	484 IGTCCCGCTCCTAGGCTCAGCCAGTGACCTGGCGTGGACGCTATGGCCGCCGCCGCCGCC 543	544 CTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGG 603	604 CTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCT 663 	664 GGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTCACTCCACTGGAGGCCCTGCT 723 	724 CTCTGACCTCTTCGGGACCGGACCAGTGCCCAGGCCTACTCTGTCTATGCCTTCAT 783	784 GATCAGTCTTGGGGCTGCCTGGCTACCTCCTGCCTGCCATTGACTGGGACACCGGTGC 843	844 CCTGGCCCCTACCTGGGCACCCAGGAGTGCCTCTTTGGCCTGCTCACCTCTTT 903	904 CCTCACCTGCGTAGCAGCCACTGCTGGTGGCTGAGGAGGGGTGGGCCCCCCCGCGA 963 	964 GCCAGCAGAAGGGCTGTGGGCCCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCG 1023	1024 CTTGGCTTTCCGGAACCTGGGCGCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCAT 1083	1084 GCCCGCACCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCACTGGATGGCACTCATGAC 1143	1144 CTTCACGCTGTTTTACACGGATTTCGTGGGGGGGGGGTGTACCAGGGCGTGCCCAGAGC 1203 	1204 TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGA	1240 1239 1261 AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGC 1320	1240 1239	1 17
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3196 3900 3256	3960 ITTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAAATTAAAGGCTTT 3316 TTATATGTTTAAAAA 3330	Db 4020 TTATATGTTTAAAAA 4034 RESULT 17	US-09-780-669-704 ; Sequence 704, Application US/09780669 ; Patent No. US20020051977A1 ; GENERAL INFORMATION:		APPLICANT: APPLICANT: APPLICANT: APPLICANT:	; APPLICANT: Retter, Marc W. ; APPLICANT: Stolk, John A. ; APPLICANT: Day, Craig H. ; APPLICANT: Vedvick, Thomas S.	Carter, Darrick Li, Samuel Wang, Aijun Skeiky, Yasir A.	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER ; FILE REFERENCE: 210121.427C24 ; CURRENT APPLICATION NUMBER: US/09/780.669	; CURRENT FILING DATE: 2001-02-09 ; NUMBER OF SEQ ID NOS: 943 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 704	; LENGTH: 4034 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-780-669-704	Query Match 75.8%; Score 2585.4; DB 10; Length 4034; Best Local Similarity 82.4%; Pred. No. 0; Matches 3325; Conservative 0; Mismatches 1; Indels 709; Gaps .3;	CCGGGTGACAGCCGCGCCTCGGCCAGGATCTGAGTG 63	7		77 (TGCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCATTGGTCCAGGGCTGTGGGT 30	

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qa	1441 TAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAA 1500	qa	1 CCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTC 258
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	CCAAGGTTAGGGTG	CCAAGGTTAGGGTG	AACCACCCICITO	TCTAGGACTGGGCT TCTAGGACTGGGCT	CCCCCAACTICCC	CCCCCAACTICCC	CAAAGTGCGGTTTC			AGGGGGGGTTTAAG	TTTATACTGTAAGT	TTATATGTTTAAAAA 		ULT 19 10-012-896-703 acquence 703, Application US/11 ublication No. US20020183251A BENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Davin C. APPLICANT: Harlocker, Susan APPLICANT: Harlocker, Susan APPLICANT: Retter, Marc W. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Carter, Darick APPLICANT: Carter, Darick APPLICANT: Carter, Darick APPLICANT: Carter, Darick APPLICANT: Greter, Darick APPLICANT: Hepler, Willam T APPLICANT: Hepler, Willam T APPLICANT: Houghton, Raymond APPLICANT: Houghton, Raymond APPLICANT: Houghton, Raymond APPLICANT: Houghton, Raymond APPLICANT: Foy, Teresa APPLICANT: Foy, Teresa APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Mandanabe, Yoshih APPLICANT: Fanger, Gary R. TITLE OF INVENTION: DIAGNOSITI
3480	836	3540		3660	3016	3720	3076	3136		3900	3256	3316		RESULT 19 Sequence 703, Applic Sequence 703, Applic Publication No. US20 GENERAL INFORMATION: APPLICANT: Xu, Jian APPLICANT: Dillon, APPLICANT: Harlock APPLICANT: Harlock APPLICANT: Greter, APPLICANT: Stolk, APPLICANT: Stolk, APPLICANT: Stolk, APPLICANT: Stolk, APPLICANT: BAPLICANT: BAPLICANT: APPLICANT: BAPLICANT: APPLICANT: Henders APPLICANT: Henders APPLICANT: Henders APPLICANT: Houghto, APPLICANT: Foy, Te APPLICANT: Foy, Te APPLICANT: Foy, Te APPLICANT: Foy, Te APPLICANT: Foy, Te APPLICANT: Foy, Te APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Fanger, APPLICANT: Wantana
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Pred. No. 0;
0; Mismatches
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 703
LENGTH: 2904
TYPE: DNA
                                                                                                                          64.48;
                                                                                                                                        Best Local Similarity 88.2
Matches 2560; Conservative
                                                                                   ; ORGANISM: Homo sapiens
US-10-012-896-703
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156 PCTOCATE CONTROL AND METHODS FOR THE THERAPY AND	۱ - ۱	Oy	
132 DOGGANITIONS NO NUMBER 1980 128 DOGGANITIONS NO NUMBER	Foy, Teresa Fanger, Gary R.	qa	81 TTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGCGTTCGGATGGGCAGCCTGGGGCTGT
139 TOTO ACCOUNTS CONTRICTED 139 TOTO ACCOUNTS ACCOU	AND METHODS FOR THE THERAPY PROSTATE CANCER	Qy Dh	o -
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189 CHICHELI	OF SEQ ID NOS: 982 E: FastSEQ for Windows Version 3.0	g qa	
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14.4 Score 2196.4; Dec. 2196.4	NISM: Homo sapiens	qa	61
100	64.4%; Score 2196.4; DB 9; Length 2904; 88.2%; Pred. No. 0;	oy O	TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
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GCTGGGGGCTGGGGCGTCCTCTCTCTCCCCCAGTCTCTAGGGCTGCCTGACTGGAGG
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                                                                  1741 CCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCATGCACTG
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
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88.2%; Pred. No. 0;
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020193296Al
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky, Yasir A.W.
Hepler, William T.
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Vedvick, Thomas (
Carter, Darrick
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Stolk, John A.
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	APPLICANT: Hepler, William	δ	1241
	ICANT: Hural, John ICANT: McNeill, Patricia D.	qq	781 TTCAGCAAGGGGGGTTGCCCAC
; APPI ; TITI	APPLICANT: Houghton, Raymond L IIILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	 Хо	
	E OF INVENTION: DIAGNOSIS OF PROSTATE CANCER REFERENCE: 210121.427024 BNU ADDITIONATION MINDED. 115.700.7100.650	qa	841 TCCTGCAGTGCGCCATCTCCCT
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U	or Wi	qa	901 TCGCCACTCGAGCAGTCTATIT
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GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.534C1

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARES: FASLSEQ for Windows Version 3.0

SEQ ID NO 703

LENGTH: 2904 1241 -----------64.4%; Score 2196.4; 88.2%; Pred. No. 0; Live 0; Mismatches Sequence 703, Application US/09822827 Patent No. US20020081680A1 Query Match 64.4 Best Local Similarity 88.2 Matches 2560; Conservative TYPE: DNA
CORGANISM: Homo sapiens
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Oy	2289	TGAGACACACCTAGAGAGAGTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA 2348
QQ	1861	GAGACACACTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA 192
Qy	2349	TCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGGGTTTCTAGG 2408
qa	1921	CTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG
QY	2409	4
QQ	1981	3AAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGAGTCCTG 204
Oy	2467	52
qq	2041	ggggcaacacacaagaaccaggrcccrcagcccacacacrgrcrrrrrgcrgarcca 210
Qy	2527	PACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCAGAGA 258
qq	2101	ccccrtraccrtrarcagardigaccrdriagrccrtcraraccarcacagaa 216
Qy	8	TTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCATTGCTAG
qq	2161	acaggcatttaaatatttaacttatttaatttaacaaagtagaagggaatccattgctag 222
Qy	2647	TTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCC 2
qq	2221	TITTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCC 228
Qy	2707	SATAGC
qq	2281	TGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCC 234
Qy	2767	CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAA 2826
qq	2341	CCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAA 240
ΟY	2827	TGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGGTTCAGGTCTCAAC 288
Dp	2401	GCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGCTTCAGGTCTCAAC 246
Qy	2887	GGCTTCCCTAACCACCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCC 2946
QQ	2461	GCTTCCCTAACCACCCTCTTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCC 252
Qy	2947	CTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAAC 300
QQ	2521	CTACTCTCTTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCAAC 258
Qy	3007	CCCACCAGCTCCACAAC
qa	2581	CCCTACCCCCAACTITCCCCACCACCTCCACAACCTGTTTGGAGCTACTGCAGGA 264
Qy	3067	CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 3126
qa	2641	cadaagcacaaagracagrirccaagccrrrcrccarcrccagcccccagagrararcr 270
Qy	3127	GIGCTIGGGGAATCTCACACAGAAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTC 3186
QQ	2701	TGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCTGCCTG
QY	3187	TTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
qa	2761	CTCTCAGGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
Qy	3247	TATGG
qa	2821	STGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAAATT
Qy	3307	AAGGCTITCITATAIGITIAAAAA 3330
qq	2881	SCTTTCTTATA

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1311 GGCATTGGTCCAGTGCTGGGCCTGGTCTGTCCCGCTCCTAGGCTCAGCCCAGTGACCAC 1370
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APPLICANT: Wantanbe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427627
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: PSESSEQ for Windows Version 3.0
LENGTH: 4894
                                                                                                                                                                                                                                                                                                                                                                                                                                     Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
                    Sequence 702, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:
                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Rales, Michael D.
APPLICANT: Rales, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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Hepler, William T.
Henderson, Robert A.
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McNeill, Patricia D.
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Best Local Similarity 80.1
Matches 2872; Conservative
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; ORGANISM: Homo sapiens
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	OLLO STATEMENT OF THE PROPERTY	1240	Qy
2750	GTCCACAGCAGGTCTCGTGCAGGAGGTACCTGTGGTTCCGCCTTCTCA	2691	QQ
1239		1240	Qy
2690	AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAAGGGTGCTGGGGAG	2631	qα
1239	1	1240	ΟŸ
2630	CAGACTACCTTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCT	2571	QQ
1239		1240	Qy
2570	GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACC	2511	qq
1239		1240	Qy
2510	ATAATCTCACCAGCGCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAG	2451	qq
1239		1240	Qy
2450	ATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAA	2391	qq
1239		1240	Οy
2390	TGACAGAAGGAAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAAGG	2331	qq
1239		1240	Οy
2330	TGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCC	2271	qq
1239		1240	Qy
2270	AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGTGGAAC	2211	qq
1239	0	1240	Qy
2210	ACACTCGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGGACTTCT	2151	qq
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-	 GATGAAGGTAAGGCCTTGGCAGCAGCAGAGGCTGGTGGGGAGCCGCCAC	2091	qq
1239	ATGA	1235	Οy
2090.	= 2	2031	qq
1234	SGGTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACAC	1175	٥y
2030		1971	qa
1174	AGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTC	1115	ογ
1970		1911	QQ
1114	CCGGGTGCACCAGCTGTGCTGCCGCATGCCCGGCACCCTGCGCCGGCTCTTC	1055	οy
1910	1 TCGCCCCACTGCTGTCCATGCCGGCCCGCTTGCCGAACCTGGGCGCCCTGCTT	1851	qq
1054	CGCCCCACTGCTGCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCT	366	٥y
1850		1791	QQ
994	CTGAGGAGGCAGGCTGGGGCCCCCAGGAGGCAGGAGGGCTGTCGGCCCCTTT	935	Οy
		1731	DÞ
934	GCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCACACTGCTGGT	7	QY

2329 CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT 2388	Qy
	QQ
2269 TTAACAGCTAGCTCCTAGTTGAGACACCCTAGAGAAGGGTTTTTGGGAGCTGAATAAA 2328	Qy
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CAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGG 226	ò
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3351 CCAGGTGCCCCATCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGC 3410	QQ
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3171 TAATGACACGTGGGTGYTGGAGGCAGTGGCCTCCTCCCACCTCCGCGCTCTGCGG 3230	qa
1609 TAATGGACACGIGGGIGCTGGAGGAGTGGCCTGCTCCCACCCGCCCTCTGCGG 1668	Qy
3111 CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGAGCCTAAGCCTGGAGCTCCCTTCC 3170	qa
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2931 CCCTGTGGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACACCTTCAGC 2990	qa
1369 CCCTGTGGCCGCTGCCGGTGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 1428	Qy
2871 GGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTT 2930	qa
1309 GGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTT 1368	ΟŊ
	q ₂
1249 GATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCAT:1308	δλ
	GANCOGCACCCTGGGGCTGTTCCTGCAGTGCCGCCATCTGCTGTTTTTCTTTTTTTT

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                    AGGTCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT
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FGATCCACCCCCTCTTACCTTATCAGGATGTGGCCTGTTGGTCC
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Db	1055 CCCGGGTGCACCAGCTGTGCCGCATGCCCGCACCTGGCCGGCTTTGTGGGT 111 1911 CCCCGGGTGCAGCTGTGCCGCATGCCCGCACCTGCGCGCGC	2051 1240 2151 1240	Db 2211 AAAGTGGAGCATGCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 2270 Qy 1240	QY 1240	1240	 Qy 1240
Xu, Jiangchun Dillon, Davin C Mitcham, Jennif Harlocker, Susa Jiang, Yuqiu	APPLICANT: Kalos, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Day, Craig H. APPLICANT: Vevick, Thomas S. APPLICANT: Carter, Darrick APPLICANT: Li, Samuel X. APPLICANT: West, West, M. APPLICANT: West, M.		; SEQ ID NO 702; SEQ for Windows Version 3.0; SEQ ID NO 702; LENGTH: 4894; TYPE: DNA; ORGANISM: Homo sapiens US-09-895-793-702	Duery Match 62.8%; Score 2142.8; DB 9; Length 4894; Best Local Similarity 80.1%; Pred. No. 0; Matches 2872; Conservative 1; Mismatches 3; Indels 708; Gaps 455 GGCATTGGTCCAGTGCTGGTCTGTGTCCCGCTCCTAGGCTCAGGCAGTGACCAC	DB 1311 GGCATTGGTCCAGTGCTGGTCTGTGTCCGGTTCTAGGCTCAGCCAGTGACCAC 1370 Qy 515 TGGCGTGGACGCTATGGCCGCCGCCGCCTTCATCATCGGCATGTCTTGGGCATCCTG Qy 517 TGGCGTGGACGTATGGCCGCCGCCGCCCTTCATCTGGCATCCTTGGGCATCCTG 574 Db 1371 TGGCGTGGACGTATGGCCGCCGCGCGCTTCATCTGGCCTGTCCTTGGCATCCTG 1430 Qy 575 CTGAGCCTTTTCATCCCAAGGGCGCGCTGCTAGCAGGCTGTGCCCGGATCC 634 1431 CTGAGCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	0y 755 CGCCAGGCCTACTCTGTCTATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 814

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RESULT 27
US-09-895-814-702
Sequence 702, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
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APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.

	1240 1239 2331 TGACAGAAGGAAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGTTAAGGCTGG 2390	1240	ATAATCTCACCAGGGCTTCCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 251	1240 1239 2571 CAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGG 2630	AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGGCTG 269	2751 TGCTCCGACCCTTCCCTGCAGGCTCTGTCTGATGCCCTCTCCCTCTGGAGGCGTTCG 1248 1249 GATGGGCAGCCTGGGGCTCTGTCTGATGGCCCCTCTCCTCTGGTCAT 1308 1111111111111111111111111111111111
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APPLICANT: Stolk, John A. APPLICANT: Day, Craig H. APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Darrick APPLICANT: Li, Samuel X. APPLICANT: Li, Samuel X. APPLICANT: Wang, Aijun APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C26 CURRENT FILING DATE: 2001-06-29 CURRENT FILING DATE: 2001-06-29 NUMBER OF SEQ ID NOS: 990 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 702 SEQ ID NO 702 SEQ ID NO 702 SEQ ID NO 891 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA	Query Match 62.8%; Score 2142.8; DB 9; Length 4894; Best Local Similarity 80.1%; Pred. No. 0; Matches 2872; Conservative 1; Mismatches 3; Indels 708; Gaps 2;	455 GGCATIGGTCCAGIGCTGGGCCTGGTCTCCGCCTCCTAGGCTCAGGCAGTGACCACTCACT	Oy 515 TGGCGTGGACCCTGCCGCCGCCGCCCTTCATCTGGGCATCCTGGGCATCCTG 574 111111111111111111111111111111111111	Oy 635 AGGCCCCTGGAGCTGCCTCTTCTTGGGGGTGGGGGCTGGACTTCTGTGGCGG 694	Qy 695 GTGTGCTTCACTGGAGGCCCTGCTCTCACCTCTTCCGGGACCCCGGACCACTGT 754 Db 1551 GTGTGTTCACTCCACTGGAGGCCCTGCTCTTCCGGGACCCGGACCACTGT 1610 Qy 755 CGCCAGGCCTACTCTCTACTCTCTACTCTTCGGGGCTGCCTCGGGCTACCTC 814 Db 1611 CGCCAGGCCTACTCTTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGGCTACCTC 1670	0y 815 CTGCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTGGCACCCAGGAGGA 0p 1671 CTGCTGCCATTGACTGGGACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGA 0y 875 TGCCTCTTGGCCTGCATCATCTCCTCACCTGGTAGCACCACTGCTGGTG 0y 875 TGCCTCTTTGGCCTCACCTCACCTTCCTCACCTGGTAGCAGCACACTGCTGGTG 0y 111111111111111111111111111111111111

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APPL	APPLICANT: Wang, Aijun APPLICANT: Skeiky, Yasir A.W.	qq	2091 G
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ογ	1240	13	239
Db	2151	ACACTCGGGGCTGTGTGTGGGGCTGGTGCCTCCATCCTGGCCCCGACTTCTCTGTCAGG 2	210
Οy	1240	7	239
QQ	2211	AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT 22	270
Qy	1240		239
Db	2271	TGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCCAGTT 23	330
Qy	1240	7.	239
QQ	2331	TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGGTTAAGGCTGG 2:	390
Οy	1240	1	239
qq	2391	ATTTCAGATCTGCCTGGTTCCAGCCGCAGTGCCCTCTGCTCCCCCCAACGACTTTCCAA 20	450
Qγ	1240		239
Db	2451	ATAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 2	510
Οy	1240		239
QQ	2511	GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTT 2	570
Qy	1240	15.	239
qq	2571	CAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGG 20	630
Qy	1240		239
qq	2631	AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGGCTG 26	069
Qy	1240	7	239
qq	2691	GTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGAC 2	750
Qγ	1240	SCGTTCG 1	248
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Qγ	1249	ATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCCATCTCCCTGGTCTTCTCTCTTGGTCAT 1	308
Db	2811	GGGCAGCCTGGGGCTGTTCCTGCAGTGCCCATCTCCCTGGTCTTCTCTCTGGTCAT 2	870
Qy	1309	SACCGGCTGCTGCAGCGATTCGGCACTCGAGCTCTATTTGGCCAGTGTGGCCAGCTTT 1	368
qq	2871	ACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCTTT 2	930
Qy	1369	CCTGTGGCTGCCGGTGCCACATGCCTACAGTGTGGCCGTGGTGACCTTCAGC 1	428
qq	2931	CTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 2	066
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QQ	2991	CCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCT 3	020
Qy	1489	CACTGGAGGTGCTAG 1	548
qq	3051	CCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAG 3	110
Qy Db	1549	CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCTTCCC 16	608
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2089 CTGAGGTGCCTAGCTGGGGGCTTGGGGTTCCTCTCTCTCT	qq	.CrGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTG 36	7716
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11	3 8	CIGAGGIGCGTAGCTGCACAGGTGGGGGCGTGCCTCTCTCTCTCTCCTCCCCAGTCTC 371	3227
11	S	TAGGGCTECCTGATTGGAGGCCTTCCAAGGGCGTTTCAGTCTGGACTTATACAGGGAGGC 220	4791
200 CARGAGGATCATGCAGGGATTTCGAGGTGGATTACCCAGGG 2268 December 2	a (rasscriscrisaciesasscrifccaasscriftcasrcissacriatacasscassc 377	3287
239 TAACAGCTAGCTCTAGTTGAGAGGGTTTTGGGGGCTGAGGG 3830 SESUIT 29 US - 05 - 780 - 69 Sequence 70 Sequence 7	<u> </u>	CAGAAGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGG 22	4851
239 TTANCAGCTACTACTACACACACACAGAGGGTTTTTGGGAGCTGATAAA 2328 381 TTANCAGCTACACACACACACACAGAGGGTTTTTGGGAGCTGATAAA 3390 232 CTCAGTCACCTGGTTTCCATCTTAAGACACACTAGAGGGTTTTTGGGAGCTGATAAA 3890 232 CTCAGTCACCTGGTTTCCATCTTAAGCCCCTTAACTGGAGTTTTAATGTAGCT 3950 2389 CTCAGTCACTGGTTTCCATCTCAAGCCCCTTAACTGGAGTTTAATGTAGCT 3950 2389 CTCAGTCACTGGTTTCTAAGACACACACACACACACACAC		CHARACTECCATGCCALGCACTGCGGGGGCTCTCTGCAGGTGGATTACCCCAGGCTCAGGG 38	
2329 CTGGTCACTGGTTTCCCATCTTAGGCCCTTAACCTGGTTGTTTAATGTACT 238 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	<u> </u>	*TAACAGCTAGGCTCCTAGTTCAGACACCCTAGAAAGGTTTTTTGGGAGCTGAATAAA 232 	RESULT 29 US-09-780-669-702
2389 CTGGGTGGTTTCCGTCTTAACCCGTGGGGTTGGTTGAGTGGT 2388 2389 CTGGCGGGGTTTCCCATCTCTAAGCCCCTTAACCGGGGTTGGTT	ò	COORDINATE STEED TO THE CONTROL OF CONTROL	; sequence /UZ, Application ; Patent No. US20020051977A
2389 CTGCAGGGGGTTCTCGGGGTGAACCCCCCAGGGGTTTGACCTTTAATGTGGTGTT 2446 2389 CTGCAGGGGGTTCTCGGGGATGAACCCCCCAGGGGTTTGACCTTGTGT 2446 [5 8	CICAGELACCIGGITICCCATCICTAAGCCCCTTAACCIGCACCTTCGTTTAATGTACCT 238	; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchu
	ì ò	CTTGCATGGCACTTRCTAGGAAACAACTTCTAACCTGCAGCTTCGTTAATGTTGCT 395	; APPLICANT: Dillon, Davi ; APPLICANT: Mitcham, Jen
2447 TTTGTAGGGAAGAGTCCTGAGGGCAACAAGAACAGGGTCCCCTCAGCCACGC 2507 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	. q <u>a</u>	CTTGCATGGGAGTTTCTAGGAATGAAAAAAAAAAAAAAA	; APPLICANT: Harlocker, Si ; APPLICANT: Jiang, Yuqui
	ογ	TTGTAGGGGAAGAGTCCTGAGGGGAACACACAAGAACTAGGTCCCTCACACACA	, APPLICANT: Henderson, K
2507 ACTGTCTTTTGCTGATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTC 2566	qa	TTGTAGGGGAAGACCCGAGGGCAACACAAGAACCAGGTCCCCTCAGCCCACAGA	APPLICANT: Fanger, Gary APPLICANT: Retter, Marc
	QY	ACTGTCTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCC 256	APPLICANT: Day, Craig H
2567 TTCTGTTGCCATCACAGACACAGGCATTTAAATATTTAACTTATTTAACAAAGT 2626	Ωp	ACTGTCTTTTCCTGATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCC	; APPLICANT: Carter, Darr ; APPLICANT: Li, Samuel
4131 TTCTGTTGCCACCACAGGGATTTAAATTTTATTTTTTTTT	Ωy	TTCTGTTGCCATCACAGAGACACGCGTTTAAATATTTAACTTATTTAACAAAGT 2	; APPLICANT: Wang, Aijun ; APPLICANT: Skeiky, Yasi.
2627 AGAAGGAATCCATTGCTAGCTTTTCTGTGTGGTGTCTAATATTTGGGTAGGGTGGGGG 2686	Op	TTCTGTTGCCATCACAGAGACACAGGCATTAAATATTAACTTATTATTAACAAAGT	; APPLICANT: Hepler, Will: APPLICANT: Hural, John
2687 ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCT 2746	Qy Dp	AGAAGGGAATCCATTGCTAGCTTTTCTGTGTGTGTCTAATATTTGGGTAGGTGGGGG 26	; APPLICANT: McNeill, Pat; ; APPLICANT: Houghton, Ra; ; TITLE OF INVENTION: COM
	٥y	ATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAAGAATCT 27	; FILE REFERENCE: 210121.
	q		CURRENT FILING DATE: 2001 ; NUMBER OF SEQ ID NOS: 943

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TCTGGCCCCCCAAATGCCTAACCCAGGACCTTGGAAATTCTACTCA 2806
                                                                                  TCTCAACGGCTTCCCTAACCACCCTCTTCTCTTGGCCCAGCCTGGT 2926
                                                                                                                            ACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCA 2986
                                                                                                                                                                                                                TGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATC 3106
                                                                                                                                                                                    TATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCC 3166
                                                                                                                                                                                                                                                                       GGAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATG 3226
                                                      CCCCAACTTTCCCCTACCCCCAACTTTCCCCACCAGCTCCACAACCC
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Inifer L.
Susan L.
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os :	FTWARE: FastSEQ for Windows Version 3.0 .	qa	2211 AAAGTGG
	SEQ ID NO 702 LENGTH 4894	Qy	1240
	IPE: DNA ROANISM: HOMO Sapiens	qa	2271 TGCGGTT
60-sn	7/80-669-7/02	Qy	1240
Gue	62.8%; Score 2142.8; DB 10; Length 4894; 80.1%; Pred. No. 0;	QC	2331 TGACAGA
Mat	2872; Conservative 1; Mismatches 3; Indels 708; Gaps	Οy	1240
δo i	GCCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCCCTCCTAGGCTCAGTGACCAC 514	qq	2391 ATTTCAG
ga ,	GGCATTGGTCCAGTGCTGGGCCTGGTCTCCCGCCCCTAGGCTCAGCCAC	Qy	1240
oy G	515 TGGCGTGGACCCTAFGGCCGCCGCCGGCCCTTCAFCTGGGCACCCTTGGGCATCCTG 1311 TILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	qq	2451 ATAATCT
n d	100C61900C17110CCCCCCCCC11CC11CC11CC11CC11CC11C	Qy	1240
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· 6		qa	2571 CAGACTA
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QQ		qa	2631 AAGAACC
ò	755 CGCCAGGCCTACTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 814	δλ	1240
7 원		qa	2691 GTCCACA
è	CTGCCTGCCATTGACTGGGACACAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAG	δλ	1240
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3 8	というできましましましました。	δλ	1249 GATGGGC
à á		qa	2811 GATGGGG
3 8	GCTGAGGAGGCAGCGCCCCACGAGCAGCAGAGGGCTGTCGCCCCCCCC	οy	1309 GGACCGG
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č		δλ	1369 CCCTGTG
; a	TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGCCGGAACCTGGGCGCCCTGCTT	qa	2931 cccrerc
ò	1055 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCTTGCGCGCTCTTCGTGGCT 1114	δλ	1429 CGCCCTC
· 6	CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCCTGCGCCCGGCTCTTCGTGGCT	<u>අ</u>	
οy	1115 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 1174	Oy.	
qa	1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 2030	g .	
ò	1175 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAAGGCCCGGAGACACTAT 1234	δλ	
7 A	1 GAGGGCTGTACCAGGGCTGCCCAGAGCTGAGCCGGGCACGAGGCCCGGAGACAGTAT	qa	
οy	1235 GATGA 1239	oy i	1609 TAATGG
qq	11111 2091 GATGAGGTAAGGCCTTGGCAGCCAGGAGGCTGGTGGGGAGCCGCCCCACCAGAGACG 2150	α ·	
δλ	1240 1239	à á	1989 GCCCTCT
QO	2151 ACACTCGGGGCTGTGTCTGGGCTGCTCTCCATCCTGGCCCCCGACTTCTCTGTCAGG 2210	3 8	
Qy	1240 1239	λ α	
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	2211	AGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG
	(7	1239
	2271	TGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTT 2330
	1240	1239
	2331	TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGG 2390
	1240	1239
	2391	ATTICAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA 2450
	1240	1239
	2451	ATAATCTCACCAGGGCCTTCCAGCTCAGGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 2510
	1240	1239
	2511	GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCCAGGAAACCTT 2570
	1240	1239
	2571	CAGACTACCTTCCTCTGCCTTCAGCAAGGGGGGTTGCCCACATTCTCTGAGGGTCAGTGG 2630
	1240	1239
	2631	AAGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGGCTG 2690
	1240	1239
	2691	GTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGAC 2750
	1240	AGGCGTTCG 1248
•	2751	TGCTCCGACCCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTCG 2810
	1249	449 GAIGGGCAGCCTGGGGCTGTTCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCAT 1308
		136
•	87	GACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCTTT 293
	1369	CCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 1428
	1429	CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCT 1488
_	1489	AGAAGCAGGTGTTCCTGCCCAAATAC
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0	3111	AGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 317)
~ 0	1609	TAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGGGTTGGGG 1668 [1618]
_	99	72
0	3231	SCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCCACCGAGGCCAGGGT 329
~ 0	1729 3291	GGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTC 1788

CTGTAAGTGAGCAATCAGAGTATAA 3286 CONTRACTOR rcregecactgreetregecarees 574 TAGCAGGGCTGCTGTGCCCGGATCCC 634 TGGGGCTGCTGGACTTCTGTGGCCAG 694 CCCTCTTCTTGGCCCAGCCTGGT 2926 ACTGGGCTGATGAAGGCACTGCCCA 2986 GCGGTTTCCCAAGCCTTTGTCCATC 3106 CCACACAGAAACTCAGGAGCACCCCC 3166 GGTTTAAGTGCCGTTTGCAATAATG 3226 5; ACTITCCCCACCAGCTCCACAACCC 3046 SGCTCCTAGGCTCAGCCAGTGACCAC 514 GACCTCTTCCGGGACCCGGACCACTGT 754 3; Indels 708; Gaps DB 10; Length 4894; FOR THE THERAPY AND NCER TGTTTAAAAA 3330 ||||||||||||| TGTTTAAAAA 4894

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RESULT 31
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                                          2927 TCCCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCA
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       CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT
                                                                              CTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATG--ACTTA
                                                                                                                 TTTGTAGGGGAAGAGTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGC
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                                  TTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAA
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5172 GGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCTA
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                                       4851 TGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTTTAAAAA 4894
COMPOSITIONS AND METHODS FOR 1
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APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasiar A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Fonger, Gary R.
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCE:
FILE REFERENCE: 210121, 427227
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT PILING DATE: 2001-12-10
NUMBER OF SEO ID NOS: 1011
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Pred. No. 0;
0; Mismatches
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                                                                                                                                             Sequence 705, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Harlocker, Susan L.
Jiang, Yuqiu
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                    Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer
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Best Local Similarity 98.7
Matches 1841; Conservative
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12 ATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCTGTTATGGGCTCCATTGTCCAG 30 TCAGCCAGTCTGTCACTGCCTATATGGTGTTGTCCAGGCCTGGTTTATGGGCTCCATTGTCCAGT 1	1950 CTTCCAGCATTGGGGTGAAGGCCTGCCTCACTGGGTCCCAGCTCCCGGCTCCTGTTA	2070 CTGCTGCCACCCTGTGCTGAGGTGCGTAGCTGCACAGCTGGGGGCTGGGGCTCCCT	190 TGGACTTATACAGGGGCCAGAAGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGT	310 TTTTGGGAGCTGAATAAACTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGC	0 TTTGAACATATGACTTATTTGTAGGGAAGGGTCCTGAGGGGCAACACACACACA	32 GGTCCCCCCCCCCCCCCCCCCCCCCCCCCCTTTTTTTTT	2608 CTTATTTATTTAACAAAGGAATCCATTGCTAGCTTTCTGTGTTGGTGTCTAA 1111111111111111111111111111111111	28 CTGATCATTGCCAGAATCTTCTCCTGGGGTCTGGCCCCCCAAATGCCTAACCGAGG 1111111111111111111111111111111
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2908 TCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGG 2967
                       6612 CTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCAACTTTCCCCTACCCCCAACTTC 6671
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TLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
LE REFERENCE: 210121.534C2
RRENT APPLICATION WHERE: US/09/895,793
RRENT FILING DATE: 2001-06-29
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FTWARE: FastSEQ for Windows Version 3.0
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Wang, Aijun.
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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lication No. US20020192763A1
ERAL INFORMATION:
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Salos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Rotter, Marc W.
APPLICANT: Rotter, John A.
APPLICANT: Caig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
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RGANISM: Homo sapiens
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Query Match 53.2%; Score 1815.8; DB 9; Length 6976; Best Local Similarity 98.7%; Pred. No. 0; Matches 1841: Conservative 0: Mismatches	TEGCCTCCTCTACCACGGGGAAAGAGGGGTGTTCCTGCCCAAATACCGGG IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1530 GGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCCTTCCTGCCAGGCCCTA 1:	590 AGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCAC 10	1650 CTCCACCGGGCTCTGGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGT7 17	1710 AGCCCACCGAGGCCAGGGTGCTTCCGGGGCGCATCTGCCTGGACCTCGCCATCCTGG 17	1770 ATAGTGCCTTCCTGCTGTCCCAGTGGCCCCATCCTGTTATGGGCTCCATTGTCGGCTCATTGTCAGCTTCTGTTTTTGTGGCTCCATTGTCAGCTCCAGC 5:	1830 TCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTT 1:	ACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAA 1	1950 CTTCCAGCACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGGCTCCTGTTA 2 1 1 1 1 1 1 1 1 1	2010 GCCCCATGGGGCTGCCGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCT 2 	6 70	2130 CTCCTCTCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTC 2	2190 TGGACTTATACAGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGT 2	2250 GGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGG 2 	2310 TITITGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGC 2 111111111111111111111111111111111111	2370 AGCTICGITTAATGIAGCICTIGCAIGGAGITTCIAGGAIGAAACACTCCTCCAIGGGA 2 	2430 TTTGAACATATGACTTATTTGTAGGGAAGAGTCCTGAGGGGCAACACACAAGAACCA 2
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2727 2787 6431 2907 2967 6611 TACCCCCAACTITCCCCTACCCCCAACTITC 3027 AAGGGAGGTCTTATCTCTGGGGGGGGTTTA 3207 TATTTAGCGGGGGGAATATTTTATACTGTAA 3267 TIGCTGATCCACCCCCTTTACCA 2547 6371 CCATTGCTAGCTTTTCTGTGTTGGTGTCTAA 2667 ATCACAGAGACACAGGCATTTAAATATTTAA 2607 CCATTGCTAGCTTTTCTGTGTTGGTGTCTAA AGGTCTCAACGGCTTCCCTAACCACCCCTCT TCCACTCCCTCTACTCTCTAGGACTGGG AGGICTCAACGGCTTCCCTAACCACCCCTCT TCCACTCCCCTCTACTCTCTAGGACTGGG

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               APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Wedvick Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foughton, Raymond L.
APPLICANT: Fanger, Taresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: UMBER: US/09/895,814
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT APPLICATION NUMBER: 2001.06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 705
                                                                                                                                                                                                                                                                                                                                                     Length 6976;
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Pred. No. 0;
0; Mismatches
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98.7%;
         Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
Li, Samuel X.
Wang, Aljun
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Matches 1841; Conservative
John A.
                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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                                                                                           GAAACTCAGGAGCACCCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTA
                               AGTGCCGTTTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAA
                                              DB 10; Length 6976;
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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
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                                                                                                                                                                                                                                                                 Sequence 705, Application US/09759143
; Patent No. US20020022248a1
; GENERAL INFORMATION:
    APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan·L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Vedvick, Thomas
Carter, Darrick
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; ORGANISM: Homo sapiens
US-09-759-143-705
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Matches 1841; Conserv
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CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 705
                                                                                                                                                                                                                                                                                                                                                                        Sequence 705, Application US/09780669 Patent No. US20020051977A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Fetter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aljun
Skeiky, Yasir A.W.
Hepler, William
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Dillon, Davin C.
Mitcham, Jennifer L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hural, John
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ORGANISM: Homo sapiens
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Score 1815.8;
Pred. No. 0;
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Query Match 53.2
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APPLICANT: Xu, Jangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR 1
TITLE OF INVENTION: DIAGNOSIS OF PROSIATE CANCER
TITLE REPERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
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                                                                                            Length
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                                                                                         Score 1815.8;
Pred. No. 0;
0; Mismatches
               Version 3.0
                                                                                         Query Match 53.2%;
Best Local Similarity 98.7%;
Matches 1841; Conservative
NOS: 982
2 for Windows
                                                            sapiens
  SEQ ID NO
FastSEQ 1
                                                        ; ORGANISM: Homo US-09-822-827-705
                      SEQ ID NO 705
LENGTH: 6976
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Sequence 851, Application US/10012896 Publication No. US20020183251A1 GENERAL INFORMATION:

US-10-012-896-851

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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Madaleline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION UNBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.3%; Score 794.6; DB 9; Best Local Similarity 99.5%; Pred. No. 4.5e-142; Matches 797; Conservative 0; Mismatches 4;
                                                                                                                                                 Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McWeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                Jiang, Yuqiu
Ralos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                        Li, Samuel X.
                                                                                                                                                                                                                                                       Foy, Teresa
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US-10-012-896-851
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LENGTH: 1203
TYPE: DNA
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859 GGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGC	QY 979 GTCGGCCCCTCCTTGTCGCCCCACTGCTGCTCCATGCCGGCCCTTGGCTTTCCGGAA 1038 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 1099 CCGGCTCTTCGTGGCTGAGCTGAGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTA 1158 1122 CCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTA 1181 QY 1159 CACGGATTCGTGGCGAGGG 1179 Dh 1182 CACGGATTCGTCGTGGCAGGG 1179	. 52 a-	C. fee	APPLICANT: VedVick, Thomas S. APPLICANT: Carter, Darrick APPLICANT: Li, Samuel X. APPLICANT: Wang, Aijun APPLICANT: Skeiky, Yasir A.W. APPLICANT: Hepler, William T. APPLICANT: Henderson, Robert A. APPLICANT: Hund. John	; APPLICANT: MCNELIL, PATITICIA D. ; APPLICANT: Houghton, Raymond, L. ; APPLICANT: Vinals de Bassols, Carlota ; APPLICANT: Foy, Teresa ; APPLICANT: Foy Teresa ; APPLICANT: Fanger, Gary R. ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER ; FILE REFERENCE: 210121.534C2 ; CURRENT APPLICATION NUMBER: US/09/895,793	; CURRENT FILING DATE: 2001-06-29 ; NUMBER OF SEQ ID NOS: 982 ; SOFTWARR: FastSEQ for Windows Version 3.0 ; SEQ ID NO 851 ; LENGTH: 1203 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-895-793-851	Query Match 23.3%; Score 794.6; DB 9; Length 1203; Best Local Similarity 99.5%; Pred. No. 4.5e-142; Matches 797; Conservative 0; Mismatches 4; Indels 0; Gaps 0; QY 379 GGCCGCAGGCATCACCTATGTCCCGCCTCTGCTGCAAGTGGGGGTAGAGGAGAAGTT 438 IIIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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                                                                                    APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: DAGMOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION UNDHER: US/09/895,814
CURRENT APPLICATION UNDHER: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: EstsEQ for Windows Version 3.0
SEQ ID NO 851
LENGTH: 1203
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                                                                                                                                                                                                                                                                                              Query Match 23.3%; Score 794.6; DB 9; Best Local Similarity 99.5%; Pred. No. 4.5e-142; Matches 797; Conservative 0; Mismatches 4;
                                        Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
               Hural, John
McNeill, Patricia D.
Henderson, Robert A.
                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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                          APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Skeiky, Yasin a.w.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C23

CURRENT APPLICATION NUMBER: US/09/759,143

CURRENT FILING DATE: 2001-01-12

NUMBER OF SEQ ID NOS: 934

SOFTWARE: FastSEQ for """

LENGTH.
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Pred. No. 4.5e-142;
0; Mismatches 4;
                                                 1159 CACGGATTTCGTGGGCGAGGG 1179
                                                                                 1182 CACGGATTTCGTGGCCGAGTG 1202
                                                                                                                                                                   ; Sequence 851, Application US/09759143; Patent No. US20020022248A1; GENERAL INFORMATION:
                                                                                                                                                                                                                      Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                                                                                                                                                                                                          Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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99.5%;
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Retter, Marc W.
Stolk, John A.
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Matches 797, Conservative
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US-09-759-143-851
                                                                                                                                     RESULT 40
US-09-759-143-851
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                GGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGGTAGAGAAGTT
                                                               CATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGG
                                                                                                                             CTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACT
                                                                                                                                                                                          Sequence 851, Application US/09822827

Patent No. US/0020081680A1

GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILLE OF INVENTION: DIAGNOSIS OF PROSITIE CANCER
FILE REPERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT APPLICATION NUMBER: US/09/822,827

CURRENT FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 982

SOFTWARE: FastSEO for Windows Version 3.0
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US-09-822-827-851.
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     762 GGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGG 821
                                    799 CTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCT
                                                     859 GGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGC
                                                                                                                   919 AGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCT
                                                                                                                                                                                APPLICANT: HALCHARY, SUSAN L.
APPLICANT: HALCHARY, SUSAN L.
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427024
CURRENT FILING DAFE: 2001-02-09
NUMBER: 2001-02-09
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Pred. No. 4.5e-142;
); Mismatches 4; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 851, Application US/09780669; Patent No. US20020051977al; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Senafer L.
; APPLICANT: Jiang, Yuqui
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Relos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Best Local Similarity 99.5
Matches 797; Conservative
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US-09-780-669-851
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Best Local Simi
Matches 745;
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                                                                                                                                                                LENGTH: 789
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                                                                                                                                                    379 GGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCAAGTGGGGGTAGAGGAGAAGTT 438 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111
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                                                                                                                                                                                                                                            439 CATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGG
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                                                                                                                   Gaps
                                                                       DB 10; Length 1203;
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                                                                                                                 Indels
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                                                                Score 794.6; DB 10
Pred. No. 4.5e-142;
0; Mismatches 4;
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                                                                   23.3%;
99.5%;
                                                            Query Match 23.33
Best Local Similarity 99.55
Matches 797; Conservative
; ORGANISM: Homo sapiens
US-09-822-827-851
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US-09-232-880-10
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1461 AGAICCTGCCCTACACACTGGCCTCCTCTACCACGGGAGAAGCAGGTGTTCCTGCCCA 1520
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                                                                                                                                                                                                                                                                                                                                                 Length 789;
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR FILE REFERENCE: 210121.428056 CURRENT APPLICATION NUMBER: US/09/232,880 CURRENT FILING DATE: 1999-01-15 NUMBER OF SEQ ID NOS: 338 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                          19.7%; Score 673.4; DB 9;
94.2%; Pred. No. 4.8e-119;
vative 0; Mismatches 40;
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                                                                                                                                                                                                                                                          LOCATION: (1)...(789)
OTHER INFORMATION: n = A,T,C
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (1)...(789)
                                                                                                                                                                                      ORGANISM: Homo sapien FEATURE:
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2058

777

657

539

1400

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1999 CGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGCCGCCAGTTTCTGTTGCTGCTGCCAAAGT 2058
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                                      1641 IGCICCCACCICCACCCGCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGG 1700
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                                                                                                                                  480 TTGTCCAGCTCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGG
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
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Vinals de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Hepler, William T.
Henderson, Robert A.
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McNeill, Patricia D.
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Kalos, Michael D.
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Li, Samuel X.
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LOCATION: 9, 380, 451, 565, 582, 716, 718, 758, 762, 765, 768, 771,
LOCATION: 779, 783
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.7%; Score 673.4; DB 9; Length 789; 94.2%; Pred. No. 4.8e-119; tive 0; Mismatches 40; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                    ; Sequence 10, Application US/10012896
; Publication No. US20020183251A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: n = A,T,C or G
US-10-012-896-10
                                                                                                                                                                          APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu APPLICANT: Alos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
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Hural, John
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Hepler, William T.
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      Li, Samuel X.
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ORGANISM: Homo sapiens
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                                                                                                                                                            GENERAL INFORMATION:
                                                                                                      US-10-012-896-10
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LENGTH: 789
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                                                                                                                             19.7%; Score 673.4; DB 9; 94.2%; Pred. No. 4.8e-119; tive 0; Mismatches 40;
                                                              : NAME/KEY: misc_feature
: LCCATION: (1)...(789)
: OTHER INFORMATION: n = A,T,C or G
US-09-895-793-10
                                                                                                                           Query Match
Best Local Similarity 94.28
Matches 745; Conservative
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                       TYPE: DNA
ORGANISM: Homo sapien
SEQ ID NO 10
LENGTH: 789
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Search completed: June 9, 2003, 22:23:03 Job time : 609 secs

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(without alignments)
10628.880 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                        OM nucleic - protein search, using frame_plus_n2p model
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                                                                                                                                                                                                                                                                                                                                                                    908470 segs, 133250620 residues
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09759143/runat_05062003_111318_23032/app_query.fasta_1.3591
-Q=/cgn2_1/USPTO_spool/US09759143/runat_05062003_111318_23032/app_query.fasta_1.3591
-DB=A_Geneseq_101002 -OFWT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LIOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45
-MODE=LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USFR=US09759413_GCN_1_1119_grunat_05062003_111318_23032 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-FGAPORT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1981. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982 A_Geneseq_101002:* Database :

Command line parameters:

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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
                                                                                                  /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

98WO-US03492.

25-FEB-1998;

WO9837093-A2 27-AUG-1998

					SUMMARIES	
ິດ 🗂	Score	* Query Match	Length	DB	GI	scription
	361	1 9		۲.	AAW7186	Amin
7	2861		553	19	6	ostate
ĸ	36	4.		21	352	in encoded
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2	98	4		22	976	n prostate
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11	m	4		23	1757	mast cell r
12	m	4		23	190	ate cancer-a
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14	m	4.		23	32	PROST 0
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19	677	9		23	9	edoxin-ubi
20	522	m		23	57	Human mast cell re
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24	14		37	22	36	gene 11
2.5		Ċ	37	23	110	albumin
26	403	-	40	22	990	n prostate
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28	ന	21.9	40	23	36	-P501S-E2
29	12	0	25	20	506	in
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ALIGNMENTS

Prostate; cancer; tumour; vaccine; immunogen; clone Amino acid encoded by prostate tumour clone L1-12. AAW71869 standard; Protein; 553 AA. (first entry) Homo sapiens 06-JAN-1999 AAW71869; RESULT 1 AAW71869

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XX

YEB-1998; 98US-0020956.

PR 25-FEB-1997; 97US-0806099.

PR 25-FEB-1997; 97US-0806099.

PR 01-AUG-1997; 97US-0904804.

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YOUNG CORL.) CORIXA CORP.

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WPI; 1998-609886/51.

PR N-PSDB; AAV61201.

XX

POlypeptides comprising immunogenic portions of prostate proteins.

PT Polypeptides comprising immunogenic portion of prostate cancer.

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POLYPEPTIAN OF THE TREATMENT Of PROSTATE CANCER.

XX

POLYPEPTIAN OF THE TREATMENT OF PROSTATE CANCER.

XX

Example 1; Page 82-84; 130pp; English.

CC

The present sequence is an immunogenic portion of a prostate tumour.

CC

Protein. The immunogen, or the DNA encoding it, can be used as a concent of prostate cancer. The immunogen was concented from a prostate tumour cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA

XX

Sequence 553 AA;
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 SQ Sequence
 553 AA;

 Alignment Scores:
 2.89e-208
 Length:
 553

 Pred. No.:
 2861.00
 Matches:
 553

 Score:
 100.00%
 Conservative:
 0

 Best Local Similarity:
 100.00%
 Mismatches:
 0

 Ouery Match:
 19
 Gaps:
 0

US-09-759-143-110 (1-3410) x AAW71869 (1-553)

Qy	284	ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG	343
QQ	Т		20
Qy	344		403
Dp	21	ValAsnLeuLeuThrPheGlyLeuGluVaļCysLeuAlaAlaGlyIleThrTyrValPro	4 0
Qy	404		463
Ωp	41	ProLeuLeuCluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	09
Qy	464		523
qq	61	ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80
Qy	524	7.1	583
οp	81	ArgTyrGlyArgArgArgProPheIleTrpAjaLeuSerLeuGlyIleLeuLeuSerLeu	100
Qy	584	to.	643
qq	101	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	120
٥y	644	c) -	703
Dp	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 1	140
Qy	704	. ن	763
Db	141	ThrproteuglualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla	160
Qy	764		823
QQ	161	TyrservalTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 1	180
Qy	824	824 ATTGACTGGGACACCAGTGCCCTGGCCCCGTACCTGGGCACCCAGGAGGAGTGCCTCTTT 8	883

200	943	1003	1063 260	1123 280	1183	1243 320	1303	1363 360	1423 380	1483	1543	1603	1663	1723	1783 500	1843	1903	
	4 GGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACCACTGCTGGTGGCTGAGAG	4 GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGCTGTCGGCCCCTCCTTGTCGCCCCAC	4 TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG	4 CACCAGCTGTGCTGCCGCATGCCCGCACCCTGCGCCCGGCTCTTCGTGGCTGAGCTGTGC	4 AGCTGGATGCCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTG	4 TACCAGGGGGGGGCGGAGAGGGGGGCACGAGGCCCGGAGACACTATGATGAGGCGGCGCGGAGACGAGGACGAGGACGAGGAGGGGGGG	4 GTTCGGATGGGCAGCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGT	4 GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGTGTGGCAGTGTGGCAGTGTGGCAGTGTGGAGAGAGA	4 GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT	4 TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC	4 TCCCTCTACCACCGGGACAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGT 	4 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC	4 TTCCCTAATGGACACGTGGGTGGAGGCAGTGGCCTGCTCCCACCTCCACCTCGCGCTC	4 TGCGGGGCCTCTGCTGTGATGTCTCCGTACGTGTGGTGGGTG	4 AGGGTGGTTCCGGGCCGGGCGATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG	4 CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC	4 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGCCCATTTACTTTGCTACACAGGCTGTGGTCTGGCCATTTACTTTGCTACACAGGCTGTGGTCTGGCCATTTACTTTGCTACACAGGCTGTGGTGTGTGT	4 GTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGGG 1942
18	888	94	100	106	112	30.	124	. 130	136.	142,	148,	154	160	1664	1724	1784	1844	1904
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                                                                                                                                                                                                                                                                                                                                                                  This sequence is encoded by a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting appostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as this protein sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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                                     AAW69385 standard; Protein; 553 AA.
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Best Local Similarity:
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25-FEB-1997;
01-AUG-1997;
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Pred. No.:
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             61 ProvalLeuGlyLeuValCysValProLeuEdlySerAlaSerAspHisTrpArgGly
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CCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCCAGTGACCACTGGCGTGGA
                                                       524 CGCTATGGCCGCCGCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTC
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Sequence

421 AlaSerSerGlukapSerLeuwerthrSerPheLeuproGlyprolysproGlyhlain 442 AlaSerSerGlukapSerLeuwerthrSerPheLeuproGlyprolysproGlyhlain 444 PheProAenoGlyHlavalGlyAlaGlyGlyserGlyceuccoccoccccccc 445 TGCGGGCCCTCCCCTGGAGCCCGCTCCCCCCCCCCCCCC
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944 GCAGCGCTGGGCCCCACCGAGCAGCAGCAGGCTGTCGGCCCCTTGTCGCCCCAC 1003
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Alignment Scores:
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                                          321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
                                                          1304 GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA
                                                                                           GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGGCCGTGGTGACAGCT
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                                                                                                                                                                     Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06591 and AAAV82000 to AAX82020 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
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                                                                                                                                                                                      New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein \,
                                                                                                                                Mitcham JL
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Mismatches:
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                                                                                                                                Yuqin J,
98US-0116134.
98US-0159812.
98US-0159822.
99US-0232149.
99US-0232880.
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Best Local Similarity:
14-JUL-1998;
23-SEP-1998;
23-SEP-1998;
15-JAN-1999;
15-JAN-1999;
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704 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 763

403

qq		Db 501 LeuSerGlnValAlaProSerLeuPheMetGlySerI
δλ	764 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTACCTCCTGCCTG	Qy 1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGG
ogo O		Db 521 ThralaTyrMetValSerAlaAlaGlyLeuGlyLeur
Oy Db	924 ATTGACTGGGACACCAGGTGCCCTGGCCCCCTGGGCACCCAGGAGGAGTGCCTCTTT 883	Oy 1904 GTAGTATTGACAAGAGCGACTTGGCCAAATACTCAC
Oy Op	884 GGCCTGCTCACCCTCACCTCGCTAGCAGCACACTCCTGGTGGCTGAGGAG 943 	RESULT 5 AAU69763 ID .AAU69763 standard; Protein; 553 AA.
'n	GCAGCGCTGGGCCCCACCAGCAGAGAGGCTGTCGGCCCCCTCTTGTCGCCCCAC	AC AAU69763;
qq		DT 30-JAN-2002 (first entry)
Oy	GGCTTTCCGGAACCTGGCGCCCTGCTTCCCCGGCTG	DE Human prostate cDNA encoded protein #3. XX
gg		
Qy Dp	1064 CACCAGCTGTGCTGCCGCATGCCCGCACCTGCGCCGCTCTTGGTGGCTGAGCTGTGC 1123 1	OS Homo sapiens. XX XX WO200173032-A2. XX
٥y	AGCTGGATGGCATCATCACCTTCACGTGTTTTACACGGATTTCGTGGGCGGGGGGGG	04-OCT-2001.
qq	281 SerTrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300	27-MAR-2001;
oy Ha	1184 TACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAGC 1243	27-MAR-2000; 09-MAY-2000; 12-MAY-2000;
3 ,	i jyicinciyvarkioargalaciukrociyinrciualaargargHisHyrAspGluGly	13-JUN-2000; 27-JUN-2000;
Oy Dp	1244 GTTCGGATGGCCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTG 1303	10-AUG-2000; 2000US-0636215 29-AUG-2000; 2000US-0651236 06-SEP-2000; 2000US-0657279
Qy Dh	1304 GTCATGGACCGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTCTGGCA 1363 	02-0CT-2000; 10-0CT-2000;
3 8	**************************************	(COKIT) COKIAA COKP.
3 8	Scilled 	PI Au J. Dillon DC, Mitcham LL, Harlocker SL, PI Fanger GR, Retter MW, Stolk JA, Day CH, Ve PI Li SX, Wang A, Skelky YAW, Hepler WT, Hend
Qy Dp	1424 TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483	XX DR WPI; 2001-639232/73. DR N-PSDB; AAS63557. XX
οy	GGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT	PT New human prostate-specific polypeptides and p PT the diagnosis and treatment of cancer, especia
Dβ	4	
٥y ط	1544 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603	AA AA C The invention relates to isolated prostate spe
3 8	TICCCTAATGGACACGTGGGTGC	CC derived from them) and antique, presptides (or CC derived from them) and antique, presenting cell CC polypeptides. The antibodies are useful for de
; A		C cancer, especially prostate cancer. The polype
Qy Db	1664 TGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGGTGAGCCCACCGAGGCC 1723 	CC of cancer especially prostate cancer. Composite CC of cancer especially prostate cancer. Composite CC polynucleotide and/or polypeptide are useful CC response, and for treating cancer. The oligonu
Qy Dp	1724 AGGGTGGTTCCGGGCCGGGCATCTGCCTGGACCTCGCATACTGCCTGC	CC detecting cancer. The present sequence is a pr CC polypeptide of the invention. XX XS Sequence 553 AA;
۷۵ •	1784 CTGTCCCAGGTGGCCCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC .1843	Alignment Scores: 2.89e-208 Length:

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(or antiquenic epitopes
cells expressing the
r detecting the presence of
r preptides, polynucleotides and
r stimulating and/or expanding
for inhibiting the development
ositions comprising the
ositions comprising the
gonucleotide is useful for
a prostate specific
                               rIleValGlnLeuSerGlnSerVal 520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Jiang Y, Kalos MD;
Vedvick TS, Carter D;
nderson RA;
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erAla 553
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                                                                                by a prostate development
                                                                                                                                                                                              nucleotide encoding polypeptide comprising a portion of umour protein useful for inhibiting development of prostate for treating prostate cancer in a patient .
                                                                                                                                                                                                                                   CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGT
                                                                                                                                                                                                                                                                CCAGTGCTGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s sequence is a partial prostate tumour protein, encoded by a mour specific cDNa. The DNa is useful for inhibiting the devel prostate cancer or for treating prostate cancer in a patient
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Matches:
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Mismatches:
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                                            prostate tumour protein useful
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             2001-440862/47
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Query Match:
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AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis
                                                                                         TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGGCTG
                                      AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTTCGTGGGCGAGGGGCTG
                                                                                                                                             GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA
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                                                                            CACCAGCTGTGCTGCCGCATGCCCCGCACCTGCGCCGGCTCTTCGTGGCTGAGCTGTGC
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and (She have cytostatic activity, antibodies to (II), flusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93394 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTCCAGAGGCTGTGGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                      Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                            Human; prostate cancer; prostate-specific; diagnosis; vaccine;
              Human prostate-specific amino acid sequence L1-12.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 267-268; 543pp; English.
                                                               cytostatic; gene therapy; metastasis
                                                                                                                                                                                                                                                                                  Xu J, Dillon DC, Mitcham JL,
Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
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2861.00
100.00%
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44.58%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553 AA;
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                                                                                                                         WO200151633-A2.
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                                                                                           Homo sapiens.
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oy oy Db	524 81 584 101	CGCTATGGCCGCCGCCGGCCCTTCATCTGGGCACTTGGGCATCCTGGTGAGCCTC 583 [
Qy Db	644	GAGCTGGCACTGCTCATCCTGGGCTGGGGCTGCTGCATTCTGTGGCCAGGTGTGCTTC 703
Qy	704	ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCGGGCC 763
Qy	764	rGCCTGGGCTA
Qy Dp	824	ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGAGTGCCTCTTT 883
Qy	884	GGCCTGCTCACCCTCATCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGGGGG 943
Qy Db	944	GCAGCGCTGGGCCCCACCAGCAGCAGAGAGGCTGTCGGCCCCCTCCTTGTCGCCCCAC 1003
Qy Db	1004	TGCTGTCCATGCCGGGCCGCTTGCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1063
Qy Dp	1064	CACCAGCTGTGCTGCCGCATGCCCGCCACCCTGCGCCGCTCTTCGTGGCTGAGCTGTGC 1123
Oy Og	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTG 1183
Qy Db	301	TACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAGCC 1243
Qy	1244	GTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTG 1303
Qy Db	1304 341	GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
Qy	1364	GCTTTCCCTGTGGCTGCCGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT 1423
Qy	1424	TCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483
Qy	1484	TCCCTCTACCACCGGGAGAGAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT 1543
Qy Db	1544	GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
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Polypeptide comprising part of the Wilm's Tumour gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI \,
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                                                                                                                                                                                                                   and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a polypeptide described in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the apecific proteins and oligonucleotides specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAHU3422 to AAH24798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG
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                                                                                                                                           Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine.
                                                                                                            Prostate tumour antigen predicted amino acid sequence for L1-12
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                   1784 CIGICCCAGGIGGCCCCCAICCTGITIAIGGGCICCAIIGICCAGCICAGCCAGICIGIC
                                                                              TTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGCGCCTC
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                                                                                                                                                                                                                                                                        Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
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14-MAR-2001; 2001US-275479P.
28-MAR-2001; 2001US-279115P.
02-APR-2001; 2001US-280143P.
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ABB77575
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state (e.g. allergic hypersensitivity, seasonal thinitis, asthma, urticaria or atopic dermatitis or mastocytosis) in a subject which unticaria or atopic dermatitis or mastocytosis) in a subject which involves determining the level of expression of (1) or (11). A computer system, comprising a database containing information identifying the expression level in a tissue or at least one mast cell of (1), is useful for presenting information to identify the relative expression level of (1). (11) is used as a marker to detect, diagnose or identify an allergic response in a patient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise polycional or monoclonal antibodies. (11) is useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agents that modulate expression of the protein or agents, such as agonists or antagonists. The agonists or antagonists are useful for modulating blotogical activity and function of (II) and thus are useful for alleviating disease conditions such as allergic hypersensitivity, seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
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      or (II) is useful for diagnosing or
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                                                                                                                       AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTG 1183
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         GTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTTCTCTCTG
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                                       TGCTGTCCATGCCGGGCCCGCTTTGCCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG
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The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a blological sample from the patient with comprises contacting a blological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that is electively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences or differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer as well as for useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABG61800-ABG61904 represent prostate cancer-associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
                                                                                  Prostate cancer; prostate tumour tissue; human; mammal; cytostatic
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                                                   Prostate cancer associated protein #101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wilson KE,
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16-MAR-2001; 2001US-27688BP.
06-APR-2001; 2001US-281922P.
24-APR-2001; 2001US-286214P.
30-APR-2001; 2001US-286514P.
04-MAY-2001; 2001US-288589P.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (EOSB-) EOS BIOTECHNOLOGY INC
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2000US-0733288.
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N-PSDB; ABK92217.
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16-MAR-2001;
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Indels:

Best Local Similarity:

Query Match:

Percent Similarity:

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US-09-759-143-110 (1-3410) x ABG61900 (1-553)

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                   104 CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGT
                               584 TITCICATCCCAAGGGCCGGCTGGTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTG
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                                                  GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC:1603
                                                                                                                                                                                                           421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
                                                                                        cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                      TCCCTCTACCACCGGGAGAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT
                                                                                                                                                                                                                               GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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                                                                                                                                                                                                                                                                                                                     Human L1-12 protein SEQ ID NO 113.
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2000US-0570737.
2000US-0593793.
2000US-0605783.
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13-JUN-2000;
27-JUN-2000;
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27-MAR-2000;
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18-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlylleThrTyrValPro
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Jillon DC, Mitcham JL, Harlocker SL, Jiang Y, SR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-0693426.
10-OCT-2000; 2000US-0685166.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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(HEPL/) HEPLER W T.
(HEND/) HENDERSON R A.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
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HARLOCKER S
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1664 TGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGGTGAGCCCACCGAGGCC 1723

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The invention relates to an isolated PROST 03 polypeptide (I) and to the polynuclectide (II) encoding PROST 03. Fragments of (I) were used to generate antibodies (III) to PROST 03. (III) is useful for selectively destroying a cell expressing (I), and for treating a disease-state associated with expression of PROST 03 in a human patient. (III) is useful for diagnosing metastasis associated with (I), in a subject. (I) is also useful for diagnosing metastasis associated with (I), in a subject. (I) is also useful for diagnosing and treating diseases of cell proliferation such as prostate cancers. (I) is also useful for generating antibodies to PROST 03. (III) is useful in detecting the levels of PROST 03 containing cells. (II) is useful in diagnostic response to PROST 03 containing cells. (II) is useful in diagnostic assays for detecting the levels of polynucleotides encoding PROST 03 in cells and tissues. (II) is useful as DNA probes, as targets for antisense and ribozyme therapy, and as templates for the production of antisense polynucleotides. (I) and (II) are useful in research, biological,
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                                                                    metastasis; prostate cancer; tumour; immune response;
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                    CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla
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20-APR-2001; 2001US-0200065.
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                                                                                  Gaps:
     clinical and therapeutic purposes. The the amino acid sequence of human PROST
                                             2.89e-208
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Polynucleotides encoding breast tumour polypeptides, useful for treating breast cancer or stimulating an immune response \dot{}
                                                              Reed SG, Xu J, Dillon DC, Retter MW, Harlocker SL;
               22-JUN-2000; 2000US-0602877.
12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
12-JUN-2001; 2001WO-US19032
                                                                               WPI; 2002-147792/19.
N-PSDB; ABK29012.
                                                 (CORI-) CORIXA CORP.
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Claim 2; Page 144-145; 150pp; English.

polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that binds to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences AAU82641-AAU82655 represent human breast tumour polypeptides of the invention. The invention relates to polynucleotides encoding breast tumour

553 AA; Sequence

Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Ouery Match:	Scol	res: arity: nilarity:	2.89e-208 2861.00 100.00% 14.58%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	553 553 0 0 0
us-09-759-	143	-110 (1-34	US-09-759-143-110 (1-3410) x AAU82643 (1-553	(1-553)	
οy	284		ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTC	GCCTGCTGCGGCAC	CGGAAAGCCCAGCTC
qa	1	MetValGln			ArgLysAlaGlnLeu
٥y	344		GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGCATCACCTA	SAGGTGTGTTTGGCC	GCAGGCATCACCTAT
Db	21			SluValCysLeuAla	
Qy	404		CCTCTGCTGCTGGAGTGGGGGTAGAGGAGGAAGTTCATGACCATGCTGGGG	SAGGAGAAGTTCATG	SACCATGGTGCTGGGC
Db	41		ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGl)	3luGluLysPheMet	ThrMetValLeuGly
Qy	464		CCAGTGCTGGGCCTGGTCTGTGTCCCTAGGCTCAGCCAGTGACCACTGG	CCGCTCCTAGGCTCA	GCCAGTGACCACTGC
Db	61	_		ProLeuLeuGlySer	AlaSerAspHisTr
Qy	524		CGCTATGGCCGCCGCCGTCATCTGGGCACTGTCCTTGGGCATCCTGTCT	ATCTGGGCACTGTCC	TTGGGCATCCTGCT
Db	81		ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLe	lleTrpAlaLeuSer	LeuGlyIleLeuLeu
Qy	584		TTTCTCATCCCAAGGCCGGCTGGCTAGGAGGCTGCTGTGTGTCCCGGATCCCGGG	CTAGCAGGGCTGCTG	TGCCCGGATCCCAG
Dp	101		PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArg	LeuAlaGlyLeuLeu	CysProAspProArg
Qy	644		GAGCTGGCACTCCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGT	GTGGGGCTGCTGGAC	CTTCTGTGGCCAGGT

CITGCIG 343

uLeuLeu 20

403

rgrecce

CATTGGT 463

yllegly 60

rValPro 40

GCGTGGA 523

pArgGly 80

GAGCCTC 583 uSerLeu 100 GCCCCTG 643 gProLeu 120 GTGCTTC 703

121 GluLeuAlaLeuLleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140 ACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 763

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q	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 1	160
ργ	764	TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	823
qq	161	yrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuPrOAla	180
Qy	824	TGGGACACCAGTGCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTT	883
qa	181	leAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe	200
٥y	884	GGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGGG (4
Db	201	lyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	
Οy	944	GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGCTGTCGGCCCCCTCCTTGTCGCCCCCA :	1003
QQ	221	laalaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	240
Qy	1004	TECTETCCATECCEGECCCCTTTGCCGAACTTGGCCCCCCCCCC	1063
Db	241	yscysprocysargalaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu	260
Qy	1064	CACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGTGCTGTGC :	1123
Db	261	isGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	280
QY	1124	AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTG	1183
qa	281	rpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu	300
Qy	1184	TACCAGGGGGGGCGCGAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGC	Ò
QQ	301	SinglyvalProargalaGluProGlyThrGluAlaArgArgHisTyrAspGluGl	320
Qy	1244	ATGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTG	1303
Db	321	alArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSerLeuValPheSerLe	340
Οy	1304	GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCGCA	1363
Db	341	lMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAl	360
Qy	1364	GCTTTCCCTGTGGCTGCCGGTGCCTGTCCCACAGTGTGCCGTGGTGACACCT	1423
QQ	361	laPheProvalAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVhrAl	380
Qy	1424	CAGCCGCCTCACCGG	1483
Db	381	laAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAl	
Qy	1484	CCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCG	1543
Db	401	rLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyG	
Qy	1544	GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGGTCCC	1603
Db	421	laSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPr	440
Qy	1604	TTCCCTAATGGACACGTGGGTGTGGAGGCAGTGGCCTCCTCCCACCTCCACCTCGCTC	1663
Db	441	eProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLe	460
٥y	1664	TGCGGGGCCTCTGCGTGATGTCTCCGTACGTGGGTGGGTG	1723
QQ	461	sGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAL	480
Qy	1724	AGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG	1783
Dp	481	gvalvalProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLe	200
Qy	1784	CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCTCAGTCTGTC	œ
qq	501	euserGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVa	520

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ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
                        284 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGGAACCCGGAAAGCCCAGGTCTTGCTG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or lits variant. (I) have extostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynuclectides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmacutical composition contening (I) are useful for inhibiting the opportion proteins and oligonuclectides specific for prostate specific proteins and oligonuclectides that hybridise to a polynuclectide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer, especially prostate cancer.

AMH0212 to AMB0713 the AMB0719 to AMB071930 are sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate tumour antigen; prostate tumour; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                    Prostate tumour antigen amino acid sequence for a fusion protein
                                                                                              GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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Matches:
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Best Local Similarity:
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Pred. No.:
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                                        CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGT
                                                   TTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGGATCCCAGGCCCCTG
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                                                                                                                          CGCTATGGCCGCCGCCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGAGCCTC
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CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 1006
                                                                                                                                                                                                                       1784 CIGICCCAGGIGGCCCCAICCCIGITIAIGGGCICCAITGICCAGCICAGCCAGICIGIC 1843
                                                                 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
                                                                                                       TICCCIAAIGGACACGIGGGIGCIGGAGGCAGIGGCCIGCICCCACCICCACCCGCGCIC 1663
                                                                                                                                            TGCGGGGCCTCTGCCTGTGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCC 1723
                                                                                                                                                                                1724 AGGGTGGTTCCGGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
                                                                                                                                                                                                                                                             ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
                                                                           946
                                      TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT
                                                                                                                Thioredoxin; ubiquitin; P501S; prostate; tumour; antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                 Thioredoxin-ubiquitin-P501S(aa55-553)-His triple fusion protein.
                                                                                                                                                                                                                                                                                                             GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= UBP1_cleavage_site
203..702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       703..710
/label= Histidine_tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1..109
/label= Thioredoxin
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/label= Linker
126..199
/label= Ubiquitin
                                                                                                                                                                                                                                                                                                                                                          AAM50661 standard; Protein; 710 AA.
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703..710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2000; 2000GB-0015619. 30-OCT-2000; 2000GB-0026484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Homo sapiens
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                                                                                                                                                                                                                     The present sequence is that of a triple fusion protein comprising, from the N-terminal end, Escherichia coli thioredoxin, human ubiquitin and amino acids 55-553 of human prostate antigen P501S, followed by a histidina effinity tail. The triple fusion protein was produced in E. coli G1724 host cells transformed by an expression vector comprising DNA (see ABA91283) encoding the fusion. This is an example of the production of triple fusion proteins of the invention that comprise ubiquitin fused between thioredoxin and a protein of interest, in this case P5015(as5-55). A ctaimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coll) under conditions which endoporotease (especially UBP1 from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the ubiquitin-specific cubiquitin-specific endoprotease in vivo. In the present case, the product is a P501-like protein of 509 amino acids. The recombinant protein of 509 amino acids. The recombinant protein of 509 amino acids. The recombinant protein of sa a vaccine for cancer therapy.
                                                                                                                    Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    440 ATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGC
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Mismatches:
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Matches:
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              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                              Example 5; Fig 9b; 87pp; English.
                                            Delisse AEF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.58e-18
2601.00
100.00%
100.00%
                                                                         WPI; 2002-147888/19
                                           Cabezon Silva TEV,
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Best Local Similarity:
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                                                                                       N-PSDB; ABA91283
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GGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCCTCATC [IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CCAGGAGGAGTGCCTCTTGGCCTGCTCACC IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	TTCCTCACCTGCGTAGCA.91. 	CCGAGCCAGCAGAGGGCTG 979 	CCGCTTGGCTTTCCGGAAC 1039	GCATGCCCGCACCCTGCGC 1099	TCATGACCTTCACGCTGTTTTAC 1159	CAGAGCTGAGCCGGCACCGAG 1219 	GGGGGTGTTCCTGCAGTGC 1279	GCAGCGATTCGCACTCGA 1339	CGGTGCCACAT	SGTTCACCTTCTCAGCCCTG 1459 	AGAAGCAGGTGTTCCTGCCC 1519 	SCCTGATGACCAGCTTCCTG 1579	GGGTGCTGGAGGCAGTGC 1639 	TGTGATGTCTCCGTACGTGG 1699 	GGGCATCTGCCTGGACCTC 1759	CCATCCCTGTTTATGGGCTCC 1819 	TGCCGCAGGCCTGGGTCTG 1879	TGACAAGAGCGACTTGGCCAAATACTCA 1939
		GGCACCCAGGAGAGTGCCTCTTTGGCCTGCTCACCCTCA 	GCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCA 	TCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGG	CTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGTIIIIIIII	CGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGCCA 	ACGATTTCGTGGCGAGGGCTGTACCAGGGCTGCC 	GCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGC	GCCATCTCCCTGGTCTTCTCTCTGGTCA: 	GCAGTCTATTTGCCCAGTGTGGCAGCTTTCCCTGTGCC 	CACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCG	CAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGIIIIIIIIII	AAATACCGAGGGGACACTGGAGGTGCTAGCAGTGGGGG 	CCAGGCCCTAAGCCTGGAGCTCCCTTCCCTATGGACACG	CTGCTCCCACCTCCACCCGCGCTCTGCCGGGGCCTCTGCC	GTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGCCC 	GCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCC	ATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTG 	GTCGCCATTTACTTTGCTACACAGGGTAGTATT

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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and the antibodies to (II), fusion proteins comprising (II), and isolated (II), and the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93137 to AAH93944 and AAM01115 to AAM01118 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 GGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGGTAGAGGAGAAGTTCATGACC 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                            Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis.
                                                                                                                                                                                 Alpha prepro-P501S recombinant protein amino acid sequence.
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501
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                        AAM01318 standard; Protein; 595 AA.
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ID, Fanger GR, Day CH,
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2596.00
96.77%
95.07%
40.45%
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                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu J, Dillon DC, M
Kalos MD, Fanger GR
Wang A, Meagher MJ;
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Best Local Similarity:
1940 GCG 1942
                            702 Ala 702
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                                                                                                                                                                                                                                                            Homo sapiens.
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- Homo sapiens.
- Escherichia coli.
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/label- L
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/label= UF
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                                                                       GGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATC
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441 LysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSer 460
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                                                       GGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCGCGCGTCTGCGGGGCCTCTGCCTGT
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WPI; 2002-508560/54
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                                                                                                                  Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 GTCCAGAGGCTGTGG----GTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG
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99.38%
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N-PSDB; ABA91284.
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vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma.
422 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis
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                                                                                                                                                                                                                   362 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla
                                                                                                                                                                                                                                                                824 ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT
                                                                                     ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC
                                                                                                                                                                           Human mast cell related protein MC14-2 SEQ ID NO 5.
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14-MAR-2001; 2001US-275479P.
28-MAR-2001; 2001US-279115P.
02-APR-2001; 2001US-280143P.
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Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity

Claim 31; Page 103-104; 119pp; English.

The invention relates to isolated nucleic acid (ABN81319-ABN81324), corresponding to genes differentially expressed in mast cells following activation or in patients with allergic hypersensitivity disease, (I) that encodes proteins (ABD77569-ABB77575) (II) or a protein fragment of (II) if at least 6 amino acids. (II) is useful for identifying binding partners. (I) or (II) is useful for diagnosing or treating a disease statioarie (e.g. allergic hypersensitivity, seasonal rhinitis, asthma, urticaria or atopic dermatitis or mastcoytosis) in a subject which involves determining the level of expression of (I) or (II). A computer system, comparising a database containing information identifying the expression level in a tissue or at least one mast cell of (I), is useful for presenting information to identify the relative expression level of (I). (II) is used as a marker to detect, diagnose or identify an allergic response in a patient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise polyclonal or monoclonal antibodies. (II) is useful for identifying agents that modulate expression of the protein or agents, such as agonists or antagonists. The agonists or antagonists are useful for modulating biological activity and function of (II) and thus are useful for alleviating disease conditions such as allergic hypersensitivity, seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.

Sequence 326 AA;

347 AACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCT 406 TATGGCCGCCGCCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTT 586 LeuLeu------AlaGlyIleGlyPro GTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGC CCACTGGAGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTAC ProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyr :::|||:::
SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrThrSer CTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGGATCCCAGGCCCCTGGAG CTGGCACTGCTCATCCTGGGCCTGGGCTGCTGGACTTCTGTGGCCCAGGTGTGCTTCACT CTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCA Length: Matches: Conservative: Mismatches: Indels: US-09-759-143-110 (1-3410) x ABB77571 (1-326) 6.64e-107 1522.50 58.85% 57.69% 23.72% Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB: Alignment Scores: 29 96 σ 467 527 26 9/ 407 587 647 707 .. 02 δy qq ò qq ò В δ g οy Op Óγ Dp à Ω ρp

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RESULT 21

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1606 1666 1726 TCCCAGGTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACT 1846 GTGGTTCCGGGGCCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTG 1786 1427 GCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCC 1486 GCGCTGGGCCCCACCGAGCCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGC 1006 TGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCAC 1066 1247 CGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTC 1306 1307 ATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCT 1366 247 1127 TGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGGAGGGGCTGTAC 1186 218 218 218 227 267 287 946 175 1067 CAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGC 1487 CTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCT 1547 AGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTC -----Gln-AlaLeuSerLeuGluLeuProSe CCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTCTGC GGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCCAGG CTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCA 1.87 CAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTT 1367 TTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCA GACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCCAGGAGGAGTGCCTCTTTGGC 216 CysProCys------218 218 -218 ----1607 1667 1001 1727 1787 287 1847 156 947 196 218 218 218 219 267 827 887 176 q òγ q Ω ОD δλ g δy g δ qq οy qq δý QQ Óγ gg óγ g δ g Qγ g óλ QQ Ω pp ŏ g Db δ Dp Óγ

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GCGCTGGGCCCCACCGAGCCAGCAGAGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGC 1006
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                                                                                      CTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGGATCCCAGGCCCCTGGAG
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29 LeuLeu------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides for antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer. Sepecially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for esponse, and for treating cancer. The oligonucleotide is useful for additional cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 AACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCT 406
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| SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrSer 28
                                                                                                                         Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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Mismatches:
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Matches:
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                                                                                              prostate cDNA encoded protein #69.
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                AA.
               AAU69875 standard; Protein; 371
                                                                                                                                                                                                                                                                                                           2000US-0605783.
2000US-0636215.
2000US-0651236.
2000US-0657279.
2000US-067279.
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2000US-0570737
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                                                                     (first entry)
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Best Local Similarity:
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                                                                                                                                                                            WO200173032-A2.
                                                                                                                                                                                                                                27-MAR-2001;
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                         27-MAR-2000;
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13-JUN-2000;
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10-AUG-2000;
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02-OCT-2000;
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Li SX,
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                                                                                                                                                                 947 GCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTTGTCGCCCCACTGC
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                                                                                                   LeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThr
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                                                                                                                                           CCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and can be used in vaccine production and gene therapy. (I), (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis can well as the prostate volume. AAH93357 to AAH9344 and AAM0115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                                                                              Reed SG;
Skeiky YAW;
                                    Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis.
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splice variant P553S-14 amino acid #2.
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Retter MW,
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GR, Day CH,
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Query Match:
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GCGCTGGGCCCCACCGAGCAGCAGAGGGCTGTCGCCCCCCCTCTTGTCGCCCCACTGC 1006
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                            -----AlaGlyIleGlyPro 35
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                                                                      TATGGCCGCCCCCCCTTCATCTGGCCACTGTCCTTGGGCATCCTGCTGAGCCTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New prostate-specific polynucleotides for diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harlocker SL, Jiang Y,
A, Day CH, Vedvick TS,
epler WT, Henderson RA;
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Conservative:
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Indels:
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Wang A, Skeiky YAW, Hepler WT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dillon DC, Mitcham JL, GR, Retter MW, Stolk J
                                                                                                                                  14-7AN-2000; 2000US-0483672.
27-MAR-2000; 2000US-0536857.
09-MAY-2000; 2000US-0568100.
12-MAY-2000; 2000US-0568100.
13-MAY-2000; 2000US-0593793.
27-UN-2000; 2000US-0593793.
27-UN-2000; 2000US-0636215.
29-MUG-2000; 2000US-0651215.
06-SEP-2000; 2000US-0651216.
06-SEP-2000; 2000US-0657279.
       980S-0020956
980S-0030607.
980S-0115453.
980S-0159812.
990S-0232149.
990S-0388946.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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RETTER M W.
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DILLON D C.
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DAY C H.
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13-JUL-1999;
12-NOV-1999;
                                                                                                                         .8-NOV-1999;
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(DAYC/)
(VEDV/)
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(MITC/)
(HARL/)
(JIAN/)
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(FANG/)
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(SKEI/)
(HEPL/)
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235

315

Human gene 11 encoded secreted protein HWBAR14, SEQ ID NO:84.

(first entry)

18-JUL-2001

AAE01362

DXXXXX

347 AACCIGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCT 406

US-09-759-143-110 (1-3410) x ABB95335 (1-371)

Gaps:

SerLeuValProLeuProLeuAlaLeuTyrLeuSerGlnProLeuThrHisThrThrSer

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AA.

AAE01362 standard; Protein; 371

AAE01362 RESULT

present sequence represents a human secreted protein of

the invention.

foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; disease; cognitive disorder; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; disease; food additive; pregnancy related disorder; endocrine disorder; allergy; pregnancy related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; protein; proliferative disorder; cancer; tumour; therapy Human; foetal gene

Homo sapiens

1..48 /label= Signal_peptide Location/Qualifiers Peptide

49..371 /label= Mature_human_secreted_protein Misc-difference Protein

/note= "Encoded by TNC' /label= Unknown

WO200134629-A1

17-MAY-2001

08-NOV-2000; 2000WO-US30654.

99US-0164835 12-NOV-1999;

27-JUL-2000; 2000US-0221142.

(HUMA-) HUMAN GENOME SCI INC

Baker KP; Ruben SM, Komatsoulis GA, Wei P, Fiscella M, 2001-308779/32.

N-PSDB; AAD05230

or New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive o preservative

Claim 11; Page 438-440; 490pp; English.

AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the proteins they encode. AAE01415-AAE0143 represent human secreted proteins they encode. AAE01415-AAE0143 represent human secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, feetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune disorders, cancer, tumours, diseases of the immune system, AIDS, autoimmune disorders, cancers, schizophrenia, asthma, skin disorders (e.g., rheunantoid arrhritis), inflammation, allergies, cognitive disorders, schizophrenia, asthma, skin disorders, cognitive disorders, schizophrenia, asthma, skin disorders, pregnancy-related disorders, addivascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The pregnancy-related disorders, endocrine disorders, and infections. The proposition of the p preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., raddoimmunoassay or enzyme linked immunosorbent assay (ELISA). proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or

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                                                                                   Conservative:
Mismatches:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or albumin, HSA). The proteins are useful for treating a disease or the shalf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein Is useful for treating and disorders such as cancer, reproductive disorders, digestive disorders (e.g. acquired immunodeficiency syndrome, AIDS), andocrine disorders (e.g. alabetes), haematopoletic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meninghtis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis), ABG653126-ABG65518 represent albumin for the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein -
                                                                                                                                                                                                                                                                                          human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; andocrine disorder; haematopoletic disorder; neural disorder; connective disorder; cytostatic; antilnfertility; antilnflammatory; antilncer; immunomodilator; anti-HIV; antilnflammatory; antilncer; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                      Albumin fusion protein; therapeutic protein X; human albumin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 1018-1019; 2102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-759-143-110 (1-3410) x ABG64105 (1-371)
                                                  ABG64105 standard; Protein; 371 AA
                                                                                                                                                                                                              Human albumin fusion protein #780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-APR-2000, 2000US-229358P.
25-APR-2000, 2000US-199384P.
21-DEC-2000, 2000US-256931P.
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1419.00
95.21%
92.12%
22.11%
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                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-010886/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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                                                                                                                                                           27-AUG-2002
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                                                                                                     ABG64105;
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RESULT 25
                         ABG64105
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GCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCCCTTGCCTTTCCGGAACCTG 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1223 CGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCC 1282
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                                                                                                                             TGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGAC 682
                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                          TTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGAC 742
                                                                                                                                                                                                                                                                                                                                                                                                                                         ACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGGCCCACCGAGCCAGCAGAAGGGCTGTCG 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AlaProSerLeuSerProHisCysCysProCysArgAlaArGLeuAlaPheArgAsnLeu 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 ArgArgHisTyrAspGluGlyLysAlaLeu-AlaAlaSerArgGlyTrpCysGlySerAr 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human prostate protein/M. tuberculosis Ral2 fusion protein RA12-P501S-E2.
SerLeuleuAlaGlyIleGlyProValLeuGlyLeuValCysValProLeuGlySer 47
                                                                                           67
                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prostate cancer; cytostatic; immunostimulant; tumour; immunogen; protein.
                                                                          ACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCTTCCTCCTCACCTGCGTAGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCC
                                                                                                                                                                                                                                                                                                                                                743 CCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCTACCTGGGC
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1076 TGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGTGATGGCA 1135
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                                                                                                                                       CCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTTGTCGCCCCCACTGCTGTCCATGC
                                                                                                                                                                                                                                                                                                                                                                                    1016 CGGCCCCCCTTGCCTTTCCGGAACCTGGCCCCTGCTTCCCCGGCTGCACCAGCTGTGC
                                                                           CTCATCCTGGGCGTGGGGCTGCTGGTGTGCCCAGGTGTGCTTCACTCCACTGGAG
                                                                                                                            GCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTAT
                                                                                                                                                                                                                              ACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACC
                                                                                                                                                                                                                                                                               CTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGC
                         AGGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTG
                                      SL, Jiang Y, Reed SG;
Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1136 CTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAG 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ral2-P501S-E2 construct amino acid sequence.
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Retter MW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
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Kalos MD, Fanger GR, Day CH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-425873/45
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                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the of cancer especially prostate cancer. The objections comprising the objounce of the and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The objouncleotide is useful for detecting cancer. The present sequence is fusion protein comprising a prostate specific polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CIGGICIGIGICCCCCCTCCTAGGCICAGCCAGTGACCACTGGCGIGGACGCTAIGGCCGC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCA 595
                                                                                                                                                                                                                                                                                                                                                          human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGC
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Carter D;
                                                                                                                                                                                                                                                                  Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400
267
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5
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Matches:
Conservative:
Mismatches:
Indels:
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  Chimeric - Microbacterium tuberculosis.
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                                                                                                                2000US-0568100.
2000US-0570737.
2000US-0593793.
                                                                                                                                                   20000S-0605783
20000S-0636215
20000S-0651236
20000S-0657279
20000S-0679426
20000S-0679426
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1403.50
97.45%
97.45%
21.87%
                                                                            27-MAR-2001; 2001WO-US09919
                                                                                                     20000S-0536857
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                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAS64153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                          WO200173032-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aliqnment Scores:
                                                                                                                                                      27-JUN-2000;
10-AUG-2000;
                                                                                                                                                                               29-AUG-2000;
                                                                                                                                                                                          06-SEP-2000;
                                                                                                                                                                                                                    10-OCT-2000;
                                                                                                    27-MAR-2000;
                                                                                                                                           JUN-2000;
                                                                                                                             12-MAY-2000;
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DB:
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (II) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400
267
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                    Claim 8; Page 504-506; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 AA;
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7.39e-98 1403.50 97.45% 97.45% 21.87% Best Local Similarity: Percent Similarity: Query Match:

US-09-759-143-110 (1-3410) x AAM01262 (1-400)

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Gaps:

371	1 GTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTG 415
416	6 GAAGTGGGGGTAGAGGAGAAGTTCATCACCATGGTGCTGGGCATTGGTCCAGTGCTGGGC 475
476	6 CIGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGGGTGGACGCTATGGCCGC 535
536 187	6 CGCCGGCCCTTCATCTGGGCACTGTCCTTGGCATCCTGCTGGCGCCTCTTTCTCATCCA 595
596	6 AGGGCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTG 655
656	6 CTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGGG 715
716	6 GCCCTGCTCTCTGACCTCTTCCGGGACCGGGACCAGTCGCCCAGGCCTACTCTGTCTAT 775
776	6 GCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG
936	6 ACCAGTGCCCTGGCCCCCTACCTGGCCACCAGGAGGAGCCCTCTTTGGCCTGCTCAC 895
307	6 CTCATCTTCCTCACCTGCGFAGCAGCCACTGCTGGTGGTGAGGAGGCAGCGCTGGGC 955

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956 CCCACCGAGCCAGCAGAAGGGCTGTCGCCCCCTTCCTTGTCGCCCCACTGCTGTCCATGC 1015
                               1016 CGGGCCCGCTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGC 1075
                                                               1076 TGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGCAGCTGGATGGCA 1135
         cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                 Ral2-P501S-E2 construct SEQ ID NO 852.
                                                                                                                                                                                                                                           Chimeric - Mycobacterium tuberculosis.
Chimeric - Homo sapiens.
                                                                                                                                                   ABB95367 standard; Protein; 400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            20000S-0483672
2000US-058857
2000US-056810
2000US-0593793
2000US-0593783
2000US-0593783
2000US-0592783
2000US-0592783
2000US-0651236
2000US-0651236
2000US-0651236
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98US-0020956.
98US-0030607.
98US-0115453.
98US-0159812.
99US-0232149.
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                                                                                                                                                                                  19-JUL-2002 (first entry)
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DILLON D C.
MITCHAM J L.
HARLOCKER S L.
JIANG Y.
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FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
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15-JAN-1999;
09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
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09-MAY-2000;
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13-JUN-2000;
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10-AUG-2000;
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(CART/)
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307 LeuilePheLeufhrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGly 326
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                                                                                                                                                                              AAW85068 standard; Protein; 255
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                                                                                                                                                                                                                                                                                                                371 GTGTGTTTGGCCGCAGGC-----ATCACCTATGTGCCGCCTCTGCTGCTG 415
                                                                                                                                                                                                                                                                                                                                  146
                                                                                                                                                                                                                                                                                                                                                  475
                                                                                                                                                                                                                                                                                                                                                                    166
                                                                                                                                                           The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu
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                                                     Kalos M
Carter
                                                                                                        New prostate-specific polynucleotides for diagnosing and tre diseases, in particular prostate cancer, and as markers for progression of cancer
                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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267
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Mismatches:
Indels:
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Matches:
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97.45%
97.45%
21.87%
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                   HENDERSON R A.
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                                                                                                                                                                                                                                                                                                                                         The present sequence is encoded by the consensus sequence for a PS108 gene. The sequences are PS108 gene-specific. They are used in the method of the invention. The specification describes a method for detecting the presence of a target PS108 polynucleotide in a test sample. The method comprises contacting the test sample with at least 1 PS108 specific polynucleotide or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatitis, prostatic intraeptihalial neoplasia (PIN) and cancer. In particular the products can be used in drug screening and gene therapy.
                                                                                                                                                                                        TGCCGCATGCCCCGCACCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCA
                                                                                                                                                     CGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; prostate disease; benign prostatic hyperplasia; BPH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by the consensus sequence of the PS108 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAG 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
Gordon J, Granados EN, Hodges SC, Klass MR, Kratoch
Roberts-Rapp L, Russell JC, Stroupe SD;
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1477
                                                                                     GGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGAT 1237
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                                                                                                                                                                                                                                                                                                                                                                               GAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCCATCTCCCTGGTCTTC
                                                                                                                                                           TCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGT
                                                                                                                                                                                                      CTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACT
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                Matches:
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       4.32e-89
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                                  Similarity:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGGCAGCTTTCCCTGTGCCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to produce antibodies which can be used in treatment. The present sequence is on of the PS108 partial protein sequences.
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                                                                                                                                                                                                                              polynucleotides
                                                                                                                                                          Granados EN;
                                                                                                                                                                   Stroupe SD,
                                                                                                                                                       ts TL, Friedman PN, Gordon J,
, Klass MR, Roberts-Rapp L, S
Russell JC, Hodges SC;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                 (ABBO ) ABBOTT LAB
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 255 AA;
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                 Billing-Medel PA,
                                                                                                                                                                           Kratochvil JD,
                                                                                                         02-MAY-1997;
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                                                         10-0CT-2000
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GCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCC 1657

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The sequence represents the amino acid sequence of prostate-specific PS108 #1, encoded by PS108 expressed sequence tag (EST) consensus sequence. The sequence was produced from overlapping PS108 ESTs sequences to produce a full length consensus sequence. This sequence was then used to produce the PS108 polypeptide which is useful in assays for detecting antibodies to prostate tissue, and as an immunogen to produce antibodies. The polypeptide is useful for screening compounds which specifically bind to the polypeptide and for screening for drugs, compounds, or any other agent which can be used to treat diseases associated with PS108. The antibody is useful to detect, or for image localisation of, PS108 antigen
                                                                                                                                                     TTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAG 1837
                                                                                                                                                                                                           TCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCCATTTACTTTGCT 1897
                                                                                              GAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCC 1777
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Prostate; PS108; immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metastasis; expressed sequence tag; EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M, Colpitts TL, Friedman PN, Gordon J;
Klass MR, Kratochvil JD, Roberts-Rapp L;
Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful in assays for detecting antibodies {\tt immunogens} to produce {\tt PS108} antibodies -
                                                                                                                                                                                                                                                                  ACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
                                                                                                                                                                                                                                                                                 Prostate-specific PS108 polypeptide #1
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                                                                                                                                                                                                                                                                                                                                                      AAU04205 standard; Protein; 255 AA.
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97US-0850713.
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Russell JC, Stroupe SD,
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N-PSDB; AAS07155.
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prostate tissue,
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delivery agents for therapeutic agents as well as for diagnostic tests and for screening for diseases or conditions associated with PS108, especially cancer. The antibody is also useful for generating chimeric antibodies for therapeutic use, for inhibiting the biological activity PS108, in therapy (for e.g. to treat prostate tissue disease including prostate cancer and its metastases), and to detect the presence of any polypeptide in a test sample which shares one or more antigenic determinants with the PS108 polypeptide.
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AAE01423 standard; Protein; 252 AA.
   AAE01423;
RESULT 32
AAE01423
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(first entry) 18-JUL-2001

Human secreted protein variant, SEQ ID NO:147.

Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; Inflammation; neurological disorder; Altheimer's disease; food additive; anglogenic disorder; kidney disorder; astrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; ell culture; chemotaxis; vulnerary; binding partner identification; gene therapy

Homo sapiens,

'note" "Corresponds to any of the naturally occuring Location/Qualifiers Key Misc-difference

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WO200134629-A1

17-MAY-2001

08-NOV-2000; 2000WO-US30654

12-NOV-1999; 99US-0164835. 27-JUL-2000; 2000US-0221142.

(HUMA-) HUMAN GENOME SCI INC

TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGC 1549

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1670 GCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCCAGGTG 1729

1730 GTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCC

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1910 TTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGG 1969

1850 TATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTA 1909

1790 CAGGTGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCC

Baker Fiscella M, Wei P, Komatsoulis GA, Ruben SM,

WPI; 2001-308779/32

diagnosing, preventing, treating or ameliorating medical conditions, such as autolmmune disease and cancer, and used as a food additive or $\,$ New nucleic acid encoding one of 21 human secreted proteins for preservative

Disclosure; Page 476-477; 490pp; English.

AAD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the proteins they encode. AAE01415-AAE01413 represent the protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, cheurological disorders (e.g., Alzheimer's disease, Parkinson's disease),

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cognitive disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, tandery disorders, gastrointestinal disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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Mismatches:
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Matches:
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/note= "potential protein kinase C phosphorylation site" 188..209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "potential casein kinase II phosphorylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying biomolecules for the diagnosis and treatment of diseases associated with cell-proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate cancer-associated gene; Incyte clone 1864683; bone cancer; cell proliferation; cancer; adrenal gland cancer; bladder cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amino acid sequence of a prostate cancer-associated protein.
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                                                                                                                                                                                                                                                                                   AAY54369 standard; Protein; 231
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                               Conservative:
Mismatches:
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Alignment Scores:
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Homo sapiens

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The prostate cancer associated gene combs sequence is associated give.

The prostate cancer associated gene combs sequence is used in the method of the invention. The specification describes a method for identifying biomolecules for the diagnosis or treatment of diseases associated with cell proliferation. The method comprises examining polynucleotides, consisting of prostate cancer-specific genes, and genes of unknown function, expressed in cDNA libraries. The patterns of both gene sets are compared to identify genes of unknown function with similar expression patterns to the prostate cancer-specific genes. The biomolecules identified by the method form pharmaccutical compositions useful for the diagnosis and treatment of diseases sociated with cell proliferation. Such diseases include cancer of the adrenal gland, bladder and bone, but especially prostate cancer. The method may also be applied using other disease-specific genes. The prostate cancer-specific genes are concer-specific genes facilitate the diagnosis and treatment of cell proliferation disorders.
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                                                                                                                                                             "potential protein kinase C phosphorylation site"
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                                                                                        "potential protein kinase C phosphorylation site"
                                                                                                                         "potential protein kinase C phosphorylation site."
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                                                                                                                                                                                             "potential cAMP and cGMP dependent protein kinase phosphorylation site"
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                                                  'note "potential N-glycosylation site"
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                  Location/Qualifiers
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Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder. ALDS; autoimmune disease; rheumatoid attritis; Parkinson's disease; cognitive disorder; schizophrania; skin disorder; psorlasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; prorlasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anniquantion; meurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; andocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                  AGGGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAG 208
                                                                                                                                                                                                                          CTGCGGCCTCTCCTTGCTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCT 148
66
                                                                                                               New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene 11 encoded secreted protein HWBAR14, SEQ ID NO:118.
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27-JUL-2000; 2000US-0221142.
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Tue Jun 10 11:28:19 2003

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AMD05220-AAD05282 represent cDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the proteins they encode. AAE01413 represent human secreted proteins they encode. CC AAE014131 represent human secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. CC Peach conditions can be diagnosed by determining the amount of the new penes. Specific uses are described for each of the 21 genes. CC based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, diseases of the immune system, AIDS, autoimmune classues in the diagnosis or treatment of proliferative disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, conditive disorders, diabetes, atherosclerosis, cardiovascular disorders, prepanary related disorders, atherosclerosis, cardiovascular disorders, prepanary-related disorders, and orders, asthma, skin disorders or proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding carteners, and in chemotaxis, and can be used as a food additive or proteins can also be used to an be used as a food additive or protein nof the invention can be used in allevatating symptoms associated with the disorders mentioned above, and in allevatating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., the present sequence represents a human secreted protein of the invention can be used in allevatating symptoms associated the invention can be used in allevatating symptoms associated adionamental and human secreted protein of the invention of the invention and human secreted protein of the invention and human secr
Claim 11; Page 456-457; 490pp; English.
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129 AA; Seguence

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3034 AGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAA 3093
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                                                                                                                                                                                                                                                                                                                                                    3154 CAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCC 3213
                                                                                                                                                            GGCCCAGCCTGGTTCCCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATG 2973
                                                                                                                                                                                                         AAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTCCCCAAC 3033
                                                                                                                                                                                                                                                                                                                  1 GlyProAlaTrpPheProProLeuProLeuProSerThrLeuSerArgThrGlyLeuMet 40
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Mismatches:
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          Length:
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         1.18e-42
673.00
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Alignment Scores:
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Query Match:
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2854 AGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTTT 2913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and disquosing disorders such as cancer, reproductive disorders, disease, disorders (e.g. crohn's disease, ulcerative collisis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzhaimer's, Parkinson's, Creutzfeldt-Jacob disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to albumin fusion proteins comprising
                                                                                                                                               Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haemactopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HTV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion protein for treating disease e.g. diabetes comprises albumin fused to a therapeutic protein -
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              ABG64102 standard; Protein; 129 AA
                                                                                                                  duman albumin fusion protein #777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2000; 2000US-229358P.
25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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100.00%
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Query Match:
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                                                ABG64102;
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ABG64102
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599 AA;

Sequence

DE SCHAR-2002 (first entry) XX XX XX DE DE SCHAR-2002 (first entry) XX DE DE SCHAR-2002 (first entry) XX DE DE SCHAR-2001 (developmental biology; cell signalling; insecticide; XX DE DE DE SCHALL (developmental biology; cell signalling; insecticide; XX DE DE SCHALL (developmental biology; cell signalling; insecticide; XX DE DE SCHAR-2001, 2001WO-US09231. XX Z1-SEP-2001. XX Z2-SEP-2001. XX Z3-MAR-2001, 2000US-191637P. PR 23-MAR-2001, 2000US-191637P. PR 23-MAR-2001, 2000US-0614150. XX AND REE) PE CORP NY. XX AND REE) PE CORP NY. XX AND REE) PE CORP NY. XX AND REE) PE CORP NY. XX AND REE) PE CORP NY. XX AND REE DE CORP NY. XX AND REE DE CORP NY. XX AND REE DE CORP NY. XX AND REE DE CORP NY. XX AND REE DE CORP NY. XX AND REE DE CORP NO. XX A	1
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977 CTGTCGGCCCCCTCCTTGTCGCCC------ 1000
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                                                                                                                                                                                                 377 TIGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGTAGAGGAAAG 436
                                                                                                                                                                                                                                                                                86 HisMetSerMetThrTrpGlyLeuSerProLeuIleGlyPhePheMetSerProLeuLeu 105
                                                                                                                                                                                                                                                                                                                GGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGGCCCGTTCATCTGGGCA 556
                                                                                                                                                                                                                                                                                                                                    146 LeuLeuGlyAspAlaGlyTyrThrTyrAlaGluSerAlaLeuAsnPheThrSerSerSer 165
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166 GlyGlySerValAlaAlaLeuValSerGlyGluAlaThrThrGlyProSerAlaSerAsp 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641 CTGGAGCTGGCA----CTGCTCATCCTGGGCGTGGGGCTGCTGGTGGACTTCTGTGGCCAG 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     206 ThrCysGlnThrProAlaArgThrTyrLeuLeuAspMetCys---ValProGluGluGln 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 CGCCAGGCCTACTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   875 TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTG---- 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          695 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         815 CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::: :::||||||||:::|||||||||| 245 IleGlyGlyValAspTrpGluThrThrHisIleGlySerPheMetGlyGlyAsnIlePro 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 GlnAlaIleLysLysGluLeuLysLysLysAsnAsnThrIleTyrTyrIleGlnGluThr 324
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325 ThrGlnLeuGluLeuGlnMetAlaSerAspAspProLysArgLeuGluAlaLeuGlnGly 344
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6 TyrAlaAlaGluThrSerPheValSerProlleLeuLeuGlnIleGlyValAspHisLys
                                                                                                                                                                                                                                                                                                                                                                           437 TTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA
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Mismatches:
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             Length:
Matches:
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519.50
39.43%
23.66%
8.09%
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Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system is a peripheral nervous system contained neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and CN.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification.
                                                               Human: nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Yang Y,
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173
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223
275
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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Matches:
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                                 Human polypeptide SEQ ID NO 3372.
                                                                                                                                                                                                                                                                                                      2000US-05488725.
2000US-0552317.
2000US-0598042.
2000US-0653450.
2000US-0653450.
2000US-0653450.
2000US-0653450.
                                                                                                                                                                                                                                                                           26-DEC-2000; 2000WO-US34263
22-OCT-2001 (first entry)
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466.00
34.00%
22.97%
7.26%
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N-PSDB; AAI59383.
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                                                                                                                                                                                                            WO200153312-A1.
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                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
                                                                                                                                                                                Homo sapiens.
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09-JUL-2000;
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                                                                                                                                                leukaemia.
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Zhao QA,
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222 CCGAGACGAGCAGTTCTGGAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCA 281

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ογ	1043	3CGCCTGCTT
qq	423	GluGlyAlaLeuThrSerGlyCysAspGlyAspIleLeuArgValGlySerLeuAspThr 442
Qy	1055	1060
QQ	443	SerLysProArgSerSerGlyIleLeuLysArgProGlnThrLeuAlaIleProAspAla 462
0y	1060	1060
QQ	463	AlaGlyGlyGlyGlyFroGluThrSerArgArgArgAsnValThrPheSerGlnGlnVal 482
Qy	1060	1060
Db	483	AlaAsnIleLeuLeuAsnGlyValLysTyrGluSerGluLeuThrGlySerSerGluArg 502
Qy	1001	CTGCACCAGCTGTGCTGCCGCATGCCCGCACC 1093
Db	503	AlaGluGlnProLeuSerValGlyArgLeuCysSerThrIleCysAsnMetProLysAla 522
Qy	1094	CACTCATGACCTTC
Db	523	LeuargThrLeuCysValAsnHisPheLeuGlyTrpLeuSerPheGluGlyMetLeuLeu 542
٥y	1154	TTTTACACGGATTCGTGGGCGAGGGCTGTACCAGGCGCGTGCCCAGAGCTGAGCCGGGC 1213
Db	543	PheTyrThrAspPheMetGlyGluValValPheGlnGlyAspProLysAlaProHisThr 562
٥y	1214	ACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCCTG 1273
Db	563	SerGluAlaTyrGlnLysTyrAsnSerGlyValThrMetGlyCysTrpGlyMetCysTle 582
Qy	1274	CAGTGGGCCATCTCCTGTCTCTCTCTGGACGGGTGGTGGTGCAGCGATTCGGC 1333
Db	583	TyrAlaPheSerAlaAlaPheTyrSerAlaIleLeuGluLysLeuGluGluPheLeuSer 602
Qy	1334	ACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGC 1393
QQ	603	
Οy	1394	CTGTCCCACAGTGTGGCGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCA 1453
Db	623	
Οy	1454	GCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCAGGGGGGAAAGCAGGTGTTC 1513
Db	643	ThrLeuCysThrLeuProTyrSerLeuLeuCysAspTyrTyrGlnSerLys 659
Qy	1514	CTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGC 1573
Db	099	LysPheAlaGly 5erSerAlaAspGlyThrArg 670
٥y	1574	TTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGC 1633
Db	670	0.00
	1634	AGTGGCCTGCTCCCACCTCCACCGGGGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTA 1693
Db	670	670
Qy	1694	SSS.
Db	671	
Qy	1754	CTGCTGTCCCAGGTGGCCCCCATCCCTGTTTAT
QQ	929	sserLeuLeuSerCysGlnTyrPheLeuAlaGlnIleLeuValSerLeuValL
Οy	1814	GGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTG 1873
qq	969	GlyPro

Page

2988

40

1 GlyLeuTrpSerTrpTrpGlyLysLeuGlyValGlyGluMetLeuGlyValGlyGluIle

3046 GGGTTGTGGAGCTGGTGGGGAAAGTTGGGGGGTAGGGGAAAG-TTGGGGGTAGGGGAAATT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to increase stem cell probliferation, to regulate hemmatopolesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; money commune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding a range of human polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                        Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
1874 GGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATT 1912
                                 705 AlaAsnGlyValMetTyrPheSerSerLeuValSerPhe 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; Page 282; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                    Novel human secreted protein #843.
                                                                                                                                                                          AAU30352 standard; Protein; 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Táng YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .71e-25
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95.60%
94.51%
7.05%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200179449-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                           18-DEC-2001
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                                                                                                                                                                                                                                    AAU30352;
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                                                                                                                   RESULT 39
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3106 GATGGACAAAGGCTTGGGAAACCGCACTTTGTGGTTCTGGTCCTGCAGTAGCTCCAAACA 3047

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2928
                                                       2927 AACCAGGCTGGCCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAGACCTGAAGCCCCA 2868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epicopes antibodies raised against the polypeptides (or antigenic epicopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for
                         9
                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                               Human; prostate cancer; cytostatic; immunostimulant; tumour; immunogen.
                                                                     Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, SR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated prostate-specific
                                                                                                               2867 CCCTCTACCTTCCAACACCCTAACCTTGGG 2835
                                                                                                                            Human prostate cDNA encoded protein #67.
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                                                                                                                                                                                                 AAU69873 standard; Protein; 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0593793
2000US-0605783
2000US-0636215
2000US-0651236
2000US-0651279
2000US-0657279
                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001; 2001WO-US09919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0568100.
2000US-0570737.
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                                                                                                                                                                                                                                                         30-JAN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS64041
                                                                                                                                                                                                                                                                                                                                                                         WO200173032-A2
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12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-2000;
06-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                      04-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fanger GR,
                                                                                                                                          81
                                                                                                                                                                                                                              AAU69873;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li SX,
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1310 GACCGCCTGGTGCAGCGATTCGGCACTCGAGCTCTATTTGGCCAGTGTGGCAGCTTTC 1369
                                                                                                                                                                                                                                              1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCC 1429
                                                                                                                                                                                                                                                                                          The present invention describes polynucleotide sequences (I) which encode
                                                                                                                                                                                                                  1 AspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPhe 40
                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                                                                           New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
detecting cancer. The present sequence is a prostate specific polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate cancer; prostate-specific; diagnosis; vaccine;
                                                              123
87
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                                                                       Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                    Gaps:
                                                                                                                                      US-09-759-143-110 (1-3410) x AAU69873 (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               P553S splice variant amino acid P553S-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 463-464; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; gene therapy; metastasis
                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                               AAM01228 standard; Protein; 123
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CH,
                                                            6.07e-24
426.00
97.83%
94.57%
6.64%
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MD, Fanger GR, Day
                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-425873/45.
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                               123 AA;
                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                   Alignment Scores:
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Kalos MD,
                                                                                                                                                                                                                                                                                        1430
                               Sequence
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                                                                                                       Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
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SSXS
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1250 ATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATG 1309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCCGTGGTGACAGCTTCAGCC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and can be used in vaccine production and gene therapy. (I), (II), and includes to (II), fusion proteins comprising (II), and isolated antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AMH93357 to AMH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 AspArgLeuValGInArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPhe 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate-specific proteins (II). (I) and (II) have cytostatic activity,
                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human P553S splice variant encoded protein SEQ ID NO 706,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1490 TACCACCGGGAGAGCAGGTGTTCCTGCCCAAATAC 1525
                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0904804.
98US-0020956.
98US-0030607.
98US-0115453.
98US-0159812.
                                                                                                                                                                                                                                                                          6.07e-24
426.00
97.83%
94.57%
6.64%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUL-2002 (first entry)
                                                                                                                                                                                                                             Sequence 123 AA;
                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2002022248-A1.
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01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
                                                                                                                                                                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2002
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                                                                                                                                                                                                                                                                             Pred. No.:
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Tue Jun 10 11:28:19 2003

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2290 CAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA-----GAG 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCT--- 2291
                                                                       Pendent group; repeating unit; enzyme recognition site; sealant; fibrin; enzymatic cross-linking; biocompatible material; structural integrity; medical adhesive; wound closure; tissue repair; transglutaminase.
         The amino acid sequence of the protein polymeric adhesion substrate (PPAS) 1-B. The protein comprises 10 repeats of the PPAS1-B monomeric repeat (AAR80326) which consists of the CLP 3.7 gene encoded sequence (AAR80321) linked to the human fibrin cross-linking substrate peptide 93.2 sequence (AAR80316). The polymers can be used in biological systems where in situ formation of a biocompatible material with structural integrity is required e.g. as medical adhesives and sealants or for wound closure or tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GlySerProGly------AlaProGlyThrProGlyGluGlyGlnGlnHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein polymers comprising repeating units and sequences of enzyme-catalysed covalent bond formation useful as a blocompatible material for wound closure and tissue repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             762
257
38
38
298
263
                                                                                                                 1490 TACCACCGGGAGAGCAGGTGTTCCTGCCCAAATAC 1525
                                                                                                                                 Conservative:
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Matches:
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                                                                                                                                                                                                                                                                                                    Protein polymeric adhesion substrate 1-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROT-) PROTEIN POLYMER TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (1-762)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-759-143-110 (1-3410) x AAR80327
                                                                                                                                                                                                           AAR80327 standard; Protein; 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0205518
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                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                            WO9523611-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-MAR-1995;
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                                                                                                                                                                                                                                                                     18-APR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cappello J;
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                        AAR80327;
                                                                                                                                                                              RESULT 43
                                                                                                                                                                                              AAR80327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTC 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Wang A, Skelky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; SEQ ID NO 706; 87pp; English.
15-JAN-1999; 99US-0232149.
09-APR-1999; 99US-0288946.
12-JUL-1999; 99US-0352616.
12-NOV-1999; 99US-043313.
18-NOV-1999; 99US-043886.
14-JAN-2000; 2000US-0483672.
27-MAR-2000; 2000US-0588100.
12-MAY-2000; 2000US-058100.
13-JUN-2000; 2000US-058110.
13-JUN-2000; 2000US-058125.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
06-SEP-2000; 2000US-0657279.
06-SEP-2000; 2000US-0657279.
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HARLOCKER S L.
JIANG Y.
KALOS M D.
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WANGA.
SKEIKYYAW.
HEPLERWT.
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RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                        STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-255649/30.
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DILLON D C.
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Best Local Similarity:
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Li SX, Wan
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(MITC/)
(HARL/)
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(KALO/)
(FANG/)
(RETT/)
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(HEPL/)
(HEND/)
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HisteuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPro TCCCGCATTCCAGTGCATGGACCCTTCTGGCTCCTGTATAAGTCCAGACTGAAACC	GCAGCACAGGG	CCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAAC	AGGAGCGGGAGCCAGTGAGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTT :::::	CTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAAT	GGCGACCAGACCCAGCCGCGGCAGACATAAGGCAGTGACAGACTGGCTGAGCTG	GACAATGGAGCCCATAAACAGGATGGGACCACCTGGGACAGCAGGAAGGCACTATCCAG		GGTGGGCTCACCCACCACACACAGAGACATCACAGGCAGAGGCCCC	GCAGAGCGGGGGGGGGGGGGCAGCCACCTCCCAGCACCCACGTGTCCATTAGG ::	GAAGGGACTCCAGGCTTAGGCCTGGCAGGAAGCTGGTCATCAGCTGCTCACTGCT	AGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAG	GGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAGGTGAACCCGGTGAGGGCGGC	TGAAGCTGTCACCACGGCCACACTGTGGGACAGGCATGTGGCACCGGCAG	CCACAGGGAAAGCTGCCACATGGCCAAATAGACTGCTCGAGTGC	CGAATCGCTGCACCGGCCGGTCCATGACCAGAGAGAAGACCAGGGAGATGGCGCACTGCA	GGAAC
91 2239 111 2179	2119	2065	2005	1945	1885	1825	1765	1717	1666	1606	1546	1486	1426	1376	1331	1271
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1070 GCTGGTGCAGCCGGGGAAGCAGGCGCCCAGGTTCC---GGAAAGCCAAGCGGGCCCGGC 1014
                                                               1244 CGCCTTCATCATAGIGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCA-----CGC 1191
                                                                                                                                                                                          1190 CCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131
                                                                                                                                                                                                                                                                                                                  1130 TCCAGCTGCACAGGTCAGCCACGAAGAGCCGGCGCGAGGGTGCGGGGCATGCGGCAGCACA 1071
351 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGlu 370
                                                                                                       371 GlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAla 390
                                                                                                                                                                                                                                        401 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 ProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998 GCGACA---AGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGCCCCAGCGCTGCCT 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 ------GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          728 CAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGCAGCCCCA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1013 ------ATGGACAGCAGTGGG 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       441 GluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGly 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       941 CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAA 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     668 CGCCCAGGATGAGCAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          625 ------GlnGlyLeuProGlySerProGlyAla------- 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 326 TCCGGT------GCCGCAGCGGCGCCTCA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652 ProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySer 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         881 AGAGGCACTCCT------CCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGGT---CCCGGAAGAGGT 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 GlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        563 AGGACAGTG --- CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCAC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 TGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA 447
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CCCACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGGCCGTTCAGG 246		AGCTTCTCAGCCCATGCTCACACCTGCTGGGGCCACCTCAGTGGGGACCGTCC 66		PPASI-B. PPASI-B; sealant; uman.			New recombinant protein polymers - containing naturally occurring repetitive units for crosslinking by enzymes, useful as medical adhesives and sealants, depots and matrices Example 4; Column 27; 70pp; English. Protein polymer adhesive substrate PPASI-B comprises 10 repeats of a monomer (see AAW49714) consisting of human fibrin gamma chain peptide 93.2 (see AAW49718) inserted into a structural backbone of collagen repeat motifs (see AAW49718). The 68 kDa PPASI-B polymer has been expressed in Escherichia coll HBDO1 transformants using plasmid perf034. Claimed recombinant protein polymers are capable of covalent crosslinking by enzymatic reaction to form products which set quickly and have good adhesive properties and high which set quickly and have good adhesive properties and high in water, allowing protein solutions of over 10 wt.% to be formed while maintaining good flow properties. CLP polymers have good tissue. The fibrin peptide 93.2 inserts of PPASI-B provide glutamine donor sites for Factor XIIIa mediated cross-linking.
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2290 CAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA-----GAG 2240
                                                                                                                                                                                                                                                                                2239 TCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAACC 2180
                                                                                                                                                                                                                                                                                                                                        2179 CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGGAGAGAGGAGAGGGACGCCC 2120
                                                                                                                                                                                                                                                                                                                                                                                              2119 CAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGT-----GGCAGCAGAGAG 2066
                                                                                                                                                                  2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCT--- 2291
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                                                                                                                                                                                                                                          1666 GCAGAGCGCGGGTGGAGGTGGGAGCAGGCCACTGCCTCCAGCACCCACGTGTCCATTAGG 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1606 GAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCT 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1546 AGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAG 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1486 GGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGC 1427
                                                                                                                                                                                                                                                                                                  160 GlnHisHisLeuGly------GlyAlaArg 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 ----- 187 ---- 187
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|------GlyAlaProGlyThrProGlyProGlnG 286
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                                           762
257
38
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qa		qa X	605 GlyThrP1 506 TGGCTGAG
ογ	1426 TGAAGCTGTCACCACCACACTGTGGGACAGCATGTGGCACCGGCAG 1377	r da	
qa	301GlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAla 319	γò	446 TGGTCATC
ХО .	ATAGACTGCTCGAGTGC	qa	625
q		Qy	386 CIGCGGC
Οy		qq	634P1
qa	GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro	Qy	326 TCCGGT-
Ολ	GGAACAGCCCCAGGCTGCCCATCCGAA	qa	652 ProGlyG
Д	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGlU	QY	302 CCCACAG
λο		qq	672 ProGlyA
go ::	3/1 GlyGinGinHisHisBeuGiyCiyarakIgGinAlaGiyaspvalCiyastriOsiyAria 550	QY	245 CACTCCA(
à â		QQ	691 yThrPro
an i	404004000000H4000000000H00004000000	Qy	185 CCGCCAA
Šī í		QQ	710
g S	GIYSEFFIOGIYAIAFFIOGIYINIFFIOGIYFIOGINGIYEEUFIOGIYSEFFIOGIYATA	QY	125 AGCTTCT
δλ	GCTGGTGCAGCCGGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCGCCCGGC	qo	725 uGlyGln
අු		Qy	65 ATCA
Qy	1013	qa	 741 ySerPro
qq	441 GluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGly 460	RESULT	JLT 45
δλ	998 GCGACAAGGAGGGGCCGACACCCTTCTGCTGGCTCGGTGGGGCCCCACCGCTCCT 942	AAW	O A
qo	461 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 477	XX	AAW57668;
οy	941 CCTCAGCCACCAGCAGTGTGGGCTACGCAGGTGAGGAAGATGAGGTGAGCCAAGGCCAA 882	XX	27-AUG-1998 (fi
qo	478 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 497	XX	Š.
οy	881 AGAGGCACTCCTCCTGGGTGCCCAGGTAGGGGCCAGGCACTGG 837	XX	Collagen-like po
Dp	498 GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHis 517	XXX	
δy	836 TGTCCCAGTCAATGGCAGGAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 783	SOX	Synthetic.
qa	518 LeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro 533	N A	US5773249-A.
ογ	782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCGGGAAGAGGT 729	DD	30-JUN-1998.
qq	534GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 548	PF	02-MAY-1996; 9
٥y	728 CAGAGAGCAGCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCA 669	P.R. 00	02-MAY-1996; 9
QQ	549 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 566	7 07 C	
Oy	rgggat(7 4 d d	06-T-004-T000 06-NOV-1990; 06-NOV-1991:
qa	567 GlyproGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGly 584	PR	
Oy	608 GCCAGCCGGCCCTTGGGATGAGAAGAGCCTCAGCAGGATGCCCA 564	XX	(PROT-) PROTEIN
qq		XX PI	Cappello J, Fer
Oy	563 AGACAGTGCCCAGATGAAGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCAC 507	XX	WPI; 1998-387004
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GCCTCTGGACCATAGTGGGCCAGGCGG---TAGGGCTCAGGGGCCGTTCAGG 246
                                                                                                                                                                                                                                                                                                                                    AGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGGCCTCTCCTTGCTG 186
                                                                                                                                                                                                                                                                                                                                                         ACTGCCTAGGAATCAGCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                     GluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySer 671
                          AGCCTAGGAGGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA 447
                                          TGAACTICTCCTCTACCCCCACTICCAGCAGCAGAGGCGGCACATAGGTGATGC 387
                                                                                                         CCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTT 327
                                                                                                                                                                         ------GCGCAGCAGCGGCTCA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oolymer; synthetic polymer; fibre coating; ice; catalytic substance.
ProGlyProGlnGlyLeuProGly-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CTCAGATCCTGGCCGA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rd; peptide; 762 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0642255.
86US-0927258.
87US-0114618.
88US-0269429.
90US-0791160.
92US-09710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0577046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                irst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        errari FA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                olymer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04/33.
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This sequence represents a unnatural collagen-like polymer of the invention. The products may be used as films, fibres, moulded objects and admixed with other natural or synthetic polymers or coatings on fibres, films, labware or other surfaces, e.g. prosthetic devices. The polymers may be used for binding a wide variety of specific binding materials, as catalytic substances (where the amino acid sequence may specifically chelate a wide variety of elements), as purification media, composites, laminates or adhesives. They may also be combined with incrganic or organic materials such as carbon fibres, nylon fibres, nitrocellulose, etc., as flask coatings or in synthetic matrices for the growth and study of cells, as affinity columns or as supports for blological materials. The polymers have collagen-like properties, but may sequences can be tailored to give the desired properties.
             Recombinant collagen-like polymers - useful for making gels, films, fibres, etc.
                                                                                                Example 7; Column 51; 93pp; English.
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762 AA; Sequence

Alignment Scores	ores:				
Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	2.42e-21 395.00 34.50% 30.06% 6.35%	Length: Matches: Conservative: Mismatches: Indels:	762 257 298 263 52	
09-759-14	13-110 (1-34	US-09-759-143-110 (1-3410) x AAW57668	(1-762)		
2347	17 GGGAAACCA	AGGTGACTGAGTTTA	TTCAGCTCCCAAAAAC	CCTTCTCTAGGTGTGTCT	2291
1		 	AlaProGlyThr	GlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHis	06
2290		AGCTAGCTGTTAAC	CCTGAGCCTGGGTAAT	CAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAG 224(2240
01	91 HisLeuGly	GlyAlaArgGlnAl	aGlyAspValGlySer	ProGlyAlaProGlyThrPro	110
2239	39 TCCCCGCAT	rtccagtgcatggag	CCCTTCTGGCCTCCCT	GTATAAGTCCAGACTGAAACC	2180
T.	111 GlyProGln	 GlyLeuProGlySe	rproGlyAlaPro	GlyproGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 126	126
2179	79 CCCTTGGAA	AGGCCTCCAGTCAGG	CAGCCCTAGAGACTGG	CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAGGAGGGACGCCC 2120	2120
1:	127 ProGln	GlyLeuProGl	ySerPro	GlyAlaProGlyThrPro	140
21:	19 CAGCCCCC	AGCTGTGCAGCTACG	CACCTCAGCAGCACAG	GGTGGCAGCAGAGAG	2066
1,	 41 GlyProGlr	::: nGlyLeuProGl	::: ySerProGlyAlaPro	141 GlyproGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGl	159
200	2065 CCACATTAC	CTTTGGCAGCAACAG	AAACTGGCGGCCAGCC	CGGCAGCCCCATGGGGCTAAC	2006
ī	::: 60 GlnHisHis	: sLeuGly		160 GlnHisHisLeuGlyGlyAlaArg	167
20	05 AGGAGCGG	GEAGCTGGGACCCAG	TGAGGCAGGCCTCCA	2005 AGGAGCGGGGAGCTGGGACCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTT	1946
1	::::: 68 GlnAlaGly	:::::: yAspValGlySerPr	oGlyAlaProGlyT	hrpro	181
19.	45 CTACGCTGA	AGTATTTGGCCAAGT	CGCTCTTGTCAAATAC	1945 CTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAAT	1886
1	82		GlyProGlnGlyL	euPro	187
18	85 GGCGACCA(GACCCAGGCCTGCGG	CAGACACCATATAGGC	AGTGACAGACTGGCTGAGCTG	1826
ı	88Gly	SerProGlyAlaPro	GlyThrProGlyProG	188GlySerProGlyAlaProGlyThrProGlyProGln	199
18	1825 GACAATGG	AGCCCATAAACAGGG	SATEGGCCCACCTGGGA	GACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAGGAGGCACTATCCAG	1766
7	200		GlyLeuProGlyS	serProGlyAlaProG	209

oy Db Oy	1765 209 1717	GATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCTGGCCTC 1718
qa	229	246
oy Db	1666 246	GCAGAGCGGGGTGGAGGTGGGAGCAGCTGCCTCCAGCACCCACGTGTCCATTAGG 1607 ::: ::: ::: ::: :::
Oy Db	1606	GAAGGGAGCTCCAGGCTAGGGCCTGGCAGGAAGCTGGTATCAGCTGTCCTCACTGCT 1547
Qy	1546	14
qo		ng 286
Qy Db	1486	GGAGGCCAGTGTGTAGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGC 1427
Oy dq	1426	TGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACCGGCAG1377
	1376	
qq	320	ProGlyThrProGlyProGlnGlyLeuProGlySerPro 332
2y Db	1331	CGAATCGCTGCACCAGCCGGTCCATGACCAGAGACCAGGGGAGATGGCGCACTGCA 1272
٥y	7	A 12
Db	351	370
Qy	1244	CGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGC 1191
Qy		
op q	391	
Qy	1130	TCCAGCTGCACAGCTCAGCCACGAAGAGCCGGCGCAGGGGGGGG
qq	401	G1
Qy Db	1070	GCTGGTGCAGCCGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGC.1014
οy	1013	
qa	441	GluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAs
Oy	866	GCGACAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCCT 9
Db	461	AlaproGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 47
Qy	941	CCTCAGCCACCAGGGGGGGGCTGCTACGCAGGTGAGGAGGAGGGTGAGGCCAA 88
Db	478	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 4
Oy	881	AGAGGCACTCCT
Q	498	GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHis 51
٥y	836	; TGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 783

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533	729	548	699	566	609	584	564	604	507	614	447	624	387	633	327	651	303	671	246		186	709	126	725	99	741		
	782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGT	534GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro	728 CAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGGAGCCCCA	549 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro	668 CGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCACCTGCTA	567 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGly	608 GCCAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCA	585 GlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro	563 AGGACAGIGCCCAGAIGAAGGGCCGGCGGCGGCCAIAGCGICCACGCCAGIGGICAC	605 GlyThrProGlyProGlnGlyLeuProGly	506 TGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA	615SerProGlyAlaProGlyThrProGlyPro	446 TGGTCATGAACTTCTCCTCTAACCCCCACTTCCAGCAGCAGAGGCGGCCACATAGGTGATGC	625GlnGlyLeuProGlySerProGlyAla	386 CTGCCGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTT	634ProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr	326 TCCGGTGCCGCAGCAGCGGCTCA	 652 ProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySer	302 CCCACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGG	672 ProGlyAlaProGlyThr-ProGlyProGlyGlyLeuProGlySerProGlyAlaProGl	245 CACTCCAGAACTGCTTTCGTCTCGGCTCTCCAGAAGCTGCGGCCTCTCCTCCTTGCTG	691 yThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly	185 CCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCC	710ProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGl	125 AGCTTCTCAGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTC	725 uGlyGlnGlnH1sH1sH1sEeuGlyGlyAlaArgGlnAlaGlyAspValGl	65 ATCACTCAGATCCTGGCCGA 46	741 ySerProGlyAlaMet-AspProGlyArg 750
Db	Οy	QQ	Qy	qq	Qy	Db	٥y	Db	Οy	Op	οy	Db	٥y	Db	٥y	qa	٥y	QQ	٥y	qq	οy	qq	λά	qq	λγ	qc	λζ	qc

Search completed: June 9, 2003, 22:24:42 Job time: 166.5 secs

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Copyright (c) 1993 : 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Full length cDNA s Prostate tumour sp cDNA sequence of h Human prostate cDN Human prostate tum Human prostate-spe Human prostate-spe Human prostate-spe Human prostate-spe Human prostate tumour an Human L1-12 cDNA s
SUMMARIES	AAV61201 AAV58586 AAC79473 AAS63557 AAS10108 AAH93465 AAH94779 AAH02530 ABL94929
ЭВ	19 119 22 22 22 22
% Query e Match Length DB	3410 3410 3410 3410 3410 3410 3410 3410
% Query Match	100000000000000000000000000000000000000
Score	3409.6 3409.6 3409.6 3409.6 3409.6 3409.6 3409.6 3409.6
Result No.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

	P553S CDNA splice Human mast cell re Thioredoxin-ubiqui Thioredoxin-ubiqui Thioredoxin-ubiqui Human secreted pro Human AM. tubercul Ral2-P501S-E2 cons Ral2-P501S-E2 cons 3' CDNA sequence o 3' fragment of pro Human immunogenic Human prostate cDN
ABK29017 AAA06349 AAS14962 AAS14962 AAS14966 AAB193868 ABB925411 AAS64039 AAH93866	AAH93869 AAB193864 ABN91328 ABN91283 ABN91284 AAN05264 AAS64153 AAH93917 AAN06250 AAN06250 AAN06368
41400440040000111010400	74444777777777777777777777777777777777
3410 44834 40334 40334 40334 40334 40334 4034	6976 6976 1667 2133 2133 11593 1203 1203 789 789 789
000 000 000 000 000 000 000 000 000 00	553.7 56.7 57.7 57.7 57.7 57.7 57.7 57.7 57
3409 32390 32390 32390 32390 32390 32390 3290 32	1815.8 1815.8 1165.2 1150.3 12
11111111111111111111111111111111111111	8888888844444 84597889048845
	o

Full length cDNA sequence of prostate tumour clone L1-12 Prostate; cancer; tumour; vaccine; immunogen; clone; AAV61201 standard; cDNA; 3410 BP 36-JAN-1999 (first entry) RESULT 1

98US-0020956. 97US-0806099. 97US-0904804. 98WO-US03492 WO9837093-A2 Homo sapiens 25-FEB-1998; 25-FEB-1997; 01-AUG-1997; 09-FEB-1998; 27-AUG-1998.

Polypeptides comprising immunogenic portions of prostate proteins -WPI; 1998-609886/51. P-PSDB; AAW71869.

(CORI-) CORIXA CORP. Dillon DC, Xu J;

180 120 180 240 300 300 360 420 480 480 540 540 900 009 720 780 9 9 of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library. GGGAACCAGCCTGCACGCGTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGA GAGTGCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGTTGTG GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG **AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT** GCCGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTG GAGTGCCTGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG GGTGAGCCGCCTGCTGCGCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTGCTAACCTT TGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT GGGGGTAGAGGAGGATTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCG GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC CGCCTGCCTAGCAGGGCTGCTGTGCCCGGATCCCCAGGCCCCTGGAGCTGGCACTGCTCAT CCTGGGCGTGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT GCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTT Gaps 3410; ö 19; Length Indels Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other; cancer ; 0 DB prostate Score 3409.6; Pred. No. 0;); Mismatches οţ Claim 3; Page 79-80; 130pp; English. ö 100.0%; 100.0%; the Best Local Similarity 100. Matches 3410; Conservative for61 121 121 181 Match 181 241 301 301 361 361 421 421 481 481 541 541 601 199 601 661 721 721 781 12 nseq g ò å ద ò g ò g ò g οŽ Op ò da ò g δ ద à a ò a δ 셤 ð Q à

1020 1020 1080 1140 1260 1380 1440 1680 1080 1200 1380 1560 1740 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1560 1680 1800 1800 1860 1860 900 960 960 TGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGAGGAGGCAGCGCTGGGGCCCCAC CATGCCCCGCACCCTGCGCCCGGCTCTTCGTGGCTGTGCAGCTGGAGCTGGATGGCACTCAT CGAGCCAGCAGAAGGGCTGTCGGCCCCCTTCTTGTCGCCCCCACTGCTGTCCATGCCGGGC CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCAGCTGTGCTGCCG GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGGGCTGTACCAGGGCGTGCCCAG AGCTGAGCCGGGCACCGGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGT CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT GGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGCTCTGCGGGGCCTCTGCCTG TGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG TGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 1021 1081 1081 1141 1201 1201 841 841 901 901 961 961 1021 1141 1261 1441 1321 1381 1441 1501 1561 1621 1741 1261 1321 1381 1501 1561 1621 1681 1681 1741 1801 1801 1861 Ω ò · q ò q ŏ g á g δy 유 ò qq οy qq QQ q QΩ à ò οy ò qq g qq g Op δ Qγ δ g Dp οχ ò ŏ à ö

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	-0	CACTGGGT	CACTGGGT	TTCTGTTG			- ₍₃	⋖	- ∢					2341 GTTTCCCATCTCTAAGCC	2401 TTTCTAGGATGAACACT	2401 TTTCTAGGATGAACACT	2461 GTCCTGAGGGGCAACACA	2461 GTCCTGAGGGCCAACACA						GGTCCCCT	GGTCCCCT						O	υ

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PACCCCCAACTTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT 3060
                                                                                                                                               This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pecific tumour protein and fragments - useful ting prostate cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 TGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 420
portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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                                                                          Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
                                                                                                       100.0%; Score 3409.6; 100.0%; Pred. No. 0;
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                                                                                                                       Best Local Similarity 100.
Matches 3410; Conservative
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QY	961	GAGCCAGCAGAAGGGTGTCGCCCCCCTTGTCGCCCCACTGCTGTCC
qa	961	GGCTGTCGCCCCCTCCTTGTCGCCCCCACTGCTGTCCATGCCGGG
Qy	1021	CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCG 1080
qq	1021	cecrrescrircesaacresscoccrecriccccsscrecaecrecress
	1081	ATCCCCCCACCCTCCCCCCCCCCCCCCTCCTTCCTCCTCTCTCTCTCTTT14
qq	1081	TGCCCCCCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCAT 114
٥y	4	20
Ор	1141	CTTCACGCTGTTTTACACGGATTTCGTGGGGGGGGGTGTACCAGGGCGTGCCCAG 120
Qy	1201	GCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGT
ρp	1201	CTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCC
Oy	1261	TGCGCCATCTCCCTGGTCTTCTCTCTGGT
Dp	1261	GGGCTGTTCCTGCAGTGCGCCATCTCCTTCTCTCTCTGGTCATGGACCGCTGG
Qy	7	38
Dp	1321	CAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCTTTCCCTGTGGCTG
٥٠ ج م	1381	CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCGCCCTCACCGG 1440
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οy	4	TTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
QQ	1441	TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
Qy	1501	AAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGAGG 156
Db	1501	GCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACA
Qy		CTAAGCCTGGAGCTCCCTTCCGTAATGGACACGT 162
Db	1561	CTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACAC
Qy	1621	GGGTGCTGGAGGCAGTGCCCTGCTCCCACCTCCGCGCTCTGCGGGGCCTCTGCCTG 1680
qq	1621	derecredaded de contracte de co
. Oy	1681	TGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 1740
Db	1681	GATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGC
QY	1741	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 1800
qq	1741	GGCATCTGCCTGGACCTCGCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCC
Qy	1801	CATTG
Db	1801	CCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGT
Qy	1861	CATTTA
Db	1861	GCCGCAGGCCTGGGTCGCTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGA
Qy	1921	SCGTAGAAACTTCCAG
Dβ	1921	GACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCC
Qy	1981	ACTEGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGT 204
qq	1981	regercccaecrecegererataececeareageceeeerage

201 TTCTGTTGCTGCCAMATANTTGGGTCTCTCTGCTGCCACCTGTGGCGCCCTA 202 TTCTGTTGCTGCCAMATANTTGGGTCTCTCTGCCCACCTGTGCGCCCTT 203 TTCTGTTGCTGCCAMATANTTGGGTCTTCTCTCTCTCTCTCTTGGGTCTGCTGCTGCTG	OY 3121 ATATCTGTGGGGAATCTCACACAGAACTCAGGAGCACCCCTGCCTG	Qy 3181 GAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT	QY 3241 TAGCGGGGTGAATATTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACA 3300 11	Qy 3301 AAATTAAAGGCTTCTTATATGTTTAAAAAAAAAAAAAAA	Oy 3361 AAAAAAARAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	RESULT 3 AAC79473 ID AAC79473 standard; CDNA; 3410 BP.	AX AC AAC79473; XX DI 07-FEB-2001 (first entry)	CDNA Se		WO200061756-A	PF 10-APR-2000; 2000WO-US09688. XX PR 09-APR-1999; 99US-0288950. PR 02-JUL-1999; 99US-0346327.	XX PA (CORI-) CORIXA CORP. XX PI Reed SG, Xu J, Dillon DC;	XX DR WPI; 2000-638568/61. DR P-PSDB; AAB28527. XX	PT A novel isolated polypeptide comprising an immunogenic portion of a PT breast cancer protein useful in the detection and treatment of breast XX	PS Claim 26; Page 91-92; 95pp; English. XX CC The present sequence was isolated from a breast tumour cDNA library. It CC is provided in a specification relating to compounds for immunotherapy			Query Match 100.0%; Score 3409.6; DB 21; Length 3410; Best Local Similarity 100.0%; Pred. No. 0; Matches 3410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
- > 2 > 0 > 0 > 0 > 0 > 0 > 0 > 0 > 0 > 0	2041 TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGCTGCGGTGCGTA	2101 GCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCCCCAGTCTCTAGGGCTCCCTG	2161 ACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTTCCAGAAGGGCTTCCAGAGGGCTTCCAGGGGGGTTTCAGTCTGGACTTATACAGGGAGGCACAAGGGCCTTCCAAGGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCCTTC	2221 ATGCACTGGAATGCGGGGACTCTGCAGGTGCATTACCCCAGGCTCAGGGTTAACAGCTTAACACTAGC	2281 CTCCTAGTTGAGACACCTAGAGAAGGGTTTTTGGGAGCTGATAAACTCAGTCACTG 	2341 GITTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGGG 	2401 TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTGTAGGGGAAGA 	2461 GTCCTGAGGGCCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT	2521 GATCCACCCCTCTTAACCTTTAACAGGATGTGGCCTGTTGGTCTTGTTGCCATCA	2581 CAGAGACACAGGCAITTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCAT 	2641 IGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA	2701 GGTCCCCTGAGATAGCTGGTCATTGGCTGATCATTGCCAGAATCTTCTCCTGGGGT 	2761 CTGGCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT	2821 TCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGG	2881 CTCAACGGCTTCCCTAACCACCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCACTTCCA	CTCCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC	CCCAACTTTCCCCTACCCCCAACTTTCCCCACAGCTCCACAACCCTGTTTGGAGCTACT	GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGT

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n the detection and treatment of breast
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Pred. No. 0;
Mismatches 0; Indels 0; GZ
0; Indels
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108]	114]	1201	1261	1321	1381	144]	1507	156 <u>1</u> 156 <u>1</u>	162]	168]	1745	180	186	192	1983	204	210:	216.
qa	Qy	Qy	Qy Db	Qy	Qy Dp	Qy Dp	QY Db	Qy	Qy QD	Qy Db	Qy Db	Qy Dp	Qy Dp	yo da	oy O	Qy Db	Qy	Oy

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Best Local Similarity
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GR, Rette
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29-AUG-2000;
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09-MAY-2000;
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2161 ACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCC 2220
                 ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 2280
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                         2221 ATGCACTGGAATGCGGGGACTCTGCAGGTTACCCAGGCTCAGGGTTAACAGTAGC
                                                                                                                               2401 TITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTGTAGGGAAGA
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                                                           2461 GTCCTGAGGGGCAACACACAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT
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                                                                                     2341 GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGAG
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polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes antibodies raised against the polypeptides (or antigenic epitopes for antiponic epitopes for antigenic epitopes polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune
                             human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer , ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalos MD;
Carter D;
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                                                                                                                                                          Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                         Jillon DC, Mitcham JL, Harlocker SL, Jiang Y, SR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prostate cDNA sequence #109.
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20000S-0605783.
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2000US-0570737
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Matches 3	3410; Conservative 0; Mismatches 0; Indels 0; Gaps ,0;		
٥٨		QY	1081 CATGCCCCG
QQ		qa	1081 CATGCCCCG
ò		VQ	1141 GACCTTCAC
	61 GTGATGAGACTGTCCCATGAGGGGGGGGGCACAAAAAAAA	qa	1141 GACCTTCACC
0y 1	AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCTTGGCTGTTATTCTTAACCAAGTT	Qy	1201 AGCTGAGCC
		qa	1201 AGCTGAGCCG
0y 1	81 GGCGGCAGCAAGGAGGAGGCGCGCAGCTTCTGGAAGCAGAACCAAAACAAAAAAAA	Qy	1261 GGGGCTGTTC
т		qa	1261 GGGGCTGTTC
Qy 2		οy	1321 GCAGCGATTC
Dp 5		QQ	1321 GCAGCGATTC
. оу	301 GGTGAGCCGCCTGCTGCGGGACCGGAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 360	δλ	1381 CGGTGCCACA
Dp 3	301 GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 360	Οp	1381 CGGTGCCACA
Oy		Qy	1441 GTTCACCTTC
Dp 3	361 TGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 420	QQ	1441 GTTCACCTTC
Ογ 4:	421 GGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGCATTGGTCCAGTGCTGGGCTGGT 480	Ολ	1501 GAAGCAGGTG
Db 4:	421 GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 480	qq	1501 GAAGCAGGTG
Oy 41	Ŋ	Oy	1561 CCTGATGACC
Db 41		q	1561 CCTGATGACC
Qy 5.	541 GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC 600	δō	1621 GGGTGCTGGA
75 qa		qa	1621 GGGTGCTGGA
Qy 6(9	Qy	1681 TGATGTCTCC
)9 qa	60] CGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGGCCCTGGAGCTGGCACTGCTCAT 660	qq	- [-
Qy 66		٥y	1741 GGGCATCTGC
Dp q0		qa	1741 GGGCATCTGC
Qy 72	721 GCTCTCTGACCTCTTCCGGGACCGGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTT 780	Qy	1801 ATCCCTGTTT
7.7 da	721 GCTCTCTGACCTCTTCCGGGACCCGGACCAGGCCTACTCTGTTTTTTTT	ପ	
Qy 78	81 CATGATCAGTCTTGGGGGCTGCCTGGCTACCTCCTGCCATTGACTGGGACACCAG 840	δλ	1861 TGCCGCAGGC
3 <i>L</i> qa		οp	1861 receeded
Oy 84		δy	1921 CGACTTGGCC
Db 841	TGCCCTGGCCCCCTACCTGGGCACCCAGGAGAACTGCCTCTTTGGCCTGCTCACCTCAT	QQ	1921 CGACTTGGCC
Qy 901		δλ	1981 CACTGGGTCC
Db 40		qa	CACTGG
Qy 961		Qy	2041 TTCTGTTGCT(
DD 961	.1 CGAGCCAGCAGAGGGCTGTCGCCCCCCTCTTGTCGCCGCTGTGTGTG	qa	TTCI
Oy 1021		ΟŸ	2101 GCTGCACAGC:
Db 1021	1 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCACCTGTGCTGCCG 1080	qa	2101 GCTGCACAGC
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Qy Db	1081	CATGCCCGCACCTGCGCCTCTTCGTGGCTGAGCTGTGCACTGGTGGTGGCACTCAT 1140
Qy Dh	1141	ACACGATTTCGTGGGCGAGGGCTGTACCAGGGCGTGCCCAG 120
λo	. 0	ACCTICACCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
Op	1201	
Qy Db	1261	GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1320
Qy	1321	CAGCGATTCGGCACTCGAGCTGTTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 138
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a ;	1381	GGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG 144
Dp Dp	4 4	GTTCACCTTCTCAGCCCTGCAGATCCTGCCTACAACTGGCCTCCCTTACCACCGGGA 1500 GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACAGGCCTCCCTC
Qy	1501	AAGCAGGTGTTCCTGCCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG 156
Db	1501	56
٥y	1561	AGCTTCCTGCCAGGCCCTAAGCCTCGCTTCCCTAATGGACACG
DÞ	1561	CTGATGACCAGCT
Oy	1621	SCTCCCACCTCCACCGGGCTCTGCGGGGGCCTCTGCCT
qq	1621	GGTGCTGGAGGCAGTGGCTGCTCC
Qy		SCCAGGGTGGTTCCGGGCCG 174
QQ	1681	GATCTCTCCGTACGTGTGGTGGTGGGTGACCCACCGAGGCCAGGGTGGTTCCGGGCCG 174
٥y	1741	CCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 18
qq	1741	GGCATCTGCCTGGACTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCCAGGTGGCCCC 180
οy	80	AGCCAGTCTGTCACTGCCTATATGGTGTC 186
qq	80	TCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGT
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λy	2101	CCAGTCTCTAGGGCTGCCTG 21
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GGCGGCAGCAAGGAGGAGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAGGACGAGTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ynucleotide encoding polypeptide comprising a portion of tumour protein useful for inhibiting development of prostate
portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 3410;
                                                                      partial tumour protein. The DNA is useful for inhibiting the der
of prostate cancer or for treating prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is a human prostate tumour cDNA which encodes a partial tumour protein. The DNA is useful for inhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer or for treating prostate cancer in a patient
                                                                                                                                                                                                                         Human; prostate tumour protein; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 3409.6; 100.0%; Pred. No. 0; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3410 BP; 667 A; 1014 C; 945 G; 783
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                                                                                                                                                                                                     Human prostate tumour cDNA L1-12
                                                                                                                                          AAS10108 standard; cDNA; 3410
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97US-0904804.
98US-0020956.
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Matches 3410; Conservative
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09-FEB-1998;
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              2221 ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC
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                                                                                  CTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG
                                                                                            GITICCCATCICIAAGCCCCTTAACCIGCAGCTICGITIAATGTAGCTCTTGCATGGGAG
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Human; prostate cancer; prostate-specific; diagnosis; vaccine;

cytostatic; gene therapy; metastasis; ss.

Homo sapiens

Human prostate-specific full length cDNA seguence

04-OCT-2001 (first entry)

AAH93465;

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SL, Jiang Y, Reed SG; Stolk JA, Skeiky YAW;

Harlocker SI Retter MW,

SE,

Mitcham 3R, Day 0

GR,

Dillon DC, MD, Fanger

Xu J, Dil Kalos MD,

(CORI-) CORIXA CORP.

Meagher MJ;

Wang A,

WPI; 2001-425873/45.

16-JAN-2001; 2001WO-US01574 14-JAN-2000; 2000US-0483672

19-JUL-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and can be used in vaccine production and gene therapy. (I), (II), (II), (II) and the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGGCAGCAAGGAGGAGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes polynucleotide sequences (I) which
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100.0%; Pred. No. 0;
iive 0; Mismatches
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Matches 3410; Conservative
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AAH93465 standard; cDNA; 3410 BP RESULT 6 AAH93465 ID AAH9 XX

301 GGTGAGCCGCCTGCTGCGGCAACGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTTGTTGTTGTTTGT

syndrome; nosome 1;

chromosome 22qil.2; prostate-specific protein; chromosome prostate specific antigen; PSA; ss.

WO200134802-A2

09-NOV-2000; 12-NOV-1999; 18-NOV-1999;

17-MAY-2001

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GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGT
                                    GATCCACCCCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
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The present invention describes an isolated polypeptide (Pl) comprising to least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (NI) encoding (Pl). (Pl) and (NI) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes 7704P, P172P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent

Isolated polypeptide comprising at least an immunogenic portion compressing prostering protein, useful in the diagnosis and therapy of

Claim 5; Page 164-165; 325pp; English.

cancer

prostate

Harlocker SL, Jiang Y, , Day CH, Skeiky YAW,

Retter MW, Stolk JA, Mitcham JL,

WPI; 2001-308785/32.

99US-0439313.

(CORI-) CORIXA CORP

Dillon DC,

Xu J,

Kalos MD,

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361 TGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 420
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illarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                   Best Local Similarity
Matches 3410; Conserv
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25-SEP-2001

AAH84779

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RESULT 7 AAH84779

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Gaps

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DB 22; Length 3410;

Seguence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

Query Match

the present invention.

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y d	1501	GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAACAGGAGACACAGGGGGGACACGGGGGGGCGCTAGCAGGAGGGGGACACGGGGGGGG	1560
λλ	1561	TGATGACGAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT	C4
ą	1561	GATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT	1620
λγ 0p	1621	CCGCGCTCTGCGGGCCTCTGCCTG	1680
ά		GANGICICCGIACGIGIGGIGGIGGIGGIGAGCCCACCGAGGCCAGGGIGGIICCIICC	4
q	1681	TGATGTCTCCGTACGTGGGTGGGTGGGTGAGCCCACGGAGGCCAGGGTGGTTCCGGGCCG	4
~	1741	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 1	0
q		GGCATCTGCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTTCCCAGGTGGCC	1800
<u>*</u>	0	AFCCCTGTTATATGGGGTCCATTGTCCAGCTCAGCCAGCTGTGTGTG	9 (
Ω	xo ox	CCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGGTGT	٥
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γ g	1921	CGACTTGGCCAAATACTCAGGGTAGAAAACTTCCACACATTGGGGTGGAGGGCTGCT	1980
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ά	2041	TCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGAGGTGCGTA	2100
q	2041	CAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTA	2100
λ,	2101	GCTGCACAGCTGGGGGCTGCGTCCTCCTCTCCCCAGTCTCTAGGGCTGCCTG	16
q	2101	CTGCACAGCTGGGGGCTGGGGGGTCCCTCTCTCTCCCCAGTCTCTAGGGCTGCCTG	21.60
¥ 4		ACTGGAGGCCTTCCAAGGGGGTTCAGTCTGGACTTATACAGGAGGCCAGAAGGGCTCC 2	2220
Q.	9	3GAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGGAGGCCCAGAAGGGCTCC	77
≿ q	2221	ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTTAACAGCTAGC 1	2280 2280
λ̈́	2281	TCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG	4
ą	2281	CICCTAGTIGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG	2340
λ̈	2341	GTTTCCCATCTCTAAGCCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 2	2400
qc	2341	TTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG	2400
λζ	2401	TITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2	2460
qo	2401	TTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA	2460
<i>≿</i> 46	2461	GTCCTGAGGGGCAACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCT 2	2520
: >	52	CCACCCCCTTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA	28
, q	i in	GATCCACCCCCTCTTTACCTTTTATCAGGATGTGGCCTGTTGGTCTTCTGTTGCCATCA 2	28

Cheever MA;

Reed SG,

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CAGAGACACACGCATTTAAATTTTAACTTATTTATTTTAACAAAGGTAGAAGGGAATCCAT
         CCCAACTITCCCCTACCCCCAACTITCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT
                                 TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA
                                                                    GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTTCTGGGGT
                                                                                                                                      Human; prostate tumour antigen; prostate tumour; therapy; diagnosis; prostate cancer; immunogenic; cytostatic; vaccine; ss.
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                                                                                                                                                                                                                                                                                                       The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have eytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynuclectides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonuclectides that hybridise to a polynuclectide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB74498 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGCAGCAAGAAGAAGAAGAGCCCCACCTCTGGAGCAGAGCCGAGACGAAGAAGTCTG
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                                                                                                                                                                                                                                Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer \cdot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 3409.6; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                              Claim 4; Page 155-156; 276pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 3410; Conservative
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61 CCTG	1621 GGGTGCTGGAGGCAGTG 	1681 TGATGTCTCCGTACGTG' 	1741 GGCCATCTGCCTGGACC' 	1801 ATCCCTGTTTATGGGCT(1861 TGCCGCAGGCCTGGGTC7 	1921 CGACTTGGCCAAATACTC 	1 CACTGGG7 	TTCTGTTGCTC		2161 ACTGGAGGCCTTCCAAGG 	221 ATGCACTGG 	281 CTCCTAGT: 281 CTCCTAGT:		2401 TTTCTAGGATGAAACACT 	2461 GTCCTGAGGGGCAACACA 	21 21	581 CAGAGACACAGGCAI 	2641 TGCTAGCTTTTCTGTGTT
qa	Oy Dp	δλ	Qy Dp	Qy Dp	Qy	Qy Dp	oy G	S S	දුරු පු	QQ Pp	Qy	Qy Dp	Qy Bp	Qy Dp	Qy Db	Qy Dp	Oy Dp	Oy Dp
	541 GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGAGCCTCTTTCTCATCCCAAGGGC 600	601 CGGCTGGCTAGCAGGGCTGCTGCCCGGGTCCCCTGGAGCTGGCACTGCTCAT 660	TTCACTCCACTGGAGGCCCT 72	CTATGCCTT 78	781 CATGATCAGTCTTGGGGGCTGCCTGGGCTACCTGCTGCCTGC	841 IGCCCIGGCCCCTACCTGGGCACCCAGAGAGAGTGCCTCTTTGGCCTGCTCAT 900	901 CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGCGCGCTGGGCCCCAC 960	961 CGAGCCAGCAGAGGCTGTCGGCCCCTCTTGTCGCCCCACTGCTGTCCATGCCGGGC 1020	1021 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCCG 1080	1081 CATGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGTGCACTGGTGGATGGCACTCAT 1140	1141 GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAGGGCGTGCCAG 1200	1201 AGCTGAGCCGGGCACCGAGGCCCGÀAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260 	1261 GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1320	1321 GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 1380	1381 CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGG 1440	1441 GTTCACCTTCTCAGCCTGCAGATCTGCCCTACACACTGGCCTCCTTACCACGGGA 1500	1501 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1560 	1561 CCTGATGACCAGCTTCCTGCCGAGGCCTAAGCCTCCCTTCCCTAATGGACAGT 1620
qq	Oy Op	Qy Db	Qy	Qy	Qy	장 입	oy qq	oy Ob	Oy Op	oy Og	Qy Db	S S	çy q	oy Op	Oy Op	oy Op	Qy	λο ,

1561	CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620
1621	GGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGGGCTTGCGGGGCCTCTGCCTG :
1681	TGATGTCTCCGTACGTGTGGTGGTGGTGGGCCCACGAGGCCAGGGTGGTTCCGGGCCG 1.
1741	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 1800
1801	ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGGTGTC 1860
1861	TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAGAG 192
1921	CGACTTGGCCAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCTGCCT 1980
1981	CACTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGT 204
2041	TTCTGTIGCTGCCAAAGTAATGIGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTA 2100
2101	GCTGCACAGCTGGGGGCTGGGGGCGTCCCTCTCTCCCCCAGTCTCTAGGGCTGCCTG 2160
2161	ACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGAGGCCAGAAGGGCTCC 2220
2221	ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 2280
2281	CTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACTG 2340
2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTGTTTAANGTAGCTCTTGCATGGGAG 2400
2401	TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2460
2461	GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCT 2520
2521	GATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580
2581	CAGAGACACAGGCATTTAAATATTTAACTTATTTAATTAA
. 2641	TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA 2700

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AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGATGAGACGTGTCCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG
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Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New prostate-specific polynucleotides for diagnosing and treatir diseases, in particular prostate cancer, and as markers for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, 3R, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
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100.0%; Pred. No. 0;
Live 0; Mismatches
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20000S-0636215.
20000S-0651236.
20000S-0657279.
20000S-067279.
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99US-0288946.
99US-0352616.
              98US-0030607.
98US-0115453.
98US-0159812.
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Matches 3410; Conservative
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WANG A.
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RETTER M W.
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KALOS M D.
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DAY C H.
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                                                                                                                                   Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
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301 G 301 G	GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT 360
361 T 361 T	TGGCCTGGAGGTGTGTTTGGCCGCAGCCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT 420
21 G 21 G	GGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 480
481 0	CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGC 540
541 0	GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC 600
	CGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCAT 660
	CCTGGCCTGGGGCTGCTGTGTTCTGTGCCAGGTGTGCTTCACTCCACTGGAGGCCCT 720
	GCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTT 780
	CATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCATTGACTGGGACACCAG 840
841	TGCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCAT 900
901 (CTTCCTCACTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGCGGCGCTGGGCCCCCAC 960
	CGAGCCAGCAGAAGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGC 1020
1021	CCGCTTGGCTTTCCGGAACTGGGCGCCCTGCTTCCCCGGCTGCACCGGTGTGCTGCCG 1080
	CATGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCAT 1140
1141	GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAG 1200
1201	AGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260

161 ACTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGAGGCCAGAAGGCCTC 222 161			3CTGGT 13 3CTGGT 13 3CTGGT 13 3CCTGC 14 11
221 ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGGTTCAGGGTTAACAGGTAGG 228	23	161 ACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAG 	36CTCC 222 3GCTCC 222
281 CTCCTAGAGACACCTAGAGAGGTTTTTGGAGCTGAATAACCTGGTCACTG 234 281 CTCCTAGTTGAGACACCTAGAGGTTTTTGGAGCTGAATAACTCAGTCACCTG 234 281 CTCCTAGTTGAGACACCTAGAGGTTTTTTGGAGCTGAATAAACTCAGTCACCTG 234		10.1 ACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAA 22.1 ATGCACTGGAATGCGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTA 22.1 ATGCACTGGAATGCGGGAATTCTCAGGAGTGATTACCAAGGTTAACAGGGTTA	366CTCC 222 AGCTAGC 228
281 CTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG 234.		281 CTCCTAGTTGAGACACCTAGAGGGGTTTTTGGGAGCTGAGGTTATTGGGAGCTGAATAAACT	TCACCTG 234
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TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA
                                                                        TITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA
                                                                                                                   GATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTCTTGGTTGCTTCTGTTGCCATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides. The sequences are useful for treating cancer, preferably breast cancer, in a patient or for stimulating an immune response. The polynucleotides and polypeptides are also useful in the diagnosis and monitoring of breast cancer. A method for detecting the presence of a cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that bind to a breast tumour polypeptide, detecting in the sample an amount of polypeptide to a predetermined cut.off value, therefore determining the presence of a cancer in the patient. Sequences ABK28020-ABK29025 represent cDNA clones encoding human breast tumour polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG
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                                                                                                                      Human; breast tumour polypeptide; gene; ss; breast cancer; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotides encoding breast tumour polypeptides, useful breast cancer or stimulating an immune response -
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                                                                                       Human breast tumour polypeptide full length cDNA clone
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ive 0; Mismatches
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12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
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Matches 3410; Conservative
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ολ	661 CCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT 720	Š E	1741 GGCCAT
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ර් සි	/81 CATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCATTGACTGGGACACCAG 840	. d	TGCCG
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Qy 1	Ч	Oy	2101 GCTGCAG
Db 1	1021 CCGCTTGCCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCCGC 1080	qq _.	2101 GCTGCA
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Qy 1		ΟŸ	2221 ATGCAC
Db 1	1141 GACCTTCACGCTGTTTTACACGGATTCGTGGCCAGGGCTGTACCAGGGCCTGCCCAG 1200	qq	
0y 1	201 AGCTGAGCCGGGCACCGAGGCCCGGAGACTATGATGAGGCGTTCGGATGGGCAGCCT 1260	ōy.	2281 CTCCTAC
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Qy 1	1261 GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1320	δ t	2341 GTTTCCC
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0y 1.	321 GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGC 1380	δ t	2401 TTTCTAC
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δδ	38	CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGACAGCTTCAGCCGCCCTCACCGG 1440
QQ	1381	CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCG
Qy	4	GITCACCITCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC
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Qy	1681	GATGICICCGIACGIGIGGIGGIGGIGGIGGICCACCGAGGCCAGGGIGGIICCGGGCCG 174
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ΟŊ	1741	GCATCTGCCTGGACTCCTGGATAGTGCCTTCCTGCTGTCCAGGTGGCCC
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QQ	1801	CCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCCATATGGTGT
οy	1861	TGCCGCAGGCCTGGGTCTGGTCGCCATTACTTTGCTACACAGGTAGTATTTGACAAGAG 1920
Ωp	1861	GCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGA
ΟŻ	1921	ACTTCCAGCACATTGGGGT
qq	1921	SACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGC
Οy	98	CACTGGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGGCTGCCGGCTGGCGCCAGT 2040
qq	1981	ACTGGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAG
ΟŽ	04	TTCTGTTGCTGCCCAAGTAATGTGGCTCTCTGCTGCCCCTGTGCTGCTGAGGTGCGTA 2100
qq	2041	CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGT
Qy	0	GCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCCCCAGTCTCTAGGGCTGCCTG 2160
qq .	2101	SCACAGCTGGGGGCTCCCTCTCTCTCCCCAGTCTCTAGGGCTGCCT
Qy	2161	ACTGGAGGCCITCCAAGGGGTTTCAGTCTGGACTTATACAGGGGGGGCCAGAAGGGCTCC 2220
qq	2161	CTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTC
ΟŸ	2221	ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 2280
οp	2221	SCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAG
Οy	2281	CTCCTAGTTCAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG 2340
Ob	2281	TCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCT
ΟY	34	GTTTCCCATCTCTAAGCCCCCTTAACCTGCAGCTTGTTTAATGTAGCTCTTGCATGGGAG 2400
qq	2341	TTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGA
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Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:110 duman; prostate cancer; diagnosis; tumour; gene therapy; detection;

immunogenic; cytostatic; vaccine; ss.

WO200004149-A2

Homo sapiens

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Length 3410;
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DB 21;
            100.0%; Pred. No. 0; ive 0; Mismatches
 Score 3408;
 99.98;
               Best Local Similarity 100.
Matches 3409; Conservative
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(first entry)

13-JUN-2000

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RESULT 11 AAA06349

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Sequence 3410 BP; 667 A; 1015 C; 945 G; 782 T; 1 other;

invention.

the present

The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used a a probe or the modulate the expression of the polypeptides. AAA06241 to AAA06691 and AAX82000 to AAX82000 represent sequences used in the exemplification of

prostate protein -

New polypeptide useful for treating and diagnosing comprises an immunogenic portion of prostate tumor

Claim 1; Page 135-136; 263pp; English.

Mitcham

Xu J,

Yuqiu J,

SL,

Harlocker

Dillon DC,

(CORI-) CORIXA CORP.

WPI; 2000-171268/15.

98US-0115453. 98US-0116134. 98US-0159812. 98US-0159822. 99US-0232149. 99US-02321880.

14-JUL-1998; 23-SEP-1998; 23-SEP-1998;

15-JAN-1999; 15-JAN-1999; 09-APR-1999;

99WO-US15838

14-JUL-1999;

27-JAN-2000

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Qy Dp	CCGCCTCTGCTGCTGGAAGT 42	Qy	1441 GITCACCITCICAGCCCIGCAGAICCIGCCCIACACACIGGCCTCCCICIACCACCGGGA 1500
Oy Dp	CCTGGT 4	Qy Dp	1501 GAAGCAGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1560
Qy Dp	\$ 9000000000000000000000000000000000000	Oy Op	1561 CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620
Oy Dp	541 GCCTTCATCTGGGCACTGTCCTTGGGCATCCTGTGGGCTCTTTCTCATCCCAAGGGC 600	У д	1621 GGGTGCTGGAGGCAGTGGCCTGCTCCACCTCGACCGGGGTCTTGCGGGGCCTCTGCCTG 1680
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Oy Op	841 IGCCCIGGCCCCTACCTGGGCACCCAGAGAGAGTGCCTCTTTGGCCTGCTCACCCTCAT 900 	QY Db	1921 CGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
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                                        CAGAGACACAGGCATTTAAATTTTAACTTTATTTAACAAAAGTAGAAGGGAATCCAT
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Novel PROST 03 polypeptides and polynucleotides useful in research, diagnosis and therapeutic applications, particularly for use in cancer

Claim 6; Fig 1; 77pp; English.

therapeutics

Steinbrecher R;

Schneider DW,

Parry G,

Ď,

Parkes

RJ,

Lau T, Lin RJ, Van Hêuit PT,

Wu J;

WPI; 2002-041404/05. P-PSDB; AAU10324.

27-APR-2000; 2000US-200065P. 20-APR-2001; 2001US-0200065. 26-APR-2001; 2001WO-US13323

(SCHD) SCHERING AG.

"PROST 03"

/product=

WO200181577-A2

01-NOV-2001

/*tag= a

Location/Qualifiers 282..1943

SS

cytostatic; vaccine;

Homo sapiens

Key

```
The invention relates to an isolated PROST 03 polypeptide (I) and to the polynucleotide (II) encoding PROST 03. Fragments of (I) were used to generate antibodies (III) to PROST 03. (III) 1s useful for selectively destroying a cell expression of PROST 03. (III) 1s useful for selectively easociated with expression of PROST 03 in a human patient. (III) is useful for diagnosing metastasis associated with (I). in a subject. (I) is also useful for diagnosing and treating diseases of cell proliferation such as prostate cancers. (I) is also useful for generating antibodies to PROST 03. (III) is useful in detecting the levels of PROST. (3) polypeptides in cells and tissues, and in targeting drugs to primary and metastatic tumours. (I) is also useful for stimulating immune response to PROST 03 containing cells. (II) is useful in diagnostic assays for detecting the levels of polynuclectides encoding PROST 03 in cells and tissues. (II) is useful as DNA probes, as targets for antisense and ribozyme therapy, and as templates for the production of antisense polynuclectides. (I) and (II) are useful in research, biological,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clinical and therapeutic purposes. The present sequence represents the coding sequence of human PROST 03.
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99.9%; Pred. No. 0;
iive 0; Mismatches
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Matches 3316; Conservative
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Human; PROST 03; metastasis; prostate cancer; tumour; immune response;

DNA encoding human PROST 03 14-FEB-2002 (first entry)

BP

AAS14962 standard; cDNA; 3320

AAS14962 RESULT

AAS14962;

2;

	1383 GYGCCACATGCCTGTCCCACAGTGTGGCCGT 	1443 TCACCTTCTCAGCCCTGCAGATCCTGCCCTA	03 A 01 A	3 TGATG TGATG	1623 GTGCTGGAGGCAGTGGCCTGCTCCCACCTCC	3 ATGICICCGIACGIGIGGIGGIC 	3 GCATCTGCCTGGACCTCGCCATC	3 CCCTGTTTATGGGC 	1 3	923 ACTTGGCCAAATACTCAGCGTAGAAP 	3 CIGGGICCCAGCICCCGGTCTG1 	3 CTGTTGCTGCCAAAGTAATGTGGCTCT 	03 T 01 T	2163 IGGAGCCTTCCAAGGGGGTTTCAGTCTGGA 	223 GCACTGG 221 GCACTGG	283 CCTAGTTGAGACAC 	4 3 1 1 1 1	2403 TCTAGGATGAAACACTCCTCCATGGGATTTG.
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243 GTGCCTGAACGGCCCCTGAGCCCTACCGGCCCACTATGGTCCAGAGGCTGTGGG 302 	303 TGAGCCCCTGCTGCGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTTTG 362 	363 GCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCGGCTCTGCTGCTGGAGTGG 422 	423 GGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCT 482	483 GIGICCGCICCTAGGCICAGCCAGIGACCACIGGCGIGGACGCIAIGGCCGCCGCCGGC 542	543 CCTICATCIGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGCCG 602 	9 9	663 IGGGCGIGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGC 722 	723 TCTCTGACCTCTTCCGGGACCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCA 782	783 TGATCAGTCTTGGGGCTGCCTGGGCTACCTCCTGCCTGCC	843 CCTGGCCCCTACCTGGGCACCCAGAGAGAGTGCCTCTTTGGCCTGCTCACCCTCATCT 902	903 TCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCG 962 	963 AGCCAGCAGAGGCTGTCGGCCCCTCTTGTCGCCCCACTGCTGCATGCCGGGCCC 1022	1023 GCTTGGCTTTCCGGAACCTGGGCGCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCA 1082	7	1143 CCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAGGGCGTGCCCAGAG 1202 	1203 CTGAGCCGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGG 1262 	1263 GGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGC 1322	1323 AGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCG 1382
Oy Dp	Oy GD	oy Op	oy od	oy Op	장 요	oy Op	oy Op	Oy Db	Oy Op	Oy Db	Qy Dp	Qy Db	Qy Db	Oy Dp	Qy	Qy Dp	Qy Dp	δÌ.

3CCAGTGTGGCAGCTTTCCCTGTGGCTGCCG 1380 1442 1562 1560 COTGGAGCTCCCTTCCCTAATGGACACGTGG 1622 1682 1742 1860 CTCTCTCCCCAGTCTCTAGGGCTGCCTGAC 2162 2282 2280 2402 ACACACTGGCCTCCTCTACCACGGGAGA 1502 CACCCGCGCTCTGCGGGCCTCTGCCTGTG 1680 GIGCCTTCCTGCTGTCCCAGGTGGCCCCAT 1802 GCCAGTCTGTCACTGCCTATATGGTGTCTG 1862 CCAGCACATTGGGGTGGAGGGCCTGCCTCA 1982 CCAGCACATTGGGGTGGAGGCCTGCCTCA 1980 CCATGGGCCTGCCGGCTGGCCGCCAGTTT 2042 CCATGGGGCTGCCGGGCTGCCCGCCAGTTT 2040 CTGCCACCTGTGCTGCTGAGGTGCGTAGC 2102 TTGGGAGCTGAATAAACTCAGTCACCTGGT 2340 GAACATATG --ACTTATTGTAGGGGAAGA 2460 STGGTGACAGCTTCAGCCGCCCTCACCGGGT ACACTGGAGGTGCTAGCAGTGAGGACAGCC CACCCGCGCTCTGCGGGGCCTCTGCCTGTG CCACCGAGGCCAGGGTGGTTCCGGGCCGGG TTCGTTTAATGTAGCTCTTGCATGGGAGTT TTGGGAGCTGAATAAACTCAGTCACCTGGT

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The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides for antigenic epitopes derived from them) and antigen presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynocheotides and the antigen-presenting cells are useful for stimulating and/or expanding r cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for teating cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                              New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels 709;
  cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
                                                                                                                                                                                                                                                                                                             illon DC, Mitcham JL, Harlocker SL, Jiang Y, FR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2585.4;
Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 483-484; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
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2000us-0636215.
2000us-0651236.
2000us-0657279.
2000us-0679426.
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                                                                                                                                     2000US-0536857.
2000US-0568100.
                                                                                                           27-MAR-2001; 2001WO-US09919
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     Human; prostate
                                                      WO200173032-A2
                              Homo sapiens
                                                                                                                                                              12-MAY-2000;
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10-OCT-2000;
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                                                                                             CTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT
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                            GTCCTGAGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT
                                        GATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
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ර් රි	504 GACCGCCTGCTGCGCACCGGAAGCCCAGCTTTGCTGCTCAACCTTTGG 363 301 GAGCCGCTGCTGCGGAAGCCCAGCTTGTTTGTTTTTTTTT	qa	1381 CGGCTTCTCATGGGTGTGGAACATCTCTGCT
Qy	CGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGG 42	oy da	1240
අු	61 CCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAGTGGG 42	ì ò	
ç, q	424 GGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTG 483	7 dd	1501 AGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGA
l ò	84 TGTCCCGCTCCTAGGCTCAGGCTCGACCACTGGGCGTGGACGCTATGGCCGCCGCCCCCCCC	Qy	1240
; <u>a</u>	81 TGTCCCGCTCCTAGGCTCAGGCTCGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGC	QQ	1561 TGTGCCCTCTGCTCCCCCAACGACTTTCCAAA
δ d	CTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGCCCGG	yo da	1240
g ,	CITCAICIGGGCACIGICCITGGGCAICCIGCIGAGCCICTITCICAICCCAAGGGCCGG 60	Qy	1240
oy O	604 CTGGCTACCAGGCTGCTGTGCCGGATCCCAGGCCCCTGGAGCTGGCATGCTCATCCT 663	qq	1681 GTCCTCACAGCTGAGACTCCCAGGAAACCTTC
άO	GGGCGTGGGGCTGCTGGACTTCTGTGGCCAAGGTGTGCTTCACTCCACTGGAAGGCCTTACT	Qy	1240
r 93		Dp	1741 GGCGTTGCCCACATTCTCTGAGGGTCAGTGGA
Qy	724 CICTGACCTTCCGGGACCCGGACCACTGTCGCCCAGGCCTACTCTGTCTATGCCTTCAT 783	Ολ	
qq	721 CTCTGACCTCTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATCTTCTTCT 780	qa ,	1801 GAAAGGGGAAGGGTGCTGGGGAGCAGGGCTGG
oy.	84 GATCAGTCTTGGGGCTGCCTGGGTACCTCCTGCCTGCCATTGACTGGGACACCAGTGC 84	රු අ	1240
අ :	GATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTTGACTGGGGACACCAGTGC 84	Qy	1240AGGCGTTCGG
දි සි	044 CCISGCCCCCTACCTGGGCACCCAGGGGGGCCTTTTGGCCTGCCT	qa	1921 CTGATGGCCCCTCTCCCTCTGCAGGCGTTCGG
λo	CCTCACCTGCGTAGCACCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCCACCGA	Oy	1278 GCGCCATCTCCCTGGTCTTCTCTCTGGTCATG
QQ	9	qa	-
oy S	64 GCCAGCAGAAGGGCTGTCGCCCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCG	oy G	1338 GAGCAGTCTATTTGGCCAGTGTGGCAGCTTTC
g è	991 GUCAGCAGAAAGGGCTGTCGCCCCCTCCTTGTCGCCCCCCACTGCTGTCCCGGGCCCG 1020	δy	1398 CCCACAGTGTGGCCGTGGTGACAGCTTCAGCC
5 A		qa	2101 CCCACAGTGTGGCCGTGGTGACAGCTTCAGCC
Qy	GCTCTTCGTGGCTGAGCTGCAGCTGGATGGCACTCATGAC 11	Qy	1458 TGCAGATCCTGCCCTACACACTGGCCTCCCTC
QQ	1081 GCCCGCACCCTGCGCCGCTCTTCGTGCTGTGCAGCTGGCATGGCATCATGAC 1140	අු	- 0
yo f	1144 CTTCACGCTGTTTTACACGGATTTCGTGGCGGAGGGCTGTACCAGGGCGTGCCCAGAGC 1203	Qy Dp	1518 CCAAATACCGAGGGACACTGGAGGTGCTAGC
8 8	CIICACCCCIOI IIIACACCCACATICCI GAGGGGGCCCIGIACCAGGGCCCIGCCAGGGCC I	Qy	1578 TGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCT
qa qa	TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGTAAGGCCTTGGCAGCCAGC	qa	81 T
οy	1240 1239	ΟŸ	1638 GCCTGCTCCCACCTCGACCGGGGTCTGCGGG
QQ	1261 AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGGGTGTGTGT	qa .	341
δy	1240 1239	ð í	1698 TGGTGGTGGGTGAGCCCACCGAGGCCAGGGTG
QQ	1321 TCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGGGATGGACCCCATCTGCATACA 1380	g ?	2401 TGGTGGTGGGTGAGCCCACCGAGGCTG
		ζ,	0

_	1240		1239
^	1381		1440
_	1240		1239
0	1441	AGGAGTCTGATCAG	1500
_	1240		1239
0	1501	STCTAGAGGGAGTG	1560
_	1240		1239
0	1561	GTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTC	1620
_	1240		1239
^	1621	TCCTAGAAGCGTC	1680
_	1240		1239
0	1681	TCCTCACAGCTGAG	1740
_	1240		1239
^	1741	CGTTGCCCACATT	1800
_	1240		1239
_	1801	AAGGGGAAGGGTGCTGGGAGCAGGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGT	1860
	1240		1239
0	1861	ICATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTC	1920
_	1240		1277
•	1921	crerecadecerredaredecadecredecrerrecrecad	1980
_	27	GCGCCATCTCCCTGGTCTTCTCTCTGTCATGACCGGCTGGTGCAGCATTCGGCACTC	33
	1981	CGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACT	2040
	1338	GAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGT	1397 2100
	1398	CCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCC	1457
•	2101	CACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGC	2160
	1458	TGCAGATCCTGCCCTACACACAGGCCTCCTCTACCACCGGGGAGAAGCAGGTGTTCCTGC	1517
•	2161	GCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCT	2220
	21	CCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCC	57
_	2	Caaataccgaggggacactggaggtgctagcagtgaggacagcctgatgaccagcttc	2280
	571	TGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTG	63
_	28	GCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGT	34
	63	GCCTGCTCCCACCTCCACCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTG	69
_	4	CCTGCTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCGTACGT	4
	1698	TGGTGGTGGTGGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGGATCTGCCTGGACC 	1757
	75	GCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTAATGGGC	81.

Db 3540 CCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGGCTTCAGGTCTCAACGGCTTCCCT 3599	QY 2896 AACCACCCTCTTTTTTTTTTGCCCAGGTTCCCCCACTTCCACTCCACTTTTTTTT	QY 2956 TCTAGGACTGGGCTGATGAGGCACTGCCCAAAATTTCCCCTACCCCAACTTTCCCTA 3015 1	OY 3016 CCCCAACTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGAAGCA 3075 111111111111111111111111111111111111	Qy 3076 CAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG 3135	QY 3136 GAATCTCACACAGAAACTCAGGGGCACCCCTGCCTGAGGAGGTCTTATCTCTC 3195 Db 3840 GAATCTCACACAGAAACTCAGGAGCACCCCCTGCCTGAGGAGGTCTTATCTCTC 3899	QY 3196 AGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT	3256 TTTATACTGTAAGTGF 	Oy 3316 TTATATGTTTAAAA 3330 	RESULT 14 AAH93868 ID AAH93868 standard; cDNA; 4034 BP.	XX AAH93868; XX DT 04-OCT-2001 (first entry)	P553S CDNA splic Human; prostate	cytostatic; gene therapy; metastasis; ss. Homo sapiens.	PN W0200151633-A2. XX PD 19-JUL-2001. XX	PF 16-JAN-2001; 2001WO-US01574. XX PR 14-JAN-2000; 2000US-0483672. XX		Wang A, Meagher MJ; WPI; 2001-425873/45.	PT New polynucleotide encoding a prostate-specific protein, for PT diagnosing, monitoring and treating prostate cancer in a patient and PT for use in vaccines .	PS Claim 1; Page 460-461; 543pp; English. XX CC The present invention describes polynucleotide sequences (I) which encode
11111111111111111111111111111111111111	1818 CCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTC 1	1878 TGGTCGCCATTACTTTGCTACAGGGTAGTATTGACAAGAGCGACTTGGCCAAATACT 1	1938 CAGCGTAGAAACTTCCAGCACATTGGGGTGAAGGCCTGCCT	1998 CCGCTCCTGTTAGCCCCATGGGGCTGCCGGCCGCCCAGTTTCTGTTGCTGCCAAAG 	2058 TAATGTGCTCTCTGCTGCCACCCTGTGCTGCTGCGTGCGT	2118 TGGGGGGTCCCTCTCCTCTCCCGGGTCTCTAGGGGTGCCTGACTGGAGGCCTTCCAAG 	2178 GGGGTTTCAGTCTGGACTTATACAGGGGCCAGAAGGGCTCCATGCACTGGAA 	2238 GACTCTGCAGGTGGATTACCCAGGGTTAACAGCTAGCTCCTAGTTGAGACACA 2297	2298 CCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC 2357 	2358 CCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACAC 2417 	2418 TCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGAAGAGTCCTGAGGGCAAC 2475	2476 ACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACC 1	2536 TACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGGCAT 2595 11111111111111111111111111111111111	2596 TTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTCTGT 265 11111111111111111111111111111111111	2656 GTTGGTGTCTAATAFTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAG 	2716 CTGGTCATTGGGCTGATCATTGCCAGAATCTTCTCCTGGGGTCTGGCCCCCCAAAAT 2775	2776 GCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 2835 111111111111111111111111111111111111	2836 CCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGCTTCCCT 289
qa	QQ .	VQ dq	Oy Ob	QΥ Ob	Qy	Qy	QY	QQ QQ	da Db	QY .	Qy B	Oy Db	Qy	do do	λο 4 <u>α</u>	Qy B	Qy	ογ

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AGGCACTGCCCAAAATTCCCCTACCCCAACTTTCCCCTA 3015
                                                                                                                                                                  GCTCCACAACCCTGTTGGAGCTACTGCÁGACCAGAAGCA 3075
                                                                                                                                                                                                                                    CCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG 3135
                                                                                                                                                                                                                                                                                                     AGGAGCACCCCTGCCTGAGCTAAGGAGGTCTTATCTCTC 3195
                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCAGAGTATAATGTTTAATGGTGACAAAATTAAAGGCTTTC 3315
                               GECCAGCCTGGTTCCCCCACTTCCACTCCCCTCTACTCC 2955
                                                                                                                                                                                                                                                                                                                                                                          TTTGCAATAATGTCGTCTTATTTATTTAGCGGGGGGAATAT 3255
                                                                                                                                                                                                                                                                                                                                                                                          GGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCT 3599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a prostate-specific protein, for reating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tate-specific; diagnosis; vaccine; tastasis; ss.
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prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and the best to (II), fusion proteins comprising (II), and isolated are also used in the detection of cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93157 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.

Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;

180 240 243 303 363 360 540 ATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGTGTTGAGCATGGGCTGAGAAG 123 CTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGC 183 CCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGG 423 GGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTG 483 GGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTG 480 543 603 GGGCGTGGGGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCT 723 CTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCAT 783 GATCAGTCTTGGGGGCTGCCTGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGC 843 63 9 GAGCCCCCTGCTGCGCCCCGGAAACCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGG GAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGG 4 AACCAGCCTGCACGCGCTGCGGGTGACAGCCGCGCGCGCCTCGGCCAGGATCTGAGTG GGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGAG CTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGG TGCCTGAACGGCCCCCTGACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGT TGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCGCC CTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCT Gaps 75.8%; Score 2585.4; DB 22; Length 4034; 82.4%; Pred. No. 0; 1; Indels 709; 0; Mismatches Matches 3325; Conservative Similarity 64 Query Match 784 61 124 121 181 244 304 301 364 361 124 121 181 544 541 604 601 564 561 724 184 721 合 g qq q g qq qq qq qq g q ò οy ò ò ò ò ò δý õ à õ ò g ò a

1239 1080 1143 1020 1083 1203 GCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGAC 1140 1141 CTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGC 1200 1321 TCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACA 1380 1381 CGGCTTCTCATGGGTGTGGAACATCTCTGCGTTTCAGGAAGGCCTCTGGCTGCTC 1440 1441 TAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAA 1500 1501 AGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAG 1560 1261 AGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCC 1320 1561 TGTGCCCTCTGCTCCCCCAAGGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTCAGG 1620 1681 GTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGG 1740 1741 GGCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA 1800 1801 GAAAGGGGAAGGGTGCTGGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTAC 1860 840 903 963 960 CCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTT CCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGGCCCCACCGA GCCAGCAGAAGGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCG GCCAGCAGAAAGGCCTGTGCGCCCCTTGTCGCCCCCACTGCTGTCCCATGCCGGGCCCG GCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGAC CTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGC 1621 CGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCTCTCACCCGCCT CCTGGCCCCCTACCTGGGCACCCAGGAGTGCCTCTTTGGCCTGCTCACCTTCATCTT CCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGA TGAGCCGGGCACCGAGGCCCGGAGACACTATGATGA-----1240 -----1240 1024 1021 1081 1144 1204 1240 1240 1240 1240 1240 1240 781 844 904 901 961 1084 1240 964 1240 Qλ 9 ò Db ò QQ Ω a ò Db ò Db ò g ò Ω ò П οy q ò q δy qq Qγ QQ ò Ω Qγ g δý g ò Db ò į,

 QY 2298 CCTAGAGAAGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC 2357 Db 3001 CCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCAAGC 3060	2 241 312	2 24	0y 2476 ACACAAGAACCAGGGCCCACAGGCACTGTCTTTTGCTGATCCACCCCCTT 2535	Qy 2536 TACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGGCAT 2595	Qy 2596 TTAAATATTTAACTAATTTAACAAAGTAGAAGGGAATCCATTGCTAGTTTTCTGT 2655 	Oy 2656 GTTGGTGTCTAATATTGGGTAGGGTGGGGGATCCCCAACAACAGGTCCCCTGAGATAG 2715	QY 2716 CTGGTCATTGGCTGATCATTGCCAGAATCTTCTTCTCGGGGTCTGGCCCCCCAAAAT 2775	OY 2776 GCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 2835	QY 2836 CCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCT 2895 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	y 2896 AACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCTC 2955	y 2956 TCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTCCCCTA 3015	y 3016 CCCCAACTTTCCCCACAGCTCCACAACCCTGTTTGGACCTACTGCAGGACCAGAAGCA 3075	y 3076 CAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGG 3135	3136 GAATCTCACACAGAAACTCAGGAGCACCCCCTGCCTGACTAAGGAGGTCTTATCTCT	y 3196 AGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTAATTTAGCGGGGTGAATAT 3255	y 3256 titatactgtaagtgaggaatcagagtataatgttatggtgagaaattaaagggtttc 3315 	y 3316 ttatatgtttaaaa 3330
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Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalos MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                             Human P553S splice variant SEQ ID NO 704.
                     ВР
                    ABL95411 standard; cDNA; 4034
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9805-0020956.
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HARLOCKER S L.
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09-APR 11999;
12-NOV 11999;
12-NOV 11999;
14-JAN 22000;
27-MAR 2000;
27-MAR 2000;
13-JUN 2000;
213-JUN 2000;
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213-JUN 2000;
29-AUG 2000;
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02-OCT-2000;
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09-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
                                                                                                Homo sapiens
                                                                                                                                        12-JAN-2001;
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                                                                                                                           21-FEB-2002
                                   ABL95411;
                                                                                                                                                                                                                                                                                                                       (DILL/)
(MITC/)
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Fanger
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                           The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
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                                                                                                                                     75.8%; Score 2585.4; DB 24; Length 4034; 82.4%; Pred. No. 0;
                                                                                                           Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;
                                                                                                                                                                       0; Mismatches
Claim 1; SEQ ID NO 704; 87pp; English.
                                                                                                                                                       Best Local Similarity 82.4
Matches 3325; Conservative
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	CGAGGGGACACTGGAGGTGCTAGCAGGACAGCCTGATGACCAGCTTCC	98 01 58 18	1878 TGGTCGCCAATTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACT 1937 1111111111111111111111111111111111	11	GGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCATGCACTGGAATGC ACTCTGCAGGGATACCCAGGGTCAGGGTTAACAGGCCTCCTAGTTGAGAC ACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGAC ACTCTGCAGGTTTTTTGGGAGCTCAGGGTTAACAGCTAGCCTCCATGTTGAGAC CTAGAGAGGTTTTTTGGGAGCTGAATAAACTCAGTCACTAGTTCCCATCTCTA CTAGAGAAGGGTTTTTGGAGGTGAATAAACTCAGTCACTGGTTTCCCATCTCTA CCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTTGCATGGATGAAA
CCTCACCTGCGTAGCAGCCACACTGCTGAGGAGGCAGCGCTGGGCCCCACCGA 963 DE	CTTCACGCTGTTTTACACGCGTTTTCGTGGGCGGGCTGTACCCAGGCGTGCCCAGAGC 1203 [11111111111111111111111111111111111	ACA 13 ACA 13 CTC 14 CTC 14	TTCAA 150 123 CGCAG 156 123 TCAGG 162	CUTCLIAGAMGLETUTIGAAGCCTATGGCCAGCTGTTTGTGTTCCTCTCACCGCCT 1680 QY GTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTTCCTCTGCCTTCAGCAAGG 1740 Dy GGCGTTGCCCACACATTCTCTGAGGATCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA 1800 QY GGCGTTGCCCACACATTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTA 1800 QY	GAAAGGGAAGGGTGCTCCACAGAGGTCTCGTGCAGCAGGTAC 1860 DD CTGTGGTTCCGCTTCTCATCTCCTGAGACTGCTCCGACCTTCCCTCCC
Qy 904 CCTCACCTGCGTAG Db 901 CCTCACCTGCGTAG Qy 964 GCCAGCAGAAGGGC Db 961 GCCAGCAGAAGGGC Qy 1024 CTTGGCTTTCCGGA Db 1021 CTTGGCTTTCCGGA Qy 1084 GCCCGCACCCTGC Qy 1084 GCCCCGCACCCTGC Db 1081 GCCCCGCACCCTGC Db 1084 GCCCCGCACCCTGC	1144 C 1141 C 1204 T 1201 T 1240 -	Oy 1240	1240	1240 . 1681 . 1240 1741	Db 1801 GAAAGGGAAGGGT Qy 1240 Db 1861 CTGTGGTTCCGCCT Qy 1240 Db 1921 CTGATGGCCCTCT Qy 1278 GCGCCATCTCCCTG Qy 1278 GCGCCATCTCCCTG

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3420 CTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCTGGGGTCTGGCCCCCCCAAAAT 3479
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                                                                                                                                                                                                                         GTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAG
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                              TCCTCCATGGGATTTGAACATATG -- ACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAAC
                                                                                       ACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCTCT
                                                                                                                                               TACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGGGCAT
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TGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contecting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially, expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in gene therapy, as a vaccine or in antisense applications.
ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes
                                                             cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72.9%; Score 2486.4; DB 24; Length 2582; 99.9%; Pred. No. 0;
                                                           Prostate cancer; prostate tumour tissue; human; mammal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2582 BP; 407 A; 822 C; 785 G; 566 T; 2 other;
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                             Prostate cancer-associated DNA sequence #103.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   are expressed in a prostate tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                           (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                  2000US-0733742.
2001US-263957P.
2001US-276791P.
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2001US-281922P.
2001US-286214P.
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                                                                           gene therapy; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mack DH,
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Matches 2499; Conserv
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                                                                                                                                        WO200230268-A2.
                                                                                                                                                                                                       12-OCT-2001;
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15-AUG-2002
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                                                                                                           Mammalia.
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2368 TTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGT. 2427
                                                                               2428 TICTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTGTAGGGGAAG 2487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer
TTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGT
                                                             2402 TICTAGGATGAAACACTCCTCCATGGGATTTGAACATATG --ACTTATTTGTAGGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                            AGTCCTGAGGGCAACACACAAGAACCAGGTCCCCTCAGCCC 2501
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A, Day CH, Vedvick TS,
Ppler WT, Henderson RA;
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                                                                                                                                                                                                                                                                                                                                 Human prosate cDNA P553S splice variant #2
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Hepler WT,
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GR, Retter MW, Stolk JA,
Wang A, Skeiky YAW, Hepl
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2000US-0651236.
2000US-0657279.
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2000US-0570737.
2000US-0593793.
2000US-0605783.
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10-OCT-2000; 2000US-0685166.
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12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
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29-AUG-2000;
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Fanger GR,
Li SX, Wang
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2342
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                                                                                                                                                                                                                                                                                                      ATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAG 1189
                                                                                                                                                                                                                                                                                                                                               1190 GGCGTGCCCAGAGCTGAGCCGGGCACCGAGACCGCAGACACTATGATGAA----- 1240
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                                                                                                                                                                                     TGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG
                                                                                                                                                                         CTGGGCCCCACCAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGT
                                                                                                                                                                                                                                                                                                                  CTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  781 TTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGCGTTCGGATGGGCAGCCTGGGGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CCAGCCGCAGTGTGCCCTCTGCTCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 CCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 TCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1389 CATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCT
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                       Indels
 DB 22;
Score 2196.4;
           Pred. No. 0;
0; Mismatches
 64.4%;
88.2%;
Ouery Match
Best Local Similarity 88.2
Matches 2560; Conservative
                                         770
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Qy	1449	TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTACCACCGGGAGAAGCAGG 1508	Ę
qq	1021	CAGCCTGCAGATCCTGCCCTACACACTGCCTCCCTCTACCACCGGGAGAAGCAG	3 8
οy	1509	TGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGA 1568	ž É
đ	1081	CTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGGAGGACGAGCCTGATGA 114	2 2
Qy	69	2	g a
qq	1141	- (7)	ΔÓ
yo q	1629	GAGGCAGTGGCCTGCTCCCACCTCCACCTCTGCGGGGCCTCTGCCTGTGATGTCT 1688	: ga
3 8		TGGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGGCGGGGGTGT. 174	Qy
7 d			Dp
Qy	1749	GCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCCATCCCTGT 1808	ž č
qq	1321	GCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGT 1380	}
Qy	1809	INTEGECTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAG 186	g qa
qq	1381	TTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAG 1440	'n
Qy	1869	GCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGG 1928	g qa
qq	1441	GCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGG 1500	ΔO
ογ	1929	~	5 원
qq	1501	CCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGCCTGCCT	00
Qy	989	04	7 名
QQ	1561	CCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTG 162	Qy
οy	2049	10	D QC
ති	1621	CAAAGTAATGTGGCTCTCTGCCACCCTGTGCTGCTGAGGTGCGTAGCTGCACA 168	Οy
οy	2109	GCTGGGGGCTGGGGCGTCCCTCTCCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGG 2168	ු ති
qq	1681	3GAG	3 8
Qy	2169	CCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGGGCCAGAAGGGCTCCATGCACTG 2228	G QQ
qq	1741	CCAAGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGC	ΔO
οy	2229	GAATGCGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGT 2288	; 음
qq	1801	CTAGT 186	
δλ	2289	TGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA 2348	RESULT 1
qq	1861	IGAGACACCACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA 1920	
٥y	2349	TCTCTAAGCCCCTTAACCTGCAGCTTCGTTAATGTAGCTCTTGCATGGGAGTTTCTAGG 2408	AAI
qq	1921	reterargecectrarecreecaecricerriaareragererreearegeagrirerage 1980	DT 04-
Qy	2409	ATGAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTG 246	DE P55
q	1981	3AAACACTCCTCCATGGGATTTGAACATATGAAGTTATTGTAGGGGGAAGAGTCCTG 204	KW Hum KW cyt
Qy	2467	Ö	
qq	2041	CCAACACACAAAAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCA 210	-
Οy	2527	CCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGA 2586	

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3186
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               2160
                                          2646
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                                         2221 CTTTCTGTGTTGTGTGTCTAATATTTGGGTAGGGTGGGGGGATCCCCAACAATCAGGTCCC
                                                                                                                                                                          2281 CTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCTCTGGGGTCTGGCC
                                                                                                                                                                                                                   2767 CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCCATCCCAAATGATAATTCCAAA
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                                                                                                                                                                                                                                                                                                                                                                                             2947 TCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                          2521 TCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITCCCCTACCCCCAACTITCCCCACCACCTCCACAACCCTGTTTGGAGCTACTGCAGGA
                                                                                                   2647 CITITICIGIGIGIGICIAATAITIGGGIAGGGIGGGGGATCCCCAACAAICAGGICCC
                                                                                                                                                             2707 CTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCTGGGGTCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                man; prostate cancer; prostate-specific; diagnosis; vaccine; tostatic; gene therapy; metastasis; ss.
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19-JUL-2001.	7310311-0M100C		
NHO-OT			
14-JAN-2000; (CORI-) CORI	N-2000; 2000US-0483672.		
Xu J, I Kalos MI Wang A,	Dillon DC, Mitcham JL, MD, Fanger GR, Day CH, N, Meagher MJ;	Harlocker SL, Jiang Y, Reed SG; Retter MW, Stolk JA, Skeiky YAW;	
WPI; 2001	01-425873/45.	,	
New polynuc diagnosing, for use in	New polynucleotide encoding a p diagnosing, monitoring and trea for use in vaccines -	New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -	
Claim 1; Page	: Page 459-460; 543pp; English.	nglish.	
The pres prostate	sent invention describes sepecific proteins (II)	The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity,	ø
and can antibodi	be used in vaccine prod les to (II), fusion prot	<pre>luction and gene therapy. (I), (II), edins comprising (II), and isolated</pre>	
(I) and patient.	Fregated using (1) of (the antibodies are also The cancer that is dia	<pre>11) are used treat cancer in a patientused in the detection of cancer in a gnosed or treated is particular;</pre>	
prostate (I) can	be used for monitoring (II) can also be used for monitoring	prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient.	
methods as well AAM01318 exemplif	methods for prostate cancer. They can ind as well as the prostate volume. AAH93357 AAMOUSIB represent polynucleotide and ami exemplification of the present invention.	for prostate cancer. They can indicate the level of metastasis as the prostate volume. AAH93357 to AAH93944 and AAM01115 to represent polynuclectice and amino acid sequences used in the iteration of the present invention.	
Sequence	Sequence 2904 BP; 542 A; 875 C;	542 A; 875 C; 773 G; 714 T; 0 other;	
Query Match Best Local Matches 256	64.4%; Similarity 88.2%; O; Conservative C	Score 2196.4; DB 22; Length 2904; Pred. No. 0;); Mismatches 1; Indels 343; Gaps 2;	.; 8
770	GTCTATGCCTTCATGATCAGTC	770 GTCTATGCCTTCATGATCAGTCTTGGGGCTGCCTGGGCTACCTCCTGCCTG	
830		CCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG 889	
61		TGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCAGGAGAGTGCCTCTTTGGCCTG 120	
890		GCGTAGCAGCCACACTGGTGGCTGAGGAGGCAGCG 949	_
121		CTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGTGGTGGTGGAGGCAGCG 180	
950		CTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCCACTGT 1009	. 60
181		CTGGGCCCCCACCGAGCCAGCAGGAAGGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGT 240	_
1010		CCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCAG 1069	6
241		TCCGGAACCTGGCCCTGCTTCCCCGGCTGCACAG 300	
1070		CTGTGCTGCCGCATGCCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGG 1129	6
301		CTGTGCTGCCGCATGCCCCGCACCTGCGCCGGGTCTTCGTGGCTGAGCTGTGCAGCTGG 360	

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ζò	1.24.1	27	340
Db	481	CTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGA 54	0
٥y	1241	12.	40
QQ	541	TTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAAGGCTGGATTTCAGATCTGCCTGGTT 60	0
٥y	1241	12	40
Db	601	CAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTT 66	0
Qy	1241		40
QQ	661	CAGCICAGGCGICCTAGAAGCGICTTGAAGCCTAIGGCCAGCIGICTIIGIGIICCCIC 72	0
Οy	1241	12	40
Db	721	CACCGGCCTGTCCTCACAGCTGGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCC 78	0
٥y	4		89
QQ	781	AGGGGCGTTGCCCACATTCTCTGAGGGCGTTCGGATGGGCAGCCTGGGGTGT 84	0
yo q	1269	ر	
3 8	, ,	CCTGCAGTGCAGTGCTCTCCCTGGTCTTCTCTCTGGTCCGGCTGGTCCGGCTGGTGCAGTGTCAGTGTTTCTCTCTC	0 0
Pp QD	06	TOGGCACTCGAGGGAGCTATTTGGCCAGTGCGGAGCTTTCCCTGTGGGTGCGGGGGGCA 18 TCGGCACTCGAGGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCA 186	æ 0
Qy	1389	SCCTGTCCCACAGTGTGGCCGTCACAGCTTCAGCCGCCCTCACCGGGTTCACCT 14	48
qq	961	0	20
Οy	1449	CTCCCTCTACCACCGGGAGAAGCAGG 15	08
qq	1021	CTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGG 10	80
ογ	1509	GTGAGGACAGCCTGATGA 15	89
QQ	1081	GTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGAGACAGCCTGATGA 11	40
٥y	1569	Greerecre 16	28
Db	1141	SAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCT	00
Qy	1629	GAGGCAGTGGCCTGCTCCCACCTCCACCGGCGCTTGGGGGCCTCTGCCTGATGTCT 168	88
DÞ	1201	GGCAGTGGCCTGCTCCCACCTCCACCGCGCCTCTGCGGGGCCTCTGCCTGTGATGTCT 12	09
Qy	1689	CCGTACGTGTGGTGGTGGGTGAGCCCACCGAGGCTAGGTGCTTCCGGGCCGGGGATCT 174	48
Dþ	1261	CGTACGTGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGCATCT 13	20
Οy	1749	CTTCCTGCTGTCCCAGGTGGCCCCCATCCCTGT 18	90
qq	1321	CCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCCATCCCTGT 13	80
Oy .	1809	TATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAG 18	89
Db	1381	ATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTCCCGC	10
Qy	1869	CCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGA	88
QQ	1441	CTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGGGACTTG	00
Qy	1929	CTGG	38
qa	1501	CAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT	09
Qy	1989	CCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTG 204	8

Db 2641 CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTGTCCATCTCAGCCCCCAGAGTATATCT 2700 Qy 3127 GTGCTTGGGGAATCTCACACAGAACTCAGGAGCACCCCCTGAGCTAAGGGAGGTC 3186	RESULT 19 AL MALDS410 standard; CDNA; 2904 BP. AC ABL95410; AL ABL95410; AL ABL95410; AL ABL95410; AL Human P553S splice variant SEQ ID NO 703. Buman P553S splice variant SEQ ID NO 703. AL Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; AL Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; AL Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; AL Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; AL Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; AL Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; AL Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; AL Human; cancer; concordate; and the concer; concer; concordate; and the concer; concer; concordate; and the concer; concordate; and the concer; concer; concordate; and the concer; concordate; and the concer; concer; concordate; and the concer; concordate; and the concer; concer; concordate; and the concer; concordate; and the concer; concer; concordate; and the concer; concordate; and the concer; concer; concordate; and the concer; concordate; and the concer; concer; concordate; and the concer; concordate; and the concer; concer; concordate; and the concer; concer; concordate; and the concer; concer; concordate; and the concer; concer; concordate; and the concer; concer; concordate; and the concer; concer; concordate; and the concer; concer;	(STOL/) (DAYC/)
	TGAGACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA TGAGACACCCCTAAACACGAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA TGAGACACCACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA TCTTTTTTTTTT	3067 CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT 3126 ·
		ογ

	(VEDV/) VEDVICK T S.	qa	601 CCAGCCGCAGTGTGCCCTCTGCTCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTT 660
		Οy	1241
	SKEIP HEDLE	qq	661 CCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTC 720
	HENDERSON	Qy	1241
	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD; Fanner GR, Reffer MW, Stolk IA, Day CH, Vedyick TS, Carter D.	qq	721 TCACCCGCCTGTCCTCACAGCTGAGACTCCCCAGGAAACCTTCAGACTACCTTCCTCTGCC 780
	1 SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA; PI; 2002-255649/30.	oy Op	1241
XX	New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer	Qy	
	Claim 1; SEQ ID NO 703; 87pp; English.	Οy	1329 TCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCA 1388
		qq	
		Qy Db	1389 CATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCT 1448
anc Jue	2304 BF; 342 A; 6/3 C; 64.48; SC	δλ	1449 TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACGGGAGAAGCAGG 1508
Bes	Pred. No. 0; 0; Mismatches 1; Ir	qq	TCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGG 108
YO da	770 GTCTATGCCTTCATGATCAGTCTTGGGGCTGCCTGGCGCTACCTCCTGCCATTGAC 829	oy Og	1509 TGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACACCCTGATGA 1568
ò	TGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTG	oy G	1569 CCAGCTTCCTGCCAGGCCCTAAGCCTCCCTTCCCTAATGGACACGTGGGTGG
9		oy Op	1629 GAGGCAGTGGCCTGCTCCACCTCCACGCGCTCTGCGGGGCCTCTGCCTGTGATGTCT 1688
3 6 7	CTGGGCCCCACCGAGCCAGCAGCGCTGCCCCCTCCTTGTCGCCGCTGCTGCTGCTGCTGCT	δγ Dp	1689 CCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCGGGTGGTTCCGGGCCGGGGCATCT 1748
a V	CCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGCCCCTGCTTCTTGTCGCCCCCACTGCTGT Z	% g	1749 GCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTGCCCAGGTGGCCCCATCCCTGT 1808
do y	CCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGGCTGCACCAG 3 CTGTGCTGCCGCATGCCCCGCACCTGCGCCGGCTCTTCGTGGCTGACTGTGCTGCACCTGC 1	Qy QD	1809 TTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAG 1868
g &	CIGIGETISCUECATIGECCUSCACUCTICUS GUITTICATES CONTRAGORISTICA GUITTICAT GUITT	y dg	1869 GCCIGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGG 1928
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qq	481 CTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAAGGAAAGGCGGA 540	g	1 CCCAGCTCCCCGCTCCTGTTAGCCCCCATGGGGGCTGCCGGGCTGGCCGCCAGTTCTGTTG
Οy		oy da	2049 CIGCCAAAGTAATGTGGCTCTCTGCTGCTGCTGTGCTGAGGTGCGTAGCTGGACA 2108 1621 CTGCCAAAGTAATGTGGCTCTTGCTGCACACCTGTGCTGCTGCTGCTGCTGCACA 1680
qa Vo	541 GCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTT 600	Qy	2109 GCTGGGGGCTGGGGCGTCCCTCTCCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGG 2168

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12-MAY-2000;
13-JUN-2000;
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                                                                            TGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCA
                                                                                                                                               1981 ATGAAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGAGTCCTG
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                                              GAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCTAGT
                                                                                                  TCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGG
                                                                                                                                ATGAAACACTCCTCCATGGGATTTGAACATATG - - ACTTATTTGTAGGGGAAGAGTCCTG
        CCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCATGCACTG
                                      GAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGT
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The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding reals specific for a tumour protein, and for inhibiting the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4894;
                                                                                                                                                                                                      Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
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dvick TS,
erson RA;
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I, Henderson
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Pred. No. 0;
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Skeiky YAW, Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 480-482; 579pp; English.
  BP
                                                                                                                                                        CDNA P553S splice
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AAS64038 standard; cDNA; 4894
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2000US-0636215.
2000US-0651236.
2000US-0657279.
2000US-06786.
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80.1%;
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2000US-0570737
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Best Local Similarity 80.1
Matches 2872; Conservative
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1311 GCCA11GG1CCAG1GCTGGGCCTGTGTCTCCGCTCCTGGCTCAGCTCA	239	rgrgcccrcrcccccacgacrrrccaa 2450
515 TGGCGTGGACGCTATGGCCGCCCCCCTTCATCTGGGCACTGTCCTTGGCATCCTG 574	Gy 1240	CACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 2510
575 CTGAGCCTCTTTCTCATCCCAAGGCCGGCTGCTAGCAGGGCTGCTGTGCCGGATCC 634	Oy 1240	CTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTT 2570
635 AGGCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGCTGGACTTCTGTGGCCAG 694	Db 2571 CAGACTACCTTCCTCTCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGT	GCGTTGCCCACATTCTCTGAGGGTCAGTGG 2630
CCACTGT 75-	Qy '1240Db 2631 AAGAACCTAGACTCCCATTGCTAGAGGTAG	AGACTCCCATTGCTAGAGGGTAGAAÄGGGGAAGGGTGCTGGGGAGCAGGGCTG 2690
ACCIC 8	Qy 1240	TGTGGTTCCGCCTTCTCATCTCCCTGAGAC 2750
8 7	Qy 1240Db 2751 TGCTCCGACCTTCCCTCCCAGGCTCTGTCT	CCGACCCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTTGAGGGTTCG 2810
TGGTG 93	QY 1249 GATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTC	SCGCCATCTCCCTGGTCTTCTCTCTGGTCAT 1308
CCTTG 994	Oy 1309 GGACCGGCTGCAGCGATTCGGCACTCGF	GCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTT 1368
SCCTGCTT 105	Qy 1369 CCCTGTGGCTGCCGGTGCCACATGCCTGTCC	CCCTGTGGCTGCCGGTGCCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGC 1428
	Qy 1429 CGCCTCACCGGGTTCACCTTCTCAGCCCTC	CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCT 1488
rgggc 1	QY 1489 CTACCACCGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGC;	CAAATACCGAGGGGACACTGGAGGTGCTAG 1548
12	OY 1549 CAGTGAGGACAGCTGATGACCAGCTTCCTGCAGGCCCTAAGCTGGAGGTCCCTTCCC I	GCCAGGCCTAAGCCTGGAGCTCCCTTCC 1608
12	0y 1609 TAATGGACACGTGGTGGAGGCAGTGGCCTGCTCCCACCTCCACCGCGCTCTGGG	CCTGCTCCCACCTCCACCCGCGCTCTGCGG 1668
123	Qy 1669 GCCTCTGCCTGTGATGTCTCCGTACGTGTC 	GTGATGTCTCCGTACGTGTGGTGGGTGAGCCCACCGAGGCCAGGGT 1728
2151 ACACTCGGGGCTGTGTGTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTGTCAGG 2210	1729 GGTTCCGGGCC	SCTGTC 1
27	3291 GGTTCC .	3CTGTC 335
123	QY 1789 CCAGGTGGCCCCATCCCTGTTTATGGGCTCC	GGCCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGC 1848
	1849 CTATAT	190
1 TGACAGAAGGAAAGGGGGAGCTTATTCAAAGTCTAGAGGGGGGGG	Db 3411 CTATATGGTGTCTGCCGCAGGCCTGGGTCTG	

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                                 GGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATC 3106
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                                                                                                                       GAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCCGTTTGCAATAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             otide encoding a prostate-specific protein, for onitoring and treating prostate cancer in a patient and ccines -
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Retter MW, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                   ne therapy; metastasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ice variant P553S-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ard; cDNA; 4894 BP.
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CH,
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ger GR, Day
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U×	exemplification of the present invention.		Ċ	
80	Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;		/77	I TGCGGTTTCAGGAAGGCCTCTGGCTC
o B	Query Match 62.8%; Score 2142.8; DB 22; Length 4894; Best Local Similarity 80.1%; Pred. No. 0:	, —	124	EECC
Ψ	tive 1; Mismatches 3; Indels 708; Gaps		12	
g g	455 GGCATIGGTCCAGTGCTGGGCCTGGTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC 514	- q ₀	239	1 ATTTCAGATCTGCCTGGTTCCAGCCC
ò	Total	Qy	1240	
3 8	1371 TGGCGTGGACCTATGCCCGCCCGCCTTCATCTGGCACTCTCTTCTCTCTC	qa	2451	1 ATAATCTCACCAGCGCCTTCCAGCTC
δ	TCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCGGGATCCC 63	QY	1240	
qq	4	qa —	251	1 GCTGTCTTTGTGTTCCCTCTCACCCG
ογ	635 AGGCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 694	δλ -	1	
qq	1491 AGGCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 1550	q _Q	2571	1 CAGACTACCTTCCTGCCTTCAGCA
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Qy	935 GCTGAGGAGCCACCGCGCCCCACCAGCAGCAAGGCTGTCGCCCCTCCTTG 994	Š 2	⊣ (GGACCGGCTGGTGCAGCGATTCGGCA
qa	1791 GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGCCCCCCTCCTTG 1850	<u> </u>	/87	
ò t	TCGCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 105		1369	CCCTGTGGCTGCCGGTGCCACATGCC
q _Q	1 TCGCCCCACTGC	_	1.4	
oy B	1055 CCCGGGCTGCACCAGCGGCTGCCGCATGCCCCGCACCTGCGCCGGGTTTTCGTGGCT 1114		2991	CGCCTCACGGGTTCACCTTCTCAG
٥y	GGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 117	0y	1489	CTACCACCGGGAGAAGCAGGTGTTCC
ф		q _Q	305	
Qy	1175 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT 1234	О		CAGTGAGGACAGCCTGATGACCAGCT
QQ	2031 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGGACCGAGGCCCGGAGACACTAT 2090	da	e e	
Qy	1235 GATGA 1239	0y	1609	TAATGGACACGTGGGTGCTGGAGGCA
qq	11111 2091 GATGAAGGTAAGGCCTTGGCAGCAGCAGAGGCTGGTGGGAGCCGCCCACCAGAGACG 2150	අ ග් 	3171	
δy	1240 1239	- O	1669	GGCCTCTGCCTGTGATGTCTCCGTAC
qq	2151 ACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGG 2210	an (3231	
ογ	1240 1239	לט לט	1/29	GGTTCCGGGCCGGGGCATCTGCCTGG
qo	2211 AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGGT 2270	2 0	1780	
ζō ΄	1240 1239	δ. —	2	

Db	2271	Æ
Qy	1240	1239
Db	2331	TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGGTGG 2390
Qy	1240	1239
QQ	2391	ATTICAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA 2450
Qy	1240	1239
Db	2451	CACCAGCGCCTTCCAGCTCAGGCGTCC
Qy	1240	1239
pp	2511	L
Qy	1240	1239
qq	2571	CAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGTGGGGTCAGTGG 2630
Qy	1240	1239
q _Q	2631	AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGGCTG 2690
QY	1240	1239
· qa	2691	GTCCACAGCAGGTCTCGTGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGAC 2750
QY	1240	GCCTTC
QQ	2751	– ∺
Qy	1249	GGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCA
QQ	2811	ATGGGCAGCCTGTGTTCCTGCAGTGCGC
Qy	1309	rgregea
Db	2871	GACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGTGT
٥y	1369	CCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACACTTCAGC 1428
Dp	2931	ccrereecreccacareccrererccacarereres
Oy	1429	CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCT 1488
Db	2991	GCCTCACGGGTTCACCTTCTCAGCCTGCAGATCCTGCCTACACACTGGCCTCCC
Qy	1489	CTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAG 1548
Db	3051	TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAG 311
٥y	1549	CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 1608
qα	3111	AGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 317
Qy	1609	AATGGACACGTGGTGCTGGAGGCAGTGCCTCCCACCTCCACCTCCGCTCTGCG
Db	3171	SGACACGTGGGTGYTGGAGG
Qy	1669	CCGAGGCC
Db	3231	CTCTGCCTGTGTTCTCCGTACGTGTGGTGGTGGTGGTGACCCCACCGAGGCCAGGG
Qy	72	GGTTCCGGGCCCGGGCATCTGCCTGGACTCGCCATCCTGGATAGTGCCTTCCTGCTGTC 1788
qa	3291	TTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGT
о _у	1789	CCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGC 1848

QY 2927 TCCCCCCACTTCCACTCCCCTC Db 4491 TCCCCCCACTTCCACTCCCCTC QY 2987 AAATTCCCCTACCCCCAACTT Db 4551 AAATTCCCCTACCCCCAACTT QY 3047 TGTTGGAGCTACTGCAGGACC QY 3107 TCAGCCCCAGAGTACTGCAGGACC QY 3107 TCAGCCCCCAGAGTATTCTGT QY 3107 TCAGCCCCCAGAGTATATCTGT QY 3167 TCAGCCCCCAGAGTATATCTGT QY 3167 TCAGCCCCCAGAGTATATCTGT QY 317 TCAGCCCCCAGAGTATATCTGT QY 317 TCAGCCCCAGAGTATATTATTAGCGGGG QY 327 TCGTCTTATTTATTTAGTTAGCGGGG QY 327 TCGTCTTATTTATTTATTTAGCGGGG QY 3287 TCGTCTTATTTATTTATTTAGCGGGG QY 3187 TCGTCTTATTTATTTATTTAGCGGGG QY 3187 TCGTCTTATTTATTTATTTAGCGGGG QY 3187 TCGTCTTATTTATTTATTTAGCGGGGG QY 3187 TCGTCTTATTTATTTATTTAGCGGGGGCTTATTATTATTAGCGGGGG QY 3187 TCGTCTTATTTA	ULT 22 95409 ABL95409 stan ABL95409; 19-JUL-2002 Human P553S s Human; cancer gene therapy;	XX PD 21-FEB-2002. XX PD 21-FEB-2002. XX PE 12-JAN-2001; 2001US-0759143. XX PR 25-FEB-1997; 97US-0806099. PR 25-FEB-1998; 98US-0020956. PR 23-SEP-1998; 98US-0020956. PR 13-JUL-1998; 98US-0115453. PR 13-JAN-1999; 99US-0159812. PR 13-JUL-1999; 99US-0138146. PR 13-JUL-1999; 99US-043813. PR 13-JUL-1999; 99US-0438672. PR 13-JUL-1999; 99US-0438672. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-05568100. PR 13-JUN-2000; 2000US-0558136. PR 06-SEP-2000; 2000US-0558136. PR 10-OCT-2000; 2000US-0658126.
3351 CCAGGTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGCTCGTCTGTCACTGC 3410 1849 CTATATGGTGTCTGCCGCAGGCTGGTCGTCGTTTACTTTCTTACTTCTACACAGGTAGT 1908 1910 ATTTGACAAGACTTGCCAAGACTTGGTCGCCATTTACTTTGCTACACAGGTAGT 3470 1909 ATTTGACAAGACTTGGCCAATACTCAGCGTAGAAAACTTCCAGCACTTGGGGTG 1968 1111111111111111111111111111111111	2269 TTAACAGCTAGCTCCTAGTTGAGACACCCTAGAGAAGGGTTTTTGGGAGCTGAATAAA 2328 [1111 11 11 11 11 11 11 11 11 11 11 11 1	ACTGTCTTTTGCTGATCCACCCCCTTTACCTTTTATCAGGATGTGGCCTGTTGGTCC 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAG 874
                                                                                                                                                                                                                                                                                   The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       515 TGGCGTGGACGCTATGGCCGCCGCCGTTCATCTGGGCACTGTCCTTGGGCATCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        1371 TGGCGTGGACGCTATGGCCGCCCCCCCTTCATCTGGGCACTGTCCTTGGGCATCCTG
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                                                                                                                                                                            Kalos MD;
Carter D;
                                                                                                                                                                                                                              New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer
                                                                                                                                                                                                                                                                                                                                                62.8%; Score 2142.8; DB 24; Length 4894; llarity 80.1%; Pred. No. 0; Conservative 1; Mismatches 3; Indels 708.
                                                                                                                                                                                                                                                                                                                                                                     3; Indels 708;
                                                                                                                                                                                                                                                                                                                               Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
                                                                                                                                                                         nn DC, Mitcham JL, Harlocker SL, Jiang Y,
Retter MW, Stolk JA, Day CH, Vedvick TS,
I A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 702; 87pp; English.
                                                                                                                   LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                 DILLON D C.
MITCHAM J L.
HARLOCKER S I
                                                                                                  VEDVICK T S.
CARTER D.
                                            JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
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                                                                                STOLK J A.
DAY C H.
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Matches 2872;
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(JIAN/)
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(FANG/)
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CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCTGCGCCCGGCTCTTCGTGGCT 1114
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                                                                                                               TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1054
                                                                                                                                                                                                                                                                                             1911 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCGGACCCTGCGCCGGCTCTTCGTGGCT 1970
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                                                                                                                                                                                                                                                                                                                                                        GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 1174
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1971 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGC
GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTCCTTG
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foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; disorder; satisfied disorder; altergy; pregnancy related disorder; altergy; pregnancy related disorder; endocrine disorder; altergy; pergnancy related disorder; undocrine disorder; altergy; pergnancy related disorder; binding partner identification; wound healing; contact the contact of the contact o Human; secreted protein; proliferative disorder; cancer; gene therapy; ss.

tumour;

Homo sapiens.

/product= "Human secreted protein" /transl_except= (pos:209..211, aa:Xaa) /note= "Xaa corresponds to any of the naturally occurring Location/Qualifiers 152..1267 /*tag= Key

/*tag= b 256.1264 /*tag= c /roduct= "Mature human secreted protein" L-amino acids" 152..295 sig_peptide

mat_peptide

WO200134629-A1

17-MAY-2001

08-NOV-2000; 2000WO-US30654.

99US-0164835 27-JUL-2000; 2000US-0221142 12-NOV-1999;

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Komatsoulis GA, Wei P, Fiscella M, Baker KP;

2001-308779/32. P-PSDB; AAE01362 New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or preservative

Claim 1; Page 388-389; 490pp; English.

AAD05220-AAD05282 represent CDNAs corresponding to 21 human secreted ABC01452-AAE01413 represent the protein grames, and AAE01352-AAE01413 represent the proteins they encode. AAE01413 represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Asthological conditions can be diagnosed by determining the amount of the new penes. Specific uses are described for each of the 21 genes, the new genes. Specific uses are described for each of the 21 genes, developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, focetal and developmental abnormalities, allowers. diseases (e.g., rheumatoid arthritis), inflammation, allergies, aucunimunt meurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, endrzophrenia asthma, skind disorders (e.g., profizophrenia asthma, skind disorders (e.g., psorlasis), sepsis, diabetes, atheroscalerosis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or

1175 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT 1234 1025 GATGAAGGTAAGGCCTTGGCAGCCAGCAGGCTGGTGTGGGAGCCGCCCACCAGAGAG 1084

L235 GATGA-----

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1240 ----

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Db ò

1085 ACACTCGGGGCTGTGTTGGGCTGGTGCTCTCCATCCTGGCCCCGACTTCTCTGTCAGG 1144

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preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioinmunoassay or.enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              995 TCGCCCCACTGCTGCTGCCGGGCCCGCTTGCCGAACCTGGGGCCCCTGCTT 1054
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                                                                                                                                                                                                                                                                                               634
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                                                                                                                                                          710; Gaps
                                                                                                                         62.7%; Score 2136.8; DB 22; Length 3878; 80.0%; Pred. No. 0; tive 5; Mismatches 4; Indels 710;
                                                                                               Sequence 3878 BP; 709 A; 1164 C; 1044 G; 951 T; 10 other;
                                                                                                                                                       Conservative
                                                                                                                                      Best Local Similarity
Matches 2885; Conserv
                                                                      the invention.
                                                                                                                            Query Match
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oy 1		Db 2225 GGTTMMGGGCCGGGGCATCTGCCTGGACCATCGTGGATAGTGCCTTCCTGCTGTC 2284
ag ,	AAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCT IZU	SGCCCCATCCCTGTTTATGGGCTC
δy	0	-8
qq	1205 TGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTT 1264	SGTGTCTGCCGCAGGCCTGGGTCTGGT
ΟŅ	1240 1239	234
qq	1265 TGACAGAAGGAAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGG 1324	1909 ATTTGACAAGGGACTTGGGCGAAATACTCAGGGTAGAAAGTTCCAGGACATTGGGGGTG 19
ογ	1240 1239	1111 11
qa	1325 ATTICAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA 1384	1969 GAGGGCTGCCTCACTGGGTCCCAGCTCCCGGCTCCTGTTAGCCCCCATGGGGCTGCCGGG 202
Οy	1240 1239	
qa	1385 ATAATCTCACCAGGGCCTTCCAGCTCAGGGGTCCTAGAAGGGTCTTGAAGCCTATGGCCA 1444	2029 CTGGCCGCCAGTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGGCGCCCCTGTGCTG 208
οy	1240 1239	2523 CIGGCCGCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCCTGTGCTG 258
qq	1445 GCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTT 1504	2089 CHGAGGHGCGTAGGHGCHGGGGGCGTCCCTCTCCTCCTCCCCCAGTCTC 21
δλ	1240 1239	2583 CTGAGGTGCGTAGCTGCACAGCTGGGGCTGGGGCGTCCCTCTCTCT
QQ	1505 CAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGG 1564	2149 TAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGG
Qy	1240 1239	264
Dp	1565 AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGTGCTGGGGAGCAGGGCTG 1624	2209 CAGAAGGGGTCCATGCAGGAATGCGGGGACTCTGCAGGTGGATTACCCAG
Qy	1240 1239	2203 CACAAACCCTTCCATCCAATCCAATTGCGGGGAATTCTCCAGGTCGATTACCAGGCTCAGGCTCAGGTCGATTACCAGGCTCAGGTCGATTACCAGGTCAATTGCAGGTCAATTGCAGGTCAATTGCAGGTCGATTGAATTGCAGGTCAATTGCAGGTCAATTGCAGGTCAATTGCAGGTCAATTGAATTGCAGGTCAATTGCAGGTCAATTGCAGGTCAATTGAATTGCAGGTCAATTGAATTGCAGGTCAATTGAATTGCAGGTCAATTGAATTGAATTGCAGGTCAATTGAAT
qa	1625 GTCCACAGGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGAC 1684	で、 女女母は女女が中のからのからからないのできないのできないのできないのできないのできないのできない。
δλ	1240AGGCGTTCG 1248	209 TIARCKIC LAGOC LICCIAGI LGAGACACAC LAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
q	1685 IGCICCGACCCTICCCICCCAGGCICTGTCAGAGGCCCCTCTCCCTCTGCAGGCGTTCG 1744	2 0.5 TEANCAGCINGCCICCINGITAGAGCAGCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAG
Qy	1249 GATGGGCAGCCTGGGGCTGTTGCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGTCAT 1308	252 CICAGICACCIGGITICCATCICIAAGCCCCTTAACCTGCAGCTTCGTTTAAGTAGCT 2883 CICAGICACCIGGATCACCTGCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAAGTAGCT 288
qq	5	2389 CTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATAT
Oy	GGACCGGCTGGTGCACCGATTCGGCACTCGACCAGTCTATTTGGCCAGTGTGGCAGCTTT 136	2883 CITGCATGGGAGITTCTAGGATGAACACTCCTCCATGGGATTTGAACATATGAAGTTA 29
අු	GGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTT 186	GTAG
Oy	1369 CCCTGTGCCGGTGCCGGTGCCACATGCCTGTCCCACACGTGGCCGTGGTGACACGTTCAGC 1428 1861	Db 2943 TTTGTAGGGGAAGAGTCCTGAGGGCCAACACACAGAACCAGGGTCCCTCAGCCCACAGG 3002
3 8	COCICIACO CONTRACTA CARACTERISTICA CONTRACTA C	Qy 2507 ACTGTCTTTTGCTGATCCACCCCCTCTTACTTATCAGGATGTGGCCTGTTGGTCC 2566
7 d		STCTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCC 3
λŏ	9 CTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAG 1	2567 TTCTGTTGCCATCACAGAGACACAGCATTTAAATATTTAACTTATTATTTAACAAAGT
: q		063 TTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAT
ò	49 CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCC 1	2627 AGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTTGTATATTTGGGTAGGGTGGGGG 268
i qa		3123 AGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGG 3.1
Qy	1609 TAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCACCCGCGCTCTGCGG 1668	4
q	:5	2747 TCTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCT
δλ	GGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGGTGAGCCCACCGAGGCCAGGGT 172	
qa ·	GGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGT 222.	Qy 2807 TCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAG
δλ	1729 GGTTCCGGGCCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTC 1788	

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3423 TCCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCA 3482
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                                                                                                                                                                                                                        TCAGCCCCCAGAGIAIAICIGIGGIAAICTCACACAGAAACICAGGAGCACCCCC 3166
                                                                                                                                                                                                                                   3603 TCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACAGAAAACTCAGGAGCACCCC 3662
                                                                                                                                                                                                                                                                     3167 IGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGGTTTAAGTGCCGTTTGCAATAATG 3226
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                                                                                                                                                                                                                                                                                                                                                                     TCCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCA
                                                                                                                                      Consensus sequence of the PS108 gene derived from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS108 gene; prostate disease; benign prostatic hyperplasia; BPH; prostatitis; prostatic intraepithelial neoplasia; PIN; cancer; drug screening; gene therapy; ss.
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Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV71181 standard; cDNA; 2152 BP.
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                                                                                                                                                                       The present sequence represents the consensus sequence for a PS108 gene. The sequences are PS108 gene-specific. They are used in the method of the invention. The specification describes a method for detecting the presence of a target PS108 polynucleotide in a test sample. The method presence of a target PS108 polynucleotide in a test sample. The method polynucleotide or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, polynucleotide. The products can be used for detecting, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatitis, prostatic intraeplithelial neoplasia (PIN) and cancer. In particular the products can be used in drug screening and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACAC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Gaps
                                                                 New isolated prostate-specific polynucleotides - used to develop products for the diagnosis and treatment of prostate diseases, e.g. benign hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2136.4; DB 20; Length 2152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2152 BP; 419 A; 622 C; 569 G; 542 T; 0 other;
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0; Mismatches
                                                                                                                                          Claim 1; Fig 1A-E; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 62.7%;
Best Local Similarity 99.9%;
Matches 2149; Conservative
               WPI; 1999-034731/03.
                                 P-PSDB; AAW85068
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                                                                      GCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAG 3094
                                                                                                                                                                                                                                                                                                                   GCCCAGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCTAGGACTGGGCTGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       olated prostate-specific polynucleotides - used to develop
ts for the diagnosis and treatment of prostate diseases, e.g.
hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene, prostate disease, benign prostatic hyperplasia; BPH;
titis; prostatic intraepithelial neoplasia; PIN; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g-Wedel PA, Cohen M, Colpitts TL, Friedman PN;
J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
s-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1711346IH, the PS108 gene contig full length sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          creening; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 standard; cDNA; 2143 BP.
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contacting the test sample with at least 1 PS108 or complement, and detecting the presence of the Polynuclectide. The products can be used for det staging, monitoring, prognosticating, in vivo im treating, or determining predisposition to diseathe prostate such as benign prostatic hyperplasi prostatic intraepithelial meoplasia (PIN) and caproducts can be used in drug screening and generations. Sequence 2143 BP; 418 A; 621 C; 563 G; 541 T; 0	Query Match 62.0%; Score 2114.8; DB 20; Length 2143; Best Local Similarity 99.8%; Pred. No. 0; Matches 2139; Conservative 0; Mismatches 2; Indels 3; Gaps 2.	1185 ACCAGGGCTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGATGAGGG 1244	1245 TTCGGATGGGCAGCCTGGTCCTGCAGTGCGCCATCTCCCTGGTCTCTCTC	1305 TCATGGACCGGCTGGTGCGGATTCGGCACTCGACCAGTTTTGGCCAGTGTGGCGG 13	1365 CTITCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTT 1424	1425 CAGCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCT 1484	1485 CCCTCTACCACGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTG 1544	1545 CTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCT 1604	1605 TCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCTCGCGCTCT 1664	1665 GCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCCA 1724	1725 GGGTGGTTCCGGGCCGGGGCATCTGCCTGGCCTCGCCATCCTGGATAGTGCCTTCCTGC 1784	1785 TGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1844	1845 CTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGG 1904	1905 TAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGGGTAGAAACTTCCAGCACATTGG 1964 	1965 GGTGGAGGCCTGCCTCACTGGGTCCCGGCTCCCGGCTCTGTTAGCCCCATGGGGCTGC 2024	2025 CGGGCTGGCCGCCAGTTCTGTTGCTGCCCAAAGTAATGTGGGTTCTTGCTGCCACCTGT 2084
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                        21; Length
        621 T; 0 other,
                      Score 2065.4; DB 2. Pred. No. 7.6e-314; 0; Mismatches 6;
        483 A; 726 C; 632 G;
                       Query Match 60.6%;
Best Local Similarity 99.6%;
Matches 2092; Conservative
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AGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGAC SCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACACCT 	CTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACC 	TTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTC 	5ACTIATTGTAGGGAAGAGTCCTGAGGGC 	CACAGCACTGFCTTTTGCTGATCCACCCCCCTCTTAC	GTTGGTCCTTCTGTTGCCATCACAGAGACACAGGCATTTAAATATT 	AACAAAGTACAAAGGGAATCCATTGCTAGCTTTTCTGTGTTTGTG 	GGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGT(SCCAGAAICTICTICTCCTGGGGTCTGGCCCCCCAAAIGCCTAACCCAGG 	aaattctactcatcccaaatgataattccaaatgctgttacccaaggttag 	GGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCT(CAGCCTGGTTCCCCCCACTCCACTCCCCTCTACTCTCTCT	ACTECCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTCCCCAC. 	CACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAA 	TGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACAGAAACT 	GCACCCCTGCCTGAGCTAAGGGGGCTCTTATCTCTCAGGGGGGGT 	CAATAATGICGTCTTATTTATTTAGGGGGGGAATATT 	CAGAGTATAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGT
1322 ATAC: 2257 CCAG: 1111 1382 CCAG:	2317 GAGG 142 GAGG	2377 TTT 1502 TTT	2437 ATATO 1562 ATATO	2495 TCAGCC 	2555 GCCTG 1682 GCCTG	2615 ATTT/ 1742 ATTT/	2675 GTAG 1802 GTAG	2735 TTGC 1862 TTGC	2795 AAA1 1922 AAA1	2855 GGAA 1982 GGAA	2915 GCCC 2042 GCCC	2975 AGGCACTG 2102 AGGCACTG	3035 GCTC 2162 GCTC	3095 CCTT	3155 AGGA(2282 AGGA(3215 TTTG 2342 TTTG	3275 ATCA 2402 ATCA
Ob Oy Dp	Qy Db	Oy Db	Qy Dp	oy og	Oy Dp	ò q	oy Db	oy Db	Qy	oy Dp	oy Db	Qy	oy Dp	oy GB	Qy Dp	Qy Dp	Qy Db

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1177 GGGCCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGA 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to produce antibodies which can be used in treatment. The present sequence is one of the PS108 partial coding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methods for detecting target prostate-specific polynucleotides or diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample
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                                                                                                                                                                                                            Human; prostate cancer; PS108; antibody; tumour; metastasis;
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Billing-Medel PA, Klass MR, Roberts-Rapp L, Stroupe SD,
Kratochvil JD, Russell JC, Hodges SC;
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98.9%; Pred. No. 2.3e-290;
tive 0; Mismatches 5;
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Best Local Similarity 98.9
Matches 2127; Conservative
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                       2462 A 2462
3335 A 3335
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                                                                                                                                                                                                Klass MR, Kratochvil JD, Roberts-Rapp
Yu H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%; Score 1915; DB 22; Length 2133;
.larity 98.9%; Pred. No. 2.3e-290;
Conservative 0; Mismatches 5; Indels 19;
/product- "Prostate-specific protein PS108"
                                                                                                                                                                                     Colpitts TL, Friedman PN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2133 BP; 414 A; 618 C; 561 G; 540 T; 0 other;
                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1; 55pp; English.
                                                                                                             98US-0071710.
97US-0850713.
                                                                                  2000US-0525397
                                                                                                                                                                                     Cohen
                                                                                                                                                                                                   Granados EN, Hodges SC,
Russell JC, Stroupe SD,
                                                                                                                                                                                                                                           WPI; 2001-424488/45.
                                                                                                                                                         (ABBO ) ABBOTT LAB.
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Matches 2127; Conserv
                                                                                                                                                                                     Billing-Medel PA,
                                                                                                                                                                                                                                                            P-PSDB; AAU04205
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                                                                                                               01-MAY-1998;
02-MAY-1997;
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301 ACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACAC
                                           TGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGG
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        2736 TGCCAGAATCTTCTTCTTCTTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGA
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                                    TAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCAT
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                                                                                                   diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample
                                                                                                                                                                                                                                                                                                                                               1185 ACCAGGGCGTGCCCAGAGCTGAGCCGGGCCCGGAGGCCGGAGACACTATGATGAAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                      1245 TTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGG
                                                                                                                                                                   The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to produce antibodies which can be used in treatment. The present sequence is on of the PS108 partial coding sequences.
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                     20;
                                                                                      for detecting target prostate-specific polynucleotides
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                                                                                                                                                                                                                                                                                           21; Length
                      Stroupe SD,
           Granados
                                                                                                                                                                                                                                                                                                                      2; Indels
                                                                                                                                                                                                                                                                  Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;
                                                                                                                                                                                                                                                                                                       .5e-288;
           Friedman PN, Gordon J,
                                                                                                                                                                                                                                                                                           DB
                      A, Klass MR, Roberts-Rapp L,
Russell JC, Hodges SC;
                                                                                                                                                                                                                                                                                           Score 1899.8;
Pred. No. 5.5e
                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                             Claim 1; Column 75-78; 55pp; English.
                                                                                                                                                                                                                                                                                          Query Match 55.7%;
Best Local Similarity 99.0%;
Matches 2121; Conservative
           Colpitts TL,
                                                              WPI; 2000-655655/63.
                         Billing-Medel PA,
                                      Kratochvil JD,
                                                                                                       diseases of
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           Cohen M,
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AGTATTTGACAAGAGCGACTTGGCCAAATACTCCAGCGTAGAAACTTCCAGCACATTGG 1964	CCCGCTCCTGTTAGCCCCATGGGGCTGC 20	GGCCCCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCTGCCGCTGT 2084	OCTAGCTGCACAGCTGGGGCTGGGGCGTCCCTCTCCTCTC	GGTGCCTGACTGGAGGCCTTCCAAGGGGTTTCAGTCTGGACTTATACAGGG 2204	GGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTC 2264	GTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAA 2324 	CACCTGGTTTCCCAT	SCATGGGAGTITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATG-AC 2443 	SAAGAGTCCTGAGGGGCAACACACAGAACCAGGTCCCCTCAGCCCAC 250 	9 /	SCCATCACAGAGACACAGGATTTAAATATTTAACTTATTTAT	AATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGG 268	TCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAA 2743 	CTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTAC 2803	CATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAG	AGGGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCTCTTCTCTTGGCCCAGCCT 2923	rcrcraggacrgggcrgargaaggcacrgc 29
TAGTATTTGA TAGTATTTGA	GGTGGAGGG(CGGGCTGGCC	GCTGCTGAGGTC	TCTCTAGGGC TCTCTAGGGC	AGGCCAGAAGGGC 	AGGGTTAACA -GGGTTAACA	TAAACTCAGTC	AGCTCTTGCA 	TTATTTGTAGGGG 	AGCACTGTCT AGCACTGTCT	TCCTTCTGTTC TCCTTCTGTTT	AGTAGAAGGG, AGTAGAAGGG,	GGGATCCCCA 	TCTTCTTCTC 	TCATCCCAAA' TCATCCCAAA	AGGTGGGGC	SGTTCCCCCC
1905	1965 781	2025	2085	2145	2205	2265	2325	1197	1256	1315	1374	2624	2684 (1551	2804 1	2864 F	2924 G 1728 G
oy Ob	Oy Db	Oy Dp	Qy Dp	Oy Op	Q Q	oy Op	oy Ob	oy Db	Oy Op	Qy Db	Qy Db	Qy Dp	Oy Dp	Qy Dp	Qy Db	Qy Db	Oy Dp

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1787 CCAAAATTTCCCCTACCCCAACTTTCCCCTACCCCCAACTTTCCCCACAGCTCCACA- 1845
                                                          3163
                                                                                                                                       1905 ATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAACTCAGGAGCA-C 1963
                                                                                                                                                                                                1964 CCCTGCCTGAGCTAAAGGAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCCGTTTGCAAF- 2022
                                                                                                                                                                                                                                           3224 AIGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTA 3283
                                                                                                                                                                                                                                                           The sequence represents the coding sequence of prostate gene PS108-specific expressed sequence tag (EST) cDNA clone 1711346IH. The sequence was used along with other overlapping cDNA clones to produce a full length consensus sequence (see AASO7155). This sequence could then be used to produce PS108 polypeptides which are useful in assays for detecting antibodies to prostate tissue, and as immunogens to produce antibodies. The polypeptide is useful for screening compounds which specifically bind to the polypeptide and for screening for drugs, compounds, or any other agent which can be used to treat diseases associated with PS108. The antibody is useful to detect, or for image
                                                                                                                    3104 ATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACC
                                                                                                                                                                               3164 CCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prostate; PS108; Immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metastasis; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel PS108 polypeptide useful in assays for detecting antibodies to prostate tissue, and as immunogens to produce PS108 antibodies - .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M, Colpitts TL, Friedman PN, Gordon J;
Klass MR, Kratochvil JD, Roberts-Rapp
Yu H;
                                                                                                                                                                                                                                                                                                    Prostate gene PS108-specific cDNA clone 1711346IH.
                                                                                                                                                                                                                                                                                                                                                                                                        AAS07601 standard; cDNA; 2124 BP
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97US-0850713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-OCT-2001 (first entry)
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Stroupe SD,
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localisation of PS108 antigen in a patient, for detecting or diagnosing a disease or condition, as delivery agents for therapeutic agents as well as for diagnostic tests and for screening for diseases or conditions associated with PS108, especially cancer. The antibody is also useful for generating chimeric antibodies for therapeutic use, for inhibiting the biological activity of PS108, in therapy (for e.g. to treat prostate tissue disease including prostate cancer and its metastases), and to detect the presence of any polypeptide in a test sample which shares one or more antigenic determinants with the PS108 polypeptide. 88888888888888

1964 2024 1664 1724 1784 1244 1364 1424 1484 CTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCT 1604 540 IGICCCAGGIGGCCCCAICCCIGITIAIGGGCICCAIIGICCAGCICAGCCAGICIGICA 1844 099 CTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGG 1904 780 840 CCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTG 1544 480 420 20; 240 300 120 09 GCTGGAGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGCTGC GGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCCATGGGGCTGC TCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGCGCGCTCT GCGGGGCCTCTGCCTGTGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCCA GCGGGGCCTCTGCCTGTGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCCA GGGTGGTTCCGGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGC GGGGGGTTCCGGGCCGGGCATCTGCCTGGCCTCCCCGGATAGTGCTTCCTGC CTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGG TAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGG TCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAG CAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCT CAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTT 1185 ACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCG TICGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGG CTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCCGTGGTGACAGCTT Gaps DB 22; Length 2124; 20; 2; Indels Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other; Score 1899.8; DB 2: Pred. No. 5.5e-288; Mismatches 0; 55.7%; 99.0%; Matches 2121; Conservative Similarity 1605 1665 481 1725 541 1785 1845 661 1905 721 1965 781 1545 1425 1485 301 421 -1305 121 181 241 361 1245 61 1365 Query Match

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2863 2983 CCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCC 3103 ATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACC 3163 1491 CCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGT-C 1904 1019 1078 2324 2204 960 AGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTTAATATTTGGGTAGGGT-G GGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAA GGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAG-A TCTTCTTCTCCTGGGGTCTGGCCCCCCCAAAATGCCTAACCCCAGGACCTTGGAAATTCTAC GGTTCCCCCCCACTTCCACTCCCTCTACTCTTCTAGGACTGGGCTGATGAAGGCACTGC -AAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGT TCCTTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAATAAAAA AGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGG AGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCT -GGGTTAACAGCTAGCCCCCTAGTTGAGACACACAGAGAGGGTTTTTGGGAGCTGAA TTATTTGTAGGGGAAGAGTCCTGAGGGCCAACACACAGAACCAGGTCCCCTCAGCCCAC AGCACTGTCTTTTTGCTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGG TCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGG AGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTC AGGGTTAACAGCTAGCTCCTAGTTGAGACACCTAGAGAAGGGTTTTTGGGAGCTGAA TAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAAACCTGCAGCTTCGTTTAATGT AGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATG-AC CGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGT 1728 3044 3104 1610 1846 1551 2804 2864 1669 2924 1787 1020 2385 2444 1256 2504 1315 2564 1374 2624 1433 2684 1492 2744 2984 2265 1079 2325 1197 2085 1138 841 g g ŏλ a Qγ q δ qq ò Dp ρy g οy òγ g g òγ g ٥y δ q $^{\circ}$ Dρ οy οy οy g g δ a Ω С ŏλ В

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1905 ATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAACTCAGGAGCA-C 1963
                               CCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATA 3223
                                                                                           ATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTA 3283
                                                                                                             2023 AIGICGICITATITITIAGCGGGGGGAAATITIATATACTGTAAGTGAGCAATCAGAGI- 2081
                                                                                                                                                                                                                                                                                                                                                                                         Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasctropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Corresponding to genes differentially expressed in mast cells following activation or in patients with allergic hypersensitivity disease, (I) that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of (II) if at least 6 amino acids. (II) is useful for identifying binding partners. (I) or (II) is useful for diagnosing or treating a disease state (e.g. allergic hypersensitivity, seasonal rhinitis, asthma, urticaria or atopic dermatitis or mastocytosis) in a subject which involves determining the level of expression of (I) or (II). A computer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated nucleic acid (ABN81319-ABN81324),
                                                                                                                                                        3284 TAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTTTA 3326
                                                                                                                                                                        2082 TAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTA 2124
                                                                                                                                                                                                                                                                                                                                                             Human mast cell related gene MC14 SEQ ID NO 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "MC14-1"
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                                                                                                                                                                                                                                                                 ABN81320 standard; cDNA; 3663 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2001; 2001US-275479P.
28-MAR-2001; 2001US-279115P.
02-APR-2001; 2001US-280143P.
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                                                                                                                                                                                                                                                                                                                               (first entry)
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                                3164
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expression level in a tissue or at least one mast cell of (i), is useful for presenting information to identify the relative expression level of (i). (II) is used as a marker to detect, diagnose or identify an allergic response in a patient. The protein can also serve as a target that modulate gene expression or activity and as an antigen to raise polyclonal or monoclonal antibodies. (II) is useful for identifying agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as modulating biological activity and function of (II) and thus are useful for alleviating disease conditions such as allergic hypersensitivity,
                                                                                                                                                                                                                                                                                                                                                                                                     62 TGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                         AGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 GCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       372 GGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTG 431
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                                                                                                                                                                                          seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis
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                                                                                                                                                                                                                                                                Score 1854.8; DB 24; Length 3663;
Pred. No. 6.2e-281;
0; Mismatches 682; Indels 303; Gaps
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73.08;
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οy	1212 GCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCC 1271	δλ	
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61 T	TGCCGCAGGCCTGGTCTGGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGA 192
21 0	CGACTTGGCCAAATACTCAGCGTAGAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT
81 C	CACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGT 204
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341 (652 (GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 24
401	TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTGTAGGGGAA 24
459 (GAGTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTG 25
519 (832 (CTGATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCAT 25
579 (892 (CACAGAGACACAGGCATTTAAATATTTAACTTATTTTAACAAAGTAGAAGGGAATCC 26
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                                    GTCTGGCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCCATCCCAAATGATA 2818
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27-JUN-2000;
10-AUG-2000;
29-AUG-2000;
06-SEP-2000;
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                                                                                                                                                                                                                                                                                           The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. The polypeptides, polynucleotides and polynucleotide and/or polypeptide are useful for stimulating the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for transling cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1710 AGCCCACCGAGGCCAGGGTGGTTCCGGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGG 1769
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                                                                                                                                                                                                         New human prostate-specific polypeptides and polynucleotides useful the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                      Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1815.8; DB 22; Length 6976;
Pred. No. 8.2e-275;
0; Mismatches 22; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
                                                                                  Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skelky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                            Claim 1; Page 484-486; 579pp; English.
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98.78;
02-OCT-2000; 2000US-0679426
10-OCT-2000; 2000US-0685166
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Matches 1841; Conservative
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                                                                                                                                                             2250 GGATTACCCAGGCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAAGGG
                                                                                                                                                                       2310 TTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGC
                                                                                                                                                                                                               GGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTCTTACCTTTATCA
                                                                                                                                                                                                                                                                                                                                                                   GGATGTGGCCTGTTGGTCCTTCTGTTGCCATCAGAGACACAGGCATTTAAATATTTAA
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GCCCCATGGGGCTGCCGGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCCTCT
                                        CTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGGCTGGGGGCGTCCCT.
                                                                                                                      TGGACTTATACAGGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGT
                                                                                                                                 AGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prostate-specific proteins (II). [1] and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. [1], [II], and tibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) can also be used to improve diagnostic and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAW01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                      GAAACTCAGGAGCACCCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTA
                                                          GAAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTTA
                                                                                                 AGTGCCGTTTGCAATAATGTCGTCTTATTTATTAGCGGGGTGAATATTTATACTGTAA
                                                                                                               New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SG;
YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SL, Jiang Y, Reed, Stolk JA, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harlocker S
Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 461-463; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        P553S cDNA splice variant P553S-6.
                                                                                                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham GR, Day
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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MD, Fanger GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meagher MJ;
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                                                                                                                                                                                                                                           6972 AAAAA 6976
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                                                                                                                                                                                                                  AAAAA 3332
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Kalos MD,
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                                                                                                                                                                                                                                                                                         RESULT 33
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Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;

Oller	. Score 1815 8.	Qy	2488 GGTCCCTCAGCCCACAGCACTGTTTTTGCT
Best	No. 8.2e-275; Schools 2; Smatches 22; Indels 2;	QQ	6132 GGTCCCTCAGCCCACAGCACTGTCTTTTGCT
δ	CTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAG	Oy Dp	2548 GGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA
g è	5112 CCTGTCCTCTTCCCCTTTTCTTCACCCCTCTGCCTTAGGTGTTCCTGCCCAAATACCGG 5171 1530 GGGACACTGGAGGTGCTAGCAGTGAGGACAGCTGATGACCAGCTTCCTGCCAGGCCTA 1589	Qy	2608 CTTATTTATTTAACAAAGTAGAAGGGAATCCAT
7 qq	GGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTA 523	qa	0
ò é	1590 AGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCTGCTCCCAC 1649	Oy Dp	2668 TATTTGGGTAGGGTGGGGGATCCCCAACAATCA [
δ δ	CTCCACCCGCGCTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGTGTTGTTTTTTTT	Qy Db	2728 CTGATCATTGCCAGAATCTTCTCTCTGGGGT
g å	5292 CTCCACCCGCGCTCTGCCGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGTG 5351 1710 AGCCCACGAGGCCAGGGTTCCGGGCCGGCCATCTGCCTGGACCTCGCCATCCTGG 1769	. ko	2788 ACCTTGGAAATTCTACTCATCCCAAATGATAAT
qa .	AGCCCACCGAGGCCAGGGTCCGGGCCGGGCCATCTGCCTGGACCTCGCCATCCTGG 541	Qy	
y Q	1//0 ATAGTGCCTTCTTGCTGCCAGGGGCCCCATCCTGGTTTTGGGGCCTTGGTGGGGGGGG	qq	~
δ d	1830 TCACCCAGTCTGTCACTGCCTATATGGTGTTCTGCCGCAGGCCTGGGTTGGTT	Qy	2908 TOTCTTGGCCCAGCCTGGTTCCCCCCACTTCCA
G &	ACTTTGCTACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAA 19	Qy	2968 CIGAIGAAGGCACIGCCCAAAAITICCCCIACC
oy Oy	5532 ACTITGCTACACAGGTAGIATITGACAAGAGGGACTIGGCCAAAIACTCAGGGTAGAAAA 5591 1950 CTICCAGCACATIGGGGTGGAGGCCTGCCTCACTGGGTCCCAGCTCCCGGTCCTGTTA 2009	Qy	3028 CCCACCAGCTCCACAACCCTGTTTGGAGCTACT
qa		a 8	6672 CCCACCAGCTCCACAACCCTGTTTGGAGCTACT
oy Ob	2010 GCCCCATGGGCTGCCGGGCTGGCCGCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCT 2069	da da	0 0
δ d	2070 CTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGCTGCAAGCTGGGGGCTGGGGCTGGGGCTTCCCT 2129 [1111111111111111111111111111111111	Qy Dp	3148 GAAACTCAGGAGCACCCCTGCCTGAGCTAAGG
6 6 F	CICCICCCCCCCCCCTAGGGCTGCCCTGAGGCCTTCCAGGGGGCTTCCAGCTCCCCCCCC	Qy	3208 AGTGCCGTTTGCAATAATGTCGTCTTATTTATT
g & 6	Z CICCICITATACAGGAGGC O TGGACTTATACAGGAGGC	Qy Db	3268 GTGAGCAATCAGAGTATAATGTTTATGGTGACA
o v	32 IGGALTIALACAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	oy 4	328 AAAAA 3332
qq	5892 GGATTACCCAGGGTCAGGGTTAACAGCTAGCTGCTTAGTTGAGACACACCTAGAGAAGGG 5951	gn	7/69
QV Oy	2310 TTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGC 2369 	RESULT ABL9541	.T.34 412 ABL95412 standard; cDNA; 6976 BP.
Qy	2370 AGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAACACTCCTCCATGGGA 2429 	AC A	ABL95412; 19-JUL-2002 (first entry)
δy	TTTGAACATATGACTTATTTGTAGGGAAGAGTCCTGAGGGGCAACACACAGAACGCA 24	X D X	man P553S splice varia
QQ	6072 TTTGAACATATGAAAGTTATTTGTAGGGGAAGAGTCCTGAGGGGCAACACACAAGAACCA 6131	KW KW	Human; cancer; prostate cancer; vaccine; c gene therapy; gene; ss.

TGATCCACCCCCTTTACCTTTATCA 2547 CAGGTCCCCTGAGATAGCTGGTCATTGGG 2727 CACTCCCTCTACTCTCTAGGACTGG 2967 STATATCTGTGCTTGGGGAATCTCACACA 6791 360AGGTCTTATCTCTCAGGGGGGGTTTA 3207 ATTECTAGCTTTTCTGTGTTGGTGTCTAA 2667 ATTCCAAATGCTGTTACCCAAGGTTAGGG 6491 CCCCCAACTTTCCCCTACCCCCAACTTTC 6671 STATATCTGTGCTTGGGGAATCTCACACA 3147 STCTGGCCCCCCAAATGCCTAACCCAGG 2787 STCTGGCCCCCCAAATGCCTAACCCAGG 6431 ATTCCAAATGCTGTTACCCAAGGTTAGGG 2847 SCCCCAACTTTCCCCTACCCCCAACTTTC 3027 TTGCAGGACCAGAAGCACAAAGTGCGGTT 3087 cytostatic; immunostimulant; us-09-759-143-110.rng

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1709

5351

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GGTCCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTTTACCTTTTATCA
                                                                                                                                    5472 TCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCTGTCATTT
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                                                  5172 GGGACACTGGAGGTGCTAGCAGTGAGGACGAGCTGATGACCAGCTTCTGCCAGGCCCTA
                                                                                  AGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCAC
                                                                                             CTCCACCCGCGCTCTGCGGGGCCTCTGCTGATGTCTCCGTACGTGTGGTGGTGGTG
                                                                                                                                                                                                                                                      TCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTT
                                                                                                                                                                                                                                                                                                                                          CTTCCAGCACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTCCTGTTA
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CCTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAG
                    5112 CCTGTCCTCTTCCCCTTTTCTTCACCCCTCTGCCTTAGGTGTTCCTGCCCCAAATACCGAG
                                         GGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.2%; Score 1815.8; DB 24; Length 6976; 98.7%; Pred. No. 8.2e-275; arive 0; Mismatches 22; Indels 2; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   r diagnosing and tre
and as markers for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New prostate-specific polynucleotides for diseases, in particular prostate cancer, a progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 705; 87pp; English.
                                                                                                                                                                                                  99US-0443686.
2000US-0483672.
2000US-058857.
2000US-0588100.
2000US-0570737.
2000US-0570737.
2000US-0636218.
2000US-0651236.
2000US-0651236.
2000US-0651236.
2000US-0651236.
                                                                                           97US-0806099,
97US-0804804,
98US-0020956
98US-0030607,
98US-01159812,
99US-0232149,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.7
Matches 1841; Conservative
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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MITCHAM J L.
HARLOCKER S I
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DAY C H.
VEDVICK T S.
CARTER D.
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KALOS M D.
FANGER G R.
RETTER M W.
                               US2002022248-A1
                                                                                                                                                                                                                                                                          10-AUG-2000; 2
29-AUG-2000; 2
06-SEP-2000; 2
02-OCT-2000; 2
10-OCT-2000; 2
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13-JUN-2000;
                                                                        12-JAN-2001;
                                                                                                                                                                                                              14-JAN-2000;
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                                                                                                                                                                              13-JUL-1999;
12-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fanger GR,
                                                    21-FEB-2002
                                                                                                                  FEB-1998
                                                                                                                           25-FEB-1998
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(MITC/)
(HARL/)
(JIAN/)
(KALO/)
(FANG/)
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(HEPL/)
(HEND/)
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(WANG/)
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                                                                                                                                                                                                                                                                                                                                          3268 GTGAGCAATCAGAGTATAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTAA 3327
                                                                                                                                                                                                                                                                                                                                                  Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
TATTIGGGTAGGGIGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGG
                                                         2968 CTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCAACTTTC
                                                                                                                                                                                                                                                                                         CTTATTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTTGGTGTCTAA
                                                                               CTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCCCCCCCAAAATGCCTAACCCAGG
                                                                                                           2788 ACCTIGGAAATICTACICAICCCAAAIGATAATICCAAAIGCIGTIACCCAAGGITAGGG
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                                                                                                                                              TCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGG
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                                                                                                                                                                                                                          3028 CCCACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTT
                                                                                                                                                                                                                                  Human mast cell related splice variant gene MC14 SEQ ID NO 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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The invention relates to isolated nucleic acid (ABNB1319-ABNB1324),

corresponding to genes differentially expressed in mast cells following

cutivation or in patients with allergic hypersensitivity disease, (I)

that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of

(II) if at least 6 amino acids. (II) is useful for identifying binding

patrners. (I) or (II) is useful for diagnosing or treating a disease

cate (e.g. allergic hypersensitivity, seasonal rhinitis, asthma,

urificaria or atopic dermaitis or mastocytosis) in a subject which

urificaria or atopic dermaitis or mastocytosis) in a subject which

corresponse in a tissue or at least one mast (I) or (II). A computer

system, comprising a database containing information identifying the

cxpression level in a tissue or at least one mast cell of (I), is useful

corresponse in a patient. The protein can also serve as a target that

modulate gene expression or activity and as an antigen to raise

polyclonal or monoclonal antibodies. (II) is useful for identifying

agents that modulate expression of the protein or agents, such as

modulating biological activity and function of (II) and thus are useful

corresponse in a lateylating disease conditions such as allergic hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCGGGCACCGGAAAGCCCCAGCTCTTGCTG
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                                                                 "MC14 alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.7%; Score 1662; DB 24;
100.0%; Pred. No. 7.5e-251;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 115-117; 119pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Einstein R;
                                                                                                                                                                                                                                                                                                                                         08-DEC-2000; 2000US-251835P.
14-MAR-2001; 2001US-275479P.
28-MAR-2001; 2001US-27515P.
22-APR-2001; 2001US-280115P.
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	Db 1441 AGC Qy 1784 CTC Db 1501 CTC Qy 1844 ACT Db 1561 ACT	Oy 1904 GTR Db 1621 GTR RESULT 36 ABA91283 ID ABA91283 Stz	XX AC ABA91283; XX DT 08-APR-2002 XX XX DE Thioredoxin- XX XW Thioredoxin-		PF 19-JUN-2001, XX X 26-JUN-2000, PR 30-OCT-2000 XX XX XX XX XX XX XX XX XX XX XX XX		CC The present CC from the 5' CC the human ul CC (amino acid CC tail. The CC which inclu CC yeast alpha CC (see AAM506 CC is an examp
524 GGCTATGGCCGCCGCCGCCGTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTC 583		481 TACTURICTERINGCUTICARGATCARGAGGGCTGCCTGGGCTACCTGCCTGCCTGCCTGCCTGCCT	944 GCAGCGCTGGGCCCCACCGAGCAGCAGGGCTGTCGGCCCCCTTGTCGCCCCAC 1003		1184 TACCAGGGCGTGCCCGAGGCTGAGGCCCGGGACACTATGATGATGAGGC		1484 TCCCTCTACCACCGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGT 1543
Oy Oy Oy	Oy Oy Oy	90 63 69 60 63 69	Oy Oy Oy	Qy Db Qy	70 40 vo	90 64 69 64 64 64	, da ya ya

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                                                                                                                                                                                                                                                                                                                     JIGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
                                                                                                                                                                                                                                                                                                                                                                                                                     sequence encoding triple fusion protein comprising ubiquitin een thioredoxin and polypeptide of interest, useful for recombinant polypeptide of interest suitable for medicinal
                                                                              of the transplant of a triple gene fusion comprising, bend, the transplant gene from Escherichia coli, ubiquitin coding sequence, the prostate antigen P501S ids 55-553 coding sequence, and DNA encoding a histidine at triple fusion was constructed in plasmid pRITI5063, luded the Saccharomyces cerevisiae CUP1 promoter and ha prepro signal sequence. The triple fusion protein b661) was produced in E. coli G1724 transformants. This mple of the production of triple fusion proteins of the comprising ubiquitin fused between thioredoxin and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                n; trxA; ubiquitin; P501S; tumour; prostate; antigen;
ccine; therapy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-ubiquitin-P501S(aa55-553)His triple gene fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAG 1945
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0; 2000GB-0026484.
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protein of interest, in this case P501S(aa55-553). A claimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coll) under conditions which allow for co-expression of the triple fusion and a ubiquitin-specific endoprotease (especially UBP1 from Saccharomyces cerevislae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the ubiquitin-specific endoprotease in vivo. In the present case, a p501-like protein of 509 amino acids is generated. The recombinant protein can used as a vaccine for cancer therapy.
                                                                                                                                                                                    44.1%; Score 1503; DB 24; Length 2133;
llarity 100.0%; Pred. No. 5.3e-226;
Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                         Sequence 2133 BP; 384 A; 656 C; 614 G; 479 T; 0 other;
                                                                                                                                                                                                   Similarity
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Best Local Simil
Matches 1503; (
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            CACAGIGIGGCGTGGTGACAGCTICAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen; cancer; vaccine; therapy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Xaa not given in amino acid sequence of Figure 12b (AAM50662), which has a Val residue at amino acid position 208 not not encoded by the present sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thioredoxin-ubiquitin-P501S(aa1-320)His triple gene fusion.
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1..1593
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Escherichia coli
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2104 GCG 2106
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1503 GTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGGAGACACTATGATGAAGG 1562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; pastrointestinal disorder; altergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                        Human secreted protein-encoding gene 11 cDNA clone HWBAR14, SEQ ID NO:55.
                                                                                                                                                                                                                                                                                                         1263 GGCAGCGCTGGGCCCCACCAGCAGCAGCAGAAAGGCTGTCGCCCCTCCTTGTCGCCCA
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                                                                                                                                                                                          883 IGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGA
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GGAGCTGGCCACTCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTT
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                                                                                                                       823 CATTGACTGGGACACCCAGTGCCCTGGCCCCTACCTGGGCACCCCAGGAGGAGTGCCTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from the 5' end, the trxA thioredoxin gene from Escherichia coli, the human ubiquitin coding sequence, the prostate antigen P501S (amino acids 1-320) coding sequence, and DNA encoding a histidine tail. The triple fusion was constructed in plasmid pRIT15115, under the control of the lambda pL promoter. Triple fusion protein (see AAM5062) was produced in E. coli GT724 transformants. This is an example of the production of triple fusion proteins of the invention comprising ubiquitin fused between thioredoxin and a the invention comprising ubiquitin fused between thioredoxin and a contain of interest, in this case P501S(aal-320). A claimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coli) under conditions which allow condorctease (especially UBP1 from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the bacterial cubiquitin-specific endoprotease in vivo. In the present case, expression was controlled by addition of tryptophan. The combinant protein can used as a vaccine for cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                 Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 TATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence is that of a triple gene fusion comprising,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1593 BP; 308 A; 472 C; 461 G; 352 T; 0 other;
                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                     19-JUN-2001; 2001WO-EP06952.
                                                                                                                                                                           30-OCT-2000; 2000GB-0026484.
                                                                                                                                                    26-JUN-2000; 2000GB-0015619
                                                                                                                                                                                                                                                                                                                      WPI: 2002-147888/19.
                                                                                                                                                                                                                                                                      Cabezon Silva TEV,
                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAM50662
                                                         03-JAN-2002
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diseases (e.g., rheumatoid arthritis), inflammation, allergies,

classes (e.g., rheumatoid arthritis), inflammation, allergies,

couplifive disorders, schizophrenia, asthma, skin disorders (e.g., instance),

cooplifive disorders, schizophrenia, asthma, skin disorders (e.g., instance),

cooplifive disorders, schizophrenia, asthma, skin disorders (e.g., instance),

cooplifive disorders, schizophrenia, asthma, skin disorders,

psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,

cooplifive disorders, kidabetes, additional disorders,

propiancy-related disorders, endocrine disorders, and infections. The

proteins can also be used to aid wound healing and epithelial cell

proteins can also be used to aid wound healing and epithelial cell

corporate transplantation, for supporting cell culture of primary tissues,

conference transplantation, for supporting cell culture of primary tissues,

conference transplantation, for supporting cell culture of prinding

conference transplantation, for supporting cell culture of prinding

conference transplantation, for supporting cell culture of prinding

conference the invention can be used as a food additive or

protein of the invention can be used in alleviating symptoms associated

with the disorders mentioned above, and in diagnostic immunoassay e.g.,

the present sequence represents a human secreted protein-encoding cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD05220-AAD05282 represent CDNAs corresponding to 21 human secreted AAE01352-AAE01413 represent the proteins they encode. AAE01413 represent human secreted protein fragments or variants. The secreted protein fragments or variants. The secreted protein fragments or variants. Or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative hamours, toetal and developmental abnormalities, hamours of the immune system, AIDS, autoimmune.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.1%; Score 925.2; DB 22; Length 1019; 98.3%; Pred. No. 8.7e-136; Live 3; Mismatches 12; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ruben SM, Komatsoulis GA, Wei P, Fiscella M, Baker KP;
                                                                                                                                                                                                                                         /*tag= c
/product= "Mature human secreted protein"
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/note= "Does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 414-415; 490pp; English.
                                                 /partial
complement (528..526)
                                                                                                                                                                                                 complement (525..142)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1999; 99US-0164835.
27-JUL-2000; 2000US-0221142.
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Best Local Similarity 98.3
Matches 941; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-308779/32.
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                                                                                              sig_peptide
                                                                                                                                                                                            mat_peptide
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2394 ATGGGAGTTTCTAGGATGAAAC-ACTCCTCCATGGGATTTGAACATATGACTTATTTGTA 2452

1; Gaps

989 AIGGGAGITICIAGGAIGAAGCGACTCNICCAIGGGAITIGAACAIATAAAGITATITGI

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2453 GGGGAAGAGTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTC 2512

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                                                                                                                                                                                                                                                                                                  2993 CCCCTACCCCCAACTITCCCCTACCCCCAACTITCCCCACCAGCTCCACAACCCTGTTTG 3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3233 TATTTATTTAGCGGGGGGAAATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTA 3292
                                                                                                                         069
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929 AGGGAAGATCCTGAGGGGCAACACACAAAAAGACCAGGTCCCCTSAGCCCACAGACTGTC 870
                                                                      630
                                                                                                                                                                                                                                                                        149 TATTTATTTAGCGGGGGGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2513 ITTTTGCTGATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGT
                               2633 GAATCCATTGCTAGCTTTTCTGTGTTGGTGTTAATATTTGGGTAGGGTGGGGGATCCCC
                                                                                                           2693 AACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCT
                                                                                                                                                   2873 CITCAGGICTCAACGGCIICCCIAACCACCCCICIICCIIGGCCCAGCCIGGIICCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
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Chimeric - Microbacterium tuberculosis.
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GTCGGCCCCCTTCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAA 1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1122 CCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCCTCATGACCTTCACGCTGTTTA 1181
                                                                                                                                                                                                                                                                                                        1001
                                                                                     821
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                  761
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1039 CCTGGGCGCCCTGCTTCCCCGGCTGCACCTGCTGCTGCCGCATGCCCCGCACCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1062 CCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCGATGCCCCGCACCCTGCG
                                                                                                                         799 CTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCT
                                                                                                                                                                                                 859 GGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGC
                                                                                                                                                                                                                                                                    919 AGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCT
                                                    GGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L, Jiang Y, Reed SG;
Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
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Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ral2-P501S-E2 construct cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGGATTTCGTGGCGAGGG 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1182 CACGGATTTCGTGGGCGAGTG 1202
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Kalos MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH93917 standard; cDNA; 1203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2000; 2000US-0483672.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-425873/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides or antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding rells specific for a tumour protein, and for inhibiting the development polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 GGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGGTAGAGGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 CATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGTGCCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCT
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                                                                                                                                                                                                                                                                                                                                                            Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%; Score 794.6; DB 22; Length 1203; 99.5%; Pred. No. 2.2e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                      Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 17; Page 542-543; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the invention.
                                                                                                                                                                         20000S-0593793.
20000S-0605783.
20000S-0636215.
20000S-0651236.
20000S-0657279.
20000S-0657279.
                                                                                     2001WO-US09919
                                                                                                                                         2000US-0568100
2000US-0570737
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Matches 797; Conservative
                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639232/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAU69907
                WO200173032-A2
                                                                                                                                                                                                                                                                 02-OCT-2000;
10-OCT-2000;
                                                                                     27-MAR-2001;
                                                                                                                                                                                                                             29-AUG-2000;
06-SEP-2000;
                                                                                                                                                                           13-JUN-2000;
27-JUN-2000;
                                                                                                                                                                                                              10-AUG-2000;
                                                                                                                       27-MAR-2000;
                                                                                                                                         09-MAY-2000;
12-MAY-2000;
                                                  04-OCT-2001
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II), the specific proteins comprising (II), and isolated are also proteins comprising (II), and isolated a realist prepared using (II) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is alagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGGTAGAGGAGGAGTT 438
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                                                                                                                                                                                                                                                                                                                                                                            tch 23.3%; Score 794.6; DB 22
al Similarity 99.5%; Pred. No. 2.2e-115;
797; Conservative 0; Mismatches 4;
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cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
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Carter D;
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
                                                                                                        Ra12-P501S-E2 construct cDNA sequence SEQ ID NO 851
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GR, Retter MW, Stolk JA, Day CH
Wang A, Skeiky YAW, Hepler WT,
                                                                                                                                                Chimeric - Mycobacterium tuberculosis.
Chimeric - Homo sapiens.
1159 CACGGATTTCGTGGGCGAGGG 1179
         1182 CACGGATTTCGTGGGCGAGTG 1202
                                                        ABL95524 standard; cDNA; 1203
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2000us-0570737
2000us-0593793
2000us-0605783
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990S-0232149.
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990S-0352616.
990S-0439313.
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2000US-0685166
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                                                                                          (first entry)
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HARLOCKER S L.
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FANGER G R.
RETTER M W.
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DILLON D C.
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DAY C H.
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WANG A.
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12-MAY-2000;
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06-SEP-2000;
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Li SX,
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                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA
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                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                           New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                               / Match 23.3%; Score 794.6; DB 24; Length 1203; Local Similarity 99.5%; Pred. No. 2.2e-115; nes 797; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                 Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
                                                                     Example 17; SEQ ID NO 851; 87pp; English.
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                                        progression of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                               Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer
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Pred. No. 1.8e-96;
0; Mismatches 40; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
                                                                                                                    Prostate; cancer; tumour; vaccine; immunogen; clone;
                                                                                             tumour clone
                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 38-39; 130pp; English
                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.7%;
94.2%;
                                                                                             cDNA sequence of prostate
                                                                                                                                                                                                                                      98US-0020956.
97US-0806099.
97US-0904804.
                                                                                                                                                                                                                   98WO-US03492.
                                                                     (first entry)
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                                                                                                                                            Homo sapiens
                                                                                                                                                                  WO9837093-A2
                                                                                                                                                                                                                   25-FEB-1998;
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CCATCCTGGATAGTG-CTTCCTGCTGTCCCANGTGGCCCCATCCCTGTTTATGGGCTCCA
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bind an immunogenic portion of a prostate protein (such as by this sequence). An antibody which binds to an immunogenic of the prostate protein, and the method can be used to detect, progression of, or treat prostate cancers. The antibody may conjugated to a therapeutic agent for use in therapy of prostate
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                                                                                    Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
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AAA06250 standard; cDNA; 789 BP

RESULT 44 AAA06250 ID AAA0

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1821 TTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGG 1880
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              241 CAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC
                                                                                                                           Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
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2000US-0657279.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and the polypeptides and the polypeptides and the polypeptides and the polypeptides and vaccines the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06591 and AAV82000 to AAX82020 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                          SEQ ID NO:10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes isolated polypeptides, comprising an
                                                                                                    Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 19.7%; Score 673.4; DB 21; Length 789; Local Similarity 94.2%; Pred. No. 1.8e-96; les 745; Conservative 0; Mismatches 40; Indels 6;
                                                                           Human immunogenic prostate tumour protein cDNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                  Хu J,
                                                                                                                    immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                  Dillon DC, Harlocker SL, Yuqiu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 99; 263pp; English.
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980S-0159812.
980S-0159822.
990S-0232149.
990S-0232880.
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                                                                                                                                                                                                                               99WO-US15838
                                               13-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention.
                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
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                                                                                                                                                                         WO200004149-A2
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polynucleotides, polypeptides, fusion proteins of the polypeptides, darkbodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for transing cancer. The oligonucleotide is useful for polyperide are useful for stimulating on immune detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                   New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer
                               Kalos MD;
Carter D;
                    Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                               invention relates to isolated prostate-specific
                                                                                                                                                                                                                                           Claim 1; Page 232-233; 579pp; English.
                                                                                                                       WPI; 2001-639232/73
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Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

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1341 CAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCC 1400 1401 ACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGC 1460 AATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGC 1580 CAGGCCCTAAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC 1640 TGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCG 1760 1641 TGCTCCCACCTCCACCGGGGGTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGG 1700 301 TGCTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGG 360 1 CAGTCTAINTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCAGTGCCTGTCCC 60 Gaps Query Match 19.7%; Score 673.4; DB 22; Length 789; Best Local Similarity 94.2%; Pred. No. 1.8e-96; Matches 745; Conservative 0; Mismatches 40; Indels 6; 1521 1581 181 1701

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1821 ITGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGG 1880

1881 TCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAG 1940

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1941 CGTAGAAAACTTCCAGCA--CATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCC 1998

1999 CGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGT 2058 2059 AATGTGGCTCTCTGCGCACCCTGTGCT-GCTGAGGTGCGTAGCTGCACAGCTGGGGGGC 2117 2118 TGGGGCGTCCC 2128 778 TNGGGNGTTCC 788 δλ q qq δ ŏ

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ALIGNMENTS

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linear				•		Vertebrata;	; Hominidae		r, M.A.	diagnosis	
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3410 bp	Patent WO012	922014				a; Chordata;	a; Primates;	10)	., Reed, S.G.	nethods for t	
329	Seguence 110 from Patent WO0125272. AX106329	AX106329.1 GI:13922014			Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 3410)	Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.	Compositions and methods for therapy and diagnosis of prostate	
AX106329	Seguence AX106329	AX106		human.		Eukar	Mamma	1 (b	Xu,J.	Compo	rancer
RESULT 1 AX106329 LOCUS	DEFINITION ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	

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atent: WO 0125272-A 110 12-APR-2001; ORIXA CORPORATION (US) Location/Qualifiers 1. 3410 /organism="Homo sapiens" /db_xref="taxon:9606" 667 a 1014 c 945 g 783 t 1 others	Similarity 100.0%; Score 3409.6; DB 6; Length 3410; Similarity 100.0%; Pred. No. 0; O; Conservative 0; Mismatches 0; Indels 0; Gaps	GGGAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCG	GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGCGTGAGCATGGGCTGAG 	AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT 	GGCGGCAGCAAGGAGGAGAGGCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTG	GAGTGCCTGAACGGCCCCTGAGCCTACCGGCTGGCCCACTATGGTCCAGAGGCTGTG	GGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTT -	TGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT	GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 	CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCATGGCGTGGACGCTATGGCGCGCCGCGCGCG	GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGCCITTIIIIIIIIII	CGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCAT	CCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT	GCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTT	CATGATCAGTCTTGGGGGCTGCCTGGCTACCTCCTGCCTG	TGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT
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Db 3061 GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGO 3121 ATATCTGTGCTTGGGGAATCTCACACAGAAACTC Db 3121 ATATCTGTGCTTGGGGAATCTCACACAGAAACTC Oy 3181 GAGTCTTATCTCTCAGGGGGGTTTAAGTGCCG	RESULT 2 AX140620 AX140620 DETINITION Sequence 110 from Patent W00134802. ACCESSION AX140620.1 GI:14280737 KEYWORDS SOURCE HOME Sapiens BUKARYOTCH MHETAZOB; CHOTGATA; CTANIA MAMMALIA: ENTHACACA; CALARYOTCH MACTAZOB; CALARY REFERENCE 1 (bases 1 to 3410) AUTHORS XU, J. Dillon, D.C., Mitcham, J.L., Ha REGGS, G., Kalos, M.D., Retter, M.W., Skeiky, Y.A. and Wang, A. TITLE CAMPOSITIONS and methods for the the COMPOSITIONS OF CORPORATION (US) FRATURES JOURNAL PATENT: WO 0134802-A 110 17-MAY-2001 CORIXA CORPORATION (US) FRATURES LOCATION/QUALIFIERS JORGANISM HOME SAPIENS LOCATION/QUALIFIERS AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AND AMD AMD AND AMD AMD AMD AMD AMD AMD AMD AMD AMD AM	Query Match 100.0%; Score 3409.6; Best Local Similarity 100.0%; Pred. No. 0; Matches 3410; Conservative 0; Mismatches Qy 1 GGGAACCAGCCTGCACGCTCGGTGCTCGGGTGAC Qy 61 GTGATCAGCCTGCACGCTGGTGCTCGGGTGAC Qy 61 GTGATCAGACGTGCTCCCACTGAGGTGCCCACACACACAC
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QY	1621	GGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTG 1680
Qy Dp	1681	TGATGTCTCCGTACGTGGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCG 1740
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Qy	1861	TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 1920
Qy	1921	CGACTIGGCCAAAIACTCAGCGIAGAAAACTICCAGCACATIGGGGIGGAGGCCIGCCT 1980
Qy	1981	CACTGGGTCCCAGCTCCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGCTGGCCGCCAGT 2040
Qy	2041	TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCCCTGTGCTGCTGAGGTGCGTA 2100
Qy	2101	3GGTCCCTCTCCTCTCCCCAGTCTCTAGGGCTGCCTG 2
Qy Db	2161	ICTGGACTTATACAGGGAGGCCAGAAGGGCTCC 222
Qy Db	2221	80 80
Qy	2281	SAGCTGAATAAACTCAGTCACCTG 234
Qy	2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 2400
Qy Db	2401	TTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2460
οχ	2461	GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTTGCT 2520

1 (bases 1 to 3410)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meegher,M.J.
Compositions and methods for the therapy and diagnosis of prostate

Patent: WO 0151633-A 110 19-JUL-2001; CORIXA CORPORATION (US)

cancer

Location/Qualifiers

.3410

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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2461 GTCCTGAGGGCAACACACAAGAACCAGGTCCCCTCAGCCCCACAGACTGTCTTTTGCT 2520
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                                                     CAGAGACACAGGCATTTAAATATTTAACTTATTTTAACAAAGTAGAAGGGAATCCAT 2640
                                                                                      TGCIAGCITITCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA 2700
                                                                                              CTCAACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCA 2940
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                                                             2761 CIGGCCCCCCAAAATGCCTAACCCAGGACCTIGGAAATTCTACTCATCCCAAATGATAAT
                                                                                                                                                                                                   CTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC
                                                                                                                                                                                                                                                                       GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTGGGGGT
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                       PAT 29-AUG-2001
                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DNA

Sequence 110 from Patent W00151633. AX200480

GI:15390293

AX200480.1 human.

AX200480 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 3

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ORGANISM

ö 120 180 180 240 240 300 300 360 360 420 420 480 480 540 540 900 900 99 9 720 720 780 780 9 9 181 GCCGCCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGGCCGAGACGAAGCAGTTCTG 1 GGGAACCAGCCTGCACGCGTGGCTCCGGGTGACAGCCGCGCGCCTCGGCCAGGATCTGA GTGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAG AAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTT GAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTG GGTGAGCCGCCTGCTGCGCCACCGGAAAGCCCCAGCTCTTGCTGGTCAACCTTGCTAACCTT TGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGT CTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCG CGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCCAGGCCCCTGGAGCTGGCACTGCTCAT CCTGGGCGTGGGGCTGCTGTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCT GGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGT 541 GCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGC 0; Gaps DB 6; Length 3410; 0; Indels 1 others ų 100.0%; Score 3409.6; 100.0%; Pred. No. 0; 0; Mismatches 783 /organism="Homo sapiens" /db_xref="taxon:9606" a 1014 c 945 g 78: Best Local Similarity 100.0%; Matches 3410; Conservative (Ø 667 241 61 61 361 Query Match 301 361 421 301 481 601 421 qq

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	841 TGCCCTGCCCCTACCTGGCCACCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCAT 900	901 CTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGCTGAGGAGGCACGCCTGGGCCCCAC 960	961 CGAGCCAGCAGCAGGAAGGCTGTCGGCCCCTTGTCGCCCCACTGCTGTCCATGCCGGGC 1020	1021 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCC 1080	1081 CATGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGTGCAGCTGGAGCTGGATGGCACTCAT 1140	1141 GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGCTGTACCAGGCGTGCCCAG 1200 	1201 AGCTGAGCCGGCACCGAGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCT 1260 	1261 GGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGT 1320	1321 GCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGTTTCCTGTGGCTGC 1380	1381 CGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGGCAGCTTCAGCCGCCTCACCGG 1440	1441 GTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACTGGCCTCCCTC	1501 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAG 1560	1561 CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGT 1620	1621 GGGTGCTGGAGGCAGTGGCCTGCTCCACCCGCGCTCTGGGGGCCTCTGCCTG 1680	1681 TGATGTCTCCGTACGTGGTGGTGGTGGGCCACCCAGGCCAGGTGGTTCCGGCCG 1740	1741 GGGCATCTGCCTGGACTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 1800	1801 ATCCTGTTTATGGGTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTC 1860 1801 ATCCTGTTTATGGGCTCCATTGTCCAGCTCAGCAGTCTGTCACTGCCATAGAGGTC 1860	1861 TGCCGCAGGCCTGGGTCGCCATTTACTTTGCTACAGGTAGTATTTGACAAGGG 1920
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2940 2880 2940 2340 2640 2640 2820 2820 2941 CICCCCTCTACTCTTAGGACTGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC 3000 2040 2040 2100 2160 2160 2280 2340 2400 2400 2460 2460 2520 2520 2700 2700 2760 2760 2941 CTCCCCTCTACTCTCTTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACG 3000 1861 TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 1920 2100 2221 ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC 2280 GATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA 2580 2761 CTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT 2821 FCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGTGGGGGCTTCAGGT CTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTG 2341 GITTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG 2401 TITCTAGGATGAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA 2581 CAGAGACACAGGCATTTAAATATTTAACTTATTTATTTAACAAAGTAGAAGGAAATCCAT 2641 TGCTAGCTTTTCTGTGTTTGTGTCTAATATTTGGGTAGGGTGGGGGGATCCCCAACAATCA 2701 GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTCCTGGGGT 2701 GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGT 2761 CTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAAT 2881 CTCAACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCCACTTCCA 2881 CTCAACGGCTTCCCTAACCACCCCTCTTCTTTGGCCCAGCCTGGTTCCCCCCACTTCCA 2341 GITICCCATCICIAAGCCCCTIAACCIGCAGCTICGITIAATGIAGCICTIGCAIGGGAG GTCCTGAGGGCCAACACACACAAAACCAGGTCCCCTCAGCCCACAGCACTGTTTTTGCT TTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTA 2101 GCTGCACAGCTGGGGGCTGGGGCGTCCTCTCTCTCTCCCCCAGTCTCTAGGGCTGCCTG ATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGC CACTGGGTCCCAGCTCCCGGTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGT 2821 2461 2041 2221 2281 2521 1981

181 GGCGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACCAAGCCAAGCCAAGCCATCTG 2	1 1 1 1 1 1 1 1 1 1	9 9 9 9 9		94 TGCCTGGCCCCTACCTGGGCACCCAGGAGGTGCCTCTTTGGCCTGCTCACCCTCAT 900	021 CCGCTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC
3001 CCCAACTITCCCCTACCCCCAACTITCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT 3060	3121 ATATCTGTGGGAATCTCACACAGAACTCAGGACCACCCCTGTTAILLING 3181 GAGGTCTTATCTCAGGGGGGTTTAAGTGCCGTTGCATAATTTATT 3240 1181 GAGGTCTTATCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT	AAATTAAAGGCTTCTTATATATATAAAAAAAAAAAAAAA	AX267136 Sequence 110 from Patent W00173032. AX267136. AX267136. AX267136. AX267136. I GI:16515920 human. Memon sapiens Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Butheria: Primates; Catarrhini; Hominidae; Homo. Xu,J.; Dillon,D.C.; Mitcham,J.L.; Harlocker,S.L.; Jaingy,Y.; Kalos,M.D.; Fander,G.R.; Retter M. W. Stolk, T. M. Diang,Y.;	epler,W.T. prostate	tch 100.0%; Score 3409.6; DB 6; Length 3410; al Similarity 100.0%; Pred. No. 0; 3410; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 1 GGGAACCAGCCTGCAGGCTGGGTGACAGCCGCGCGCCTGGCCAGGATCTGA 60

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qc	2341	GTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAG	2400
YG 4	2401	TITCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGA ;	2460
n A	9	1C1FGGGGCGAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTTTTTGCT	2.5
- q0	4		2520
λζ	25	GATCCACCCCCTCTTACCTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA :	in i
qo	2521	ATCCACCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCCTTCTGTTGCCATCA	28
Ka i	58	CAGAGACACAGGCATTTAAATTTAACTTATTAATTTAACAAAGTAGAAGGGAATCCAT	2640
qq	χ,	AGAGACACATTTAAATATTTAACTTTATTTATTTAACAAAGGGGGTTTATTAACAAAGGGGGGTTAATTTAACAAAGGGGGGTTAATTTAACAAAGGGGGGTTAATTTAACAAAGGGGGGGG	, ,
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٥y	2701	GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGG	9 /
qa	2701	rcccridadaracridatroggcrgarcarroccagaarcrrcrrccrgg	2760
٥y	7	CIGGCCCCCCAAATGCCTAACCCAGGACCTIGGAAATICTACTCATCCCAAATGATAAT	82
qq	2761	3GCCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGAT	2820
όy	2821	TCCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGG	88
qa	2821	CCAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGTGGGGGCTTCAG	88
٥y	88	CTCAACGCTTCCCTAACCCCTTTTTTTTGCCCAGCCTGGTTCCCCCCACTTCCA	94
Db	2881	AACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCÇCCCACTTCC	4
٥y	4	CTCCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACC	8
qq	2941	CCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTT	300
Οy	3001	CCCAACTTTCCCCTACCCCCAACTTTCCCCACAGCTCCACAACCCTGTTTGGAGCTACT	306
Dp	3001	CCCTACCCCAACTTTCCCCACCAGCTCCACAACCCTGTTTC	306
οy	3061	GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCCAGAGT	12
Db	3061	GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCC	312
QY	3121	ATATCTGTGCTTGGGGAATCTCACACAGAACTCAGGAGCACCCCCTGCCTG	318
QD	3121	ATATCTGTGCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCTGCCTG	3180
٥y	3181	GAGGTCTTATCTCTCAGGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTTATTATT	3240
.qa	3181	GAGGICTTATCTCTCAGGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTAT	3240
٥y	3241	TAGCGGGGTGAATATTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACA	30
Db	3241	TAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGAC	ō
Qy	3301	AAATTAAAGGCTTTCTTATATGTTTAAAAAAAAAAAAAA	36
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721 GCTCTCTGACCTCTTCCGGGACCCGGACCAGGCCTACTCTGTCTATGCCTT 780		1021 CCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCTGTGCTGCCG 1080	1141 GACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAG 1200	1261 GGGGCTGTTCCTGCAGTGCCCATCTCCCTGGTCATGGACCGGCTGGT 1320	1381 CGGTGCCACATGCCTGTCCCACAGTGTGGTGGTGACAGCTTCAGCCGCCTCACCGG	1501 GAAGCAGGTGTTCCTGCCCAAATACCGAGGGAACTGGAGGTGGTAGCAGGACAG 1560	1621 GGGTGCTGGAGGCAGTGCTCCCACCTCCACCGGGGCCTCTGCGGGGCCTCTGCCTG 1680	GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCCCCC
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DEFINITION Sequence 100 from Patent W00198339. AX429961 AX429961 AX429961 AX429961 AX429961 AX429961 AX429961 AX429961 AX42961 AX429961 A	Cancer WO 0198339-A 100.27-DEC-2001; CORIXA CORPORATION (US) FEATURES Location/Qualifiers 1. 3410 /organism="Homo sapiens" Abse COUNT 667 a 1014 c 945 g 783 t 1 others	/ Match Local Similarity 100.0%; Score 3409.6; DB 6; Length 3410; Local Similarity 100.0%; Pred. No. 0; les 3410; Conservative 0; Mismatches 0; Indels 0; Gaps 1 GGGAACCAGCCTGCACGCTCGGCTCCGCTCACCAGCACCAGCACCAGGATCTGA	GYGATGAGGCGCCCAGGGCTCCGGGGTGACAGCGGGGGGCGTCGGCCAGGGATCTGA bu GYGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGGTTGAGCATGGGCTGAG 12 [CAGTT	GGTGAGCCGCCTGCTGCGCAAAGCCCCTGGCCCACTATGGTCCAGAGG GGTGAGCCGCCTGCTGCGCACCGGAAAGCCCCACTTGCTGGTCAACCTGCTA IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GGGGGTAGAGGAGATTCATGACCATGGTGCTGCTGTGCCCCCTTGCTGCTGGGAGGT		:닭 었=었

Qy 2941 CTCCCC Qy 2941 CTCCCC Qy 3001 CCCAAC Qy 3121 ATATCT Qy 3131 AAAAAA Qy 3131 AAAAAAA Qy 3301 AAAAAAA Qy 331 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1801 ATTOCKTOSTITATIGGGCTCCANTTGTCCAGCTCAGCTCACTCACTCACTCACTCARATGGTCCT 1800 1801 ATTOCKTOSTITATIGGGCTCCANTTGTCCACCTCAGCTCACCTCACTCACTCACTCACTCACT
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission

Submitted (127-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama I-chome, Shinjuku-ku, Tokyo 162-8640, Japan CE-mail: khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-Illi(ex.2120), Fax:81-3-5285-Il81)
         PRI 13-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R. Sitel: DraIII (CACATGTG)

R. Site2: DraIII (CACATGTG)

Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to product was digested with Sfil and size selection was performed to arclude fragments <1.5kb.The Sfil and size selection was performed to into distinct DraIII sites of PME185-FL3. AhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="WVORLWVSRLERHRKAQLLINLLFGLEVCLAAGITYVPPLLL
EVGVEEKFWIMVLGIGPVLGLVSVPLINGSASDHWRGRYGRRFPFWAGIGILLSLEU
IPRAGWLAGLLCPPREFLEILLIGVGLLDFCGQVCFTPLEALLSDLFRDPHCRQA
XSVYAFWISLGGCLGYLLPAIDWDTSALAPYLGTQEECLFGLLTLIFLTCVAATLLVA
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AELCSWMALWTFTLFYTDFVGEGLYQGVPRAELGTEARRHYDEGVRMGSLGLFLQCAI
SLVFSLVMDRLVQREGTRAVYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTFSAL
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SGLLPPPPALCGASACDVSVRVVVGEPTEARVVPGRGICLDLAILDSAFLLSQVAPSL
FMGSIVQLSQSVTAYMVSAAGLGLVAIYFATQVVFDKSDLAKYSV"
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                 to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Sugano et al., , Institute of Medical Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                   Osada.N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K. Isolation of full-length cDNA clones from macaque brain cDNA
                                clone:QtrA-11310, full insert
                                                                                                                                                   oligo capping; fis (full insert sequence).
Macaca fascicularis adult male temporal lobe right cDNA to
clone_lib:macaque brain cDNA library QtrA clone:QtrA-11310.
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/clone_lib="macaque brain cDNA library QtrA"
/dev_stage="adult"
454. .2115
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/db_xref="taxon:9541"
/clone="QtrA-11310"
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/protein_id="BAB46871.1"
/db_xref="GI:13874497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Custom primer used for sequencing (5' end primer [CTTCTGCTCTAAAAGCTGCG]; 3' end primer [CGACCTGCAGCTGGAGCACA]).
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                                Macaca fascicularis brain cDNA
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AUTHORS
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85.0%; Score 2900.2; DB 9; Length 3514; imilarity 94.8%; Pred. No. 0; ;; Conservative 0; Mismatches 118; Indels 54; Gaps	CAGGATCTGAGTGATGAGGGGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGC	ATGGGCTGAGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTC 	CTAGGCAGTTGGCGGCAGCAAGGGGGGGGGCGCCAGCTTCTGGAGCAGGCCGAGACGA 	AGCAGITCIGGAGIGCCIGAACGGCCCCCIGAGCCCIACCGCCIGGCCCACIAIGGICC	AGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACC	TGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGC	TGCTGGAAGTGGGGGTAGAGGAGAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGC	TGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATG	GCCGCCGCCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCA 	TCCCAAGGCCGGCTGGCTAGCAGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGG	CACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCAC	IGGAGGCCTGCTCTCTGACCTCTTCCGGACCCGGACCACTGTCGCCAGGCCTACTCTCTCT	TCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	GGGACACCAGTGCCCTGGCCCCTACCTGGGCACCAGGAGGAGTGCCTCTTTGGCCTGC	TCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGC	TGGGCCCCACCGAGCCAGCAGAGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGTC	CATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGC
/ Match Local S es 3155	51	111	171 341	231	291	351	411	471	531	591	651 821	711	771	831 1001	891 1061	951 1121	1011
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λi		TGTGCTGCCGCATGCCCGCCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGA 1	13
Q Q	4 (GTGCTGCCGCATGCCCGCACCCTGCGCCCGTCTTCGTGGCTGAGCTGTGGA	5 6
∆. q	1131	TGGCALTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCCAAGGGCTGTACCAGG 	1360
, Y		CGTGCCCAGAGCTGAGCCGGGCCAGCAGGCCCGGAGACACTATGATGAAGCGTTCGG	Š
ą		GCGTGCCCCAGAGCTGGGCTGGGCACCGGAGACACTATGATGAAGGCGTTCGGA 1	Ō
λ	1251	TGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGG 1	
q	1421	GGGCAGTCTGGGGGTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGG	1480
λλ	31	ACCGGTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTTCC 1	m 1
ð	œ	CCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATCTGGCCAGTGTGGCAGCTTTCC	4
λλ	37	CTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCG 1	1430
ą		TGTGGCTGCCGGTGCCACGTGCCTGTCCCACAGTGTGGCTGTGGTGACGGCTTCAGCO	0
<u>۲</u>	43	3GGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCTCT	4 (
Q Q	09	CHCACHGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTTGGCCTCCTCT	9
γ	1491	ACCACGGGAGAGAGGGGTGTTCCTGCCCAAATACCGGGGGACACTGGAGGTGCTAGCA 	1550 1720
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2 g	1721	GEGAGGACAGCCTGATGACTACCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTA	1780
λλ	1611	TGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGCTCTGGGG	1670
q	1781	ATGGACACGTGGGTGCTGGACGCAGTGGCCTGCTTCCACCCCCCGCGTCTGGGGG	1840
λλ	1671	CCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGGTGGGTG	1730
qc	1841	CTCTGCCTGCGATGTCTCTGTACGTGGTGGGTGGGTGAGCCCACCGAGGCCAGGGTGG	1900
λλ	1731	TTCCGGGCCGGGGCATCTGCCTGGACCTCGCATACTGGATAGTGCCTTCCTGCTGTGCC 3	1790
qc	1901	TCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCC	1960
λλ	1791	AGGIGGCCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCT	1850
qo	1961	3TGGCCCCGTCCTTCTTCATGGCTCCATCGTCCAGCTCAGCCAGTCTGTCACTGCCT	2020
λζ	1851	ATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTAT	1910
qo	2021	ATGGTGTCTGCTGCAGGCCTGGGTCTGGTTGCTTTACTTTGCTACACAGGTAGTAT	2080
λζ	1911	TIGACAAGAGCGACTIGGCCAAAIACICAGCGTAGAAAACTICCAGCACAITGGGGTGGA	1970
qo	2081	TGACAAGAGCGACTTGGCCAAATACTCGGTGTAGAAACTTCCAGCACATTGGGGTGGA	2140
λχ	1971	GGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTC-CTGTTAGCCCCATGGGGCTGCCGGGC	02
qa	2141	GGCCTGCCTCACTGGGTCCCAGCTCCCCACTTTGTTAGCCCCCATGGGGCTGCTGGG	2200
οy	2030	TGGCCGCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCTGCCACCCTGTGCTGC	2089
QQ	2201	GGCCGCCAGTITCIGITGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTG	2260
δÿ	2090	TGAGGTGCGTAGCTGCACACGGGGCTGGGGCGTCCCTCTCCTCTCTCCCCAGTCTCT	2149
qq	2261	GAGGIGCGIAGCICCACAGGIGGGGGTGGGGCAICCCICTCCCICCICCCAGICI	2320
δÿ	2150	AGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGAGGCC	2209

Db 3373 TGCCGTTTGC	Qy 3270 GAGCAATCAG; Db 3430 GAGCAATC;	Qy 3330 AAAAAAAAA Db 3488 AAAAAAAAA		DEFINITION Sequence 625 ACCESSION AX200995 VERSION AX200995.1 (KEYWORDS		REFERENCE 1 (bases 1 t AUTHORS Xu,J., Dillor Reed,S.G., Ke Stolk,J.A., &	TITLE Compositions cancer JOURNAL Patent: WO 01 CORIXA CORPOR	(1)	COUNT 721 & N FY Match	Best Local Similarity Matches 3325; Conserve Ov 4 AACCAGCCTGG		Oy 64 ATGAGACGTGT	Db 61 ATGAGACGTGT Qy 124 CTGGACCGGCP	121	Db 181 GGCAGCAGG	Qy 244 TGCCTGAACGC	Db 241 TGCCTGAACGG	301	Qy 364 CCTGGAGGTGT	361	UY 424 GGTAGAGGAGA
111111111111111 1111111111111111111111	2210 AGAAGGGCTCCATGCACTGGAATGCGGGACTCTGCAGGTGGAT 2253 	AACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTT 231		2373 TTCGTTTAATGTAGCTCTTGCATGGGAGTTCTAGGATGAAACACTCCTCCATGGGATTT 2432 	2433 GAACATATGACTTATTTGTAGGGAAGAGTCCTGAGGGGCAACACACAAGAACCAGGT 2490 	2491 CCCCTCAGCCCACAGCACTGTCTTTTTGCTGATCCACCCCCCTCTTACCTTTTATCAGGA 2550	2551 TGTGGCCTGTTGGTCCTTCTGTTGCATCACAGGACACAGGCATTTAAATATTTAACTT 2610 111111	2611 ATTATTTAACAAAGTAGAAAGGGAATCCATTGCTAGCTTTTCTGTGTGTG	2671 TTGGTAGGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGCTG 2730 	2731 ATCATTGCCAGAATCTTCTCTGGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACC 2790	2791 TTGGAAATTCTACTCAAATGATAATTCCAAATGCTGTTACCCAAGGTTAGGGTGT 2850	2972 TIGGAANTITIACTCATCCGACTGATAATTCCAAATGCTGTTACCCAAGGTTAGGGGGT 3031	2851 TGAAGGAAGGTAGAGGGTGGGGCTTCAAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCT 2910 11111111111111111111111111111111111	2911 CITGGCCCAGCTTCCCCCACTTCCACTCCCCTCTACTCTCTAGGACTGGCCTG 2970	ATGAAGGCACTGCCCAAAATTTGCCCTACCCCCAACTTTCCCC	3152 ATGAAGGCACTGCCTGAAATTTCCCTCACCCCCCAACTTTCCCC 3194	3031 ACCAGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGGACAAAGTGCGGTTTCC 3090 11		3255 CAGGCCTTTGTCCATCTCAGCCCCCCAGAGTATCTGTGTGTG	3150 AACTCAGGAGCACCCCTGCCTGAGCTAAGGAGGTCTTATCTCTCAGGGGGGTTTAAG 3209 3315 BACTCAGGAGCAACCCTGCTGAACTAAAAAAAAAAAAAAA	210 TGCCGTTTGCAATAATGTCGTCTTATTTAGCGGGGGTGAATATTTATATACTGTAAGT 326
qq	oy Ob	Qy	oy Op	Qy Db	Qy Dp	oy op	6y 6y	oy Op	oy Op	oy Oy	δλ	qq	Qy	oy op	δ	QQ	oy B	ογ	QQ	کې و	70

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CAATAAT --- GTCTTATTTATTTAGCGGGCAAATATTTTATACTGTAAGT 3429
                                   GAGTATAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTTTAAAA 3329
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Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Skelky,Y.A., Wang,A. and Meagher,M.J.
is and methods for the therapy and diagnosis of prostate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3AGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STCCCCACTGAGGTGCCCCACAGCAGCTGTTGAGCATGGGCTGAGAAG 123
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utheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                               DNA
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82.4%; Pred. No. 0;
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedyick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A. Compositions and methods for the therapy and diagnosis of prostate
                                                      PAT 26-OCT-2001
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                                          GAATCTCACACACAAACTCAGGAGCACCCCTGCCTGAGCTAAGGGAGGTCTTATCTCTC 3195
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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2461 TCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCT 2520	1818 CCATTGTCCAGCTCAGCCAGTCTGTCACTATGGTGTCTGCCGCAGGCCTGGGTC 1877	1878 TGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACT 1937 	1938 CAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCTGCCT	1998 CCGCTCCTGTTAGCCCCATGGGGCTGCCGGCCGCCAGTTTCTGTTGCTGCCAAAG 2057	TAATGTGG TAATGTGG	2118 IGGGGGTCCCTCTCTCTCCCCAGTCTCTAGGGCTGCCTGACGAGGCTTCCAAG 2177	2178 GGGGTTTCAGTCTGGACTTATACAGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGG 2237 	223B GACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTGAGACACA 2297	2298 CCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGC 2357 	2358 CCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAAACAC 2417 	2418 TCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGGAAGAGTCCTGAGGGGCAAC 2475	2476 ACACAAGAACCAGGTCCCCTCAGCCCAGCACTGTCTTTTGCTGATCCACCCCCTCT 2535 11111111111111111111111111111111111	2536 TACCTTTATCAGGATGTGGCCTGTTGGTCCTTGTGCCATCACAGAGACACAGGCAT 2595 11111111111111111111111111111111111	2596 TTAAATATTTAACTTATTTAACAAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGT 2655 	2656 GTTGGTGTCTAATATTTGGGTAGGGTGGGGATCCCCAACAATCAGGTCCCCTGAGATAG 2715 11111111111111111111111111111111111	2716 CTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGCCCCCCAAAAT 2775 11111111111111111111111111111111111	2776 GCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTAC 2835 	2836 CCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCT 2895
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Macaca fascicularis brain cDNA clone:QmoA-10594, full insert
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Macaca fascicularis
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                            2956 TCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTA
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Osada.N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M.,
Terao,R., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
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LLSLFLIFRAGWLAGILCPDPRPLELALLILGVGLLDFCGGVCFTPLEALLSDLFRDP
DHCRQATSVYTFWISLGGCLGYLLFALAPVLGTGPGECLFGTLTLLFETCVA
ATLLVABEAALGPBARGLSAPSLPSHCCFWARLAFRINGALLFRLHQTCYA
ATLLVABELCSWMALMTFTLFYTDFVGEGLYGCVPRAELGTEARRHYDEGVRWGSLGI
FLQCAISLYFSLVVDRLVQYRGFGTARVTASVAAFPVAAGGTCLSHSYNVTASAALTG
FTFSALOILPYTLASTYHREROYFLRYKYGDAGGTSSEDSLMTSFLGPRFPNG
HVGAGGSGLLPPPALCGASACDVSVRVVVGEPTEARVYPGRGITCDLAILLSAFLLS
QVAPSLEMGSIVQLSQSYTAYWYSAAGLGLVVBKSDLAKYSV"
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                                                                                                                           /tissue_type="medulla oblogata"
/clone_lib="macaque brain cDNA library QmoA"
/dev_stage="adult"
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74.7%; Score 2545.6; DB 9; Length
Best Local Similarity 94.6%; Pred. No. 0;
Matches 2792; Conservative 0; Mismatches 104; Indels
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oligo-capping method
nstitute of Medical Science,
                                                                                                                                                                             /product="hypothetical protein"
/protein_id="BAB60745.1"
/db_xref="GI:14388391"
                                                                                   /organism="Macaca fascicularis"
                                         er [CTTCTGCTCTAAAAGCTGCG];
[CGACCTGCAGCTCGAGCACA]).
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                                sequencing
                                                                                            /db_xref="taxon:9541"
/clone="QmoA-10594"
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         (Sugano et al., , Institute
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                                1017 GGCCCGCTTGGCTTTCCGGAACCTGGCCCCCTGCTTCCCCGGCTGCACCAGCTGTGCT
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Eukaryota: Metzoca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 2904)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Steed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate
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                                                                 2793 TIGCAATAAT---GTCTTATTTAGCGGGGCAAATATTTATACTGTAAGTGAGCAA
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88.2%; Pred. No. 0;
iive 0; Mismatches 1
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1.2904
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Sequence 624 from Patent WO0151633.
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Matches 2560; Conservative
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	qq	13 Lysser
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CGCCAACTGCCTAGGAATCA	Qy	2942 -AGTGG
AlaGlyProLysGlyAlaHisGlyProAlaGlyPr	da ,	45 rProGly
	ο _γ	2883 GAGACCT
::: roLys-G	qq	64 rGlyPrc
OY 113 CATGCTCAACATGCTGCTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATC 54	Qy	2823 GGAATTP
	qq	72
•	Qy	2763 CAGACCC
	QQ	89 yArgPro
RESULT 42	Qy	2703 ACCTGAT
US-08-931-820-4 ; Sequence 4, Application US/08931820	qa	104 yProAla
Patent No. 6010863 GENERAL INFORMATION:	ογ	2650
APPLICANT: TITLE OF INVENTION: Assay for collagen degradation	qa	121 spGlyAr
	δλ	2607 TTAAATA
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	qq	:: 135 euLysGl
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)	Qy	2547 TGATAAA
A: US/08/931,820	qa	155 lyAlaPr
FILING DATE: CLASSIFICATION: 435	QY	2487 TGGTTCT
PRIOR APPLICATION DATA: APPLICATION NUMBER: EP 96202596.1	qq	174
FILING DATE: INFORMATION FOR SEC ID NO: 4:	QŸ	2427 CCATGGA
S: cid	qq	174
= =	Qy	2367 AGGTTAA
TOPOLOGY: linear MOLECULE TYPE: protein	qq	175
HYPOTHETICAL: NO ORIGINAL SOURCE:	Qy	2313 AAAACCC
ORGANISM: Homo sapiens TISSUE TYPE: Collagen type III	qa	 187 roGlyPr
MO	Qy	2253 ATCCACC
Modified	qq	:: 198 erProGl
; OTHER INFORMATION: /note= "Ala may be Pro" US-08-931-820-4	Qy	2199 TATAAGT
ment Scores:	qa	218 ly-
6.85e-19 351.50	Οy	2139 GAGAG
Tarity: 29.85% Conservative:	qa	227 lyHisAl
	QY	2085 CACAGGG

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GGGTTGTGGAGCTGGGGAAAGTTGGGGGGTAGGGGGAAAGTTGGGGGGTAGGGGA 2992
                                                                                                                                       TGGGCAGTGCCTTCATCAGCCCAGTCCTAGAGAGTAGAGGGG----- 2943
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--AlalleGlyProSerGlyProAlaGlyLysAsp6lyGluSerGlyArgProGl 89
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у 127	G 218 - 141	A 212 153	A 206 1 9 171	- 202(r 197	A 1910 - 217	7	G 1790 G 250	C 174: H 270	C 170: P 290	A 166;	G 1601	G 158: - - - -	3	A 1467 . a 381	:A 1407		12
nGl	TCCAC	CAGCCCTAGAGACTGGGGAGAGGAGA 	GCAG	GlyA	GCCC pPro	TCAA	ATAT - OGly	CACCT	-GGTCCAGGCAGATGCC OGlyProProGlyAlaH	-CCACCTGGCCTCGGTGGGCTCACCAC 	-GCAGAGGCCCCGCAGA ::: yAlaGlnGlyPro	CATTA 	-TTAGGGCCTG AlaGlyProG	SGTAT SlyPr	AGGGCA ProAla	20990	CCAAP ProGl	AspPr
/AlaGl	ATAAG	AGAGA I YG1yS	recc. yglys	3C erArç	GGCAC	TCTTC	ACACO - ProP1	GGGC(GlyP1	GGCA(GCTC Alah	GCCC	GLYP	TTAG AlaG	CCTC -	rgrgr	ACCA	CTGG	3A gGly
ProGlyA1	CTGT	GGGGA(roGly	AGGG rog1	GGCA Glys	AGTGA erarg	STCGC	SGCAG	3GATG SpPro	STCCA yPro	sGTGG :: ysGly	CAGAG ::: aGln	ccacc	lyPro	rgrcc GlyPr	CCAGI	CTGTC	CCACA 	GAGA(SerAi
Pro	CCTCC yProF	AGACT aGlyF	AGCAC aGlyF	AGCCC roGly	ACCCA Glyse	CCAAC	CTGC	ACAG(Glyas	Prog	CCIC : ProL	G GlyA	GCAC		CCAG aGln	GAGG I -y	GAAG	AGCTG	3ACCA LyGly
rogl	rcreccrecter	CCTAG ProAl	CAGC	GGCC GlyP	TIGGG 	TTTGG	7AGGC rogly	SATAA erArg	lyAsp	ccrgg lagly	roLys	CICCA roPro	 1yAla	CACCT GlyAl	AGAGG ::: GlnG]	CGGCJ oGly:	GGAA! gGly?	CCAT(ProG
yAspE	CCCTT PPro-	CAGCC	CACCI	CTGGC	GGAG(19	AGTA	GACC(AspP	AGCC(ArgG	CCAC ProA	GlyP	CTGC	ProG	CTAG	STGGT YAla	3AGGG ProPr	SerAr	CCGGT aGly
erArgGlyAspProGly	GCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCA 	CAGG	TACG	GAGCCACATTACTTTGGCAGCACAGAAACTGGCGGCCAGCCGGCAGC- ::: AsproglyProprogly-AlaGlnGlyProAlaGlyProGlyGlySerA	CCCATGGGGCTAACAGGAGCGGGGAGCTGGGACCCAGTGAGGCAGGCCCT	SGCTG	SACCA rgGly	AATGG roGly	GGACAGCAGGAAGGCACTATCCAGGATGGCGAGGTCCAGGCAGATGCC 	CCGGCCCGGAA	CACCACACGTACGGAGACATCACAG	CGCGGGTGGAGGTGGGAGCAGGCCACTGCCTCCAGCACCCACGTGTCCATTAG	GGAAGGGAGCTCCAGGCTTAGGGCCTG 	GCAGGAAGCTGGTCATCAGGCTGTACTGCTAGCACCTCCAGTGTCCCCTCGGTATT	TGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGGCCAGTGTGTAGGCCA 	GGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTGTCACCACGGCCA 	CACTGTGGGACAGGCATGTGGCACCGGCACACGGGAAAGCTGCCACACTGGCCAAAT	AGACTGCTCGAGTGCCGAATCGCTGCACCAGCGGTCCATGACCAGAGAGA
-Ser	TGCA7 rarg(AGGCCTCCAGT - GlyAlaGln-	GCAGO aGln	CAAC	GA 1yPro	TCTA	TGGC SerA	GGAC GlyP	GGAT 		CACCACACGTACGGAGACATCACAG 	GCGCGGGTGGAGGTGGGAGCAGG AlaGlyProGlyGlySerArgGlyA	CCAG 	STCCT spPro	CTTCT	SAACC ::: AspPr	ACCGG ProG1	creca lnGly
	rccag 31yse	GGCCT yal	SCTGT 31yAl	3GCAG 31y-A	AACAG aGlnG	AGTTT	GTAAA lyGly	GAGCT roAla	ATCCA yPrc	 ysG1 ₃	ATCAC	GCAG	GAGCT 1yasi	GGCT(CCTG 	AGGT(-Gly	11GGC -	AlaG
1	GCAT OGly(GGAA(CCCA	CTTT	GGCT.	ACCCCAATGTGCTGGAAGTT ProProGlyAlaGlnGly	CAAA	GGCT GlyP	SCACT SAlaG	yProL	SAGAC : sGlya	rggga yglys	-AAGG ::: rArgG	CATCA erArg	SAACA yAsp	TGAGA erArg	GCATC ala-	9555
	rcccc 31yPr	CCCTT	CAGCC 31yPr	CATTA	CATGG	rgrgc lyAla	TGTAC laGly	AGACT	GAAGC yPrc	AA	TACGO :: roLys	GAGG	1ySe	TGGT(ArgG	.66667 	TGTGGGACAGGCAT aGlnGlyProAla-	GAGT
GlyGly	AGAG a(AACC	GCCC PPro(GCCA(:	CC 1yPr	CCAA 	ACCTG ProA	TGAC	AGCAG 	CCGCCCGGAA- isGlyProAlaG	ACACG aGlyP	SGGTG aGlyP	 oGlyG	AGGAAGC -Gly	CA 1yser	CTGCA roGly	GTGGC GlnG]	TGCTC
G1	CCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTT ProAlaGlyProGlyGlySerArgGlyAspPro-	ACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGA	GGGACGCCCCAGCCCCAGCTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAA 	GAGCCACATACTTTGGCAGCAACAGAAACTGGCGGCCCACCCGGCAGC ::: :::	pProG	ccaccccaatgtgctggaagttttctacgctgagtatttggccaagtcgctcttgtcaaa 	TACTACCTGTGTAGCAAAGTAAATGGCGACCAGCCCAGGCCTGCGGCAGACATAA 	GGCAGTGACAGACTGGCTGACAGTGGAGCCCATAAACAGGGATGGGGCCACCTG	GGACA yala	00000 1861	CACCA	GCGC(GG JyPro	GCAG	TGGGCA GlyGlySe	GGAT	CACT	AGAC
114	2248 (2188	2128 (2068	2019	1969	1909	1849	1789	1741 270	1702	1661 309	1607 328	1580	1520 366	1466 382	1406 395	1346
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Qy Dp

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Qy Db δ QQ Oy Oy Dp

οy	1295	AGACCAGGGAGATGGCGCACTGCAGGAACAGCC	2
qa	427	GlySerArgGlyAspF	46
٥y	1253	CATCCGAACGCCTTCATCATGTGTCTCCGGGCCTCGGTGCCCCGGCTCAGCTCTGGGCA	1194
qq	447	ProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgGly 4	09
Qy	1193	SCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTG	1134
qq	461		472
QY	3	TGCGGGCATGCGGCAGC	0
Db	m	-	
Qy	1073	ACAGCTGGTGCAGCCGGGGAAGCAGGGGGCGCCCAGGTTCCGGAAAGCCAAGCGGCCCGGC 1	1014
рþ	491		510
Qy	1013		696
Db	511		530
Qy	962		918
Db	531	sGlyAlaHisGlyProAlaGlyProLys	546
٥y	917	:	873
qq	547		562
Οy	872	CCTCCTGGGTGCCCAGGGAGGGGGCCAGGG	843
QQ	563	:	581
οy	842	CACTGGTGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 7	783
qq	582		588
Qy	782	TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAG	726
QQ	589	_	602
Qy	725		9
Db	603	17	
Qy	899		989
QQ	619		638
Qy	635	TGGGATCCGGGCACAGCAGCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGC	579
QQ	639		658
Qy	578	TCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCGATAGCGTCCAC	519
qq	629		699
Οy	518		459
Db	670	GlyproGlyGlySerArgGlyAspProGlyProFroGlyAlaGln	684
Qy	458	TGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGGGGGCAA	399
qq	685		703
QY	398	CATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA	339
Op	704		715

2287		ΟŻ
Qy 2347 GGGAAACCAGGTGACTGAGTTTATTCA 	281 TGGGCCAGGCGGGTAGGGCTCAGGGGGCCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225	do Op
1 3-110 (1-3410) x US-08-642-	338 AGAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCTCACCCACAGCCTCTGGACCATAG 282	Qy Db
+.025-1 e: 353.50 ent Similarity: 32.33% Local Similarity: 30.10%	398 CATAGGTGATGCCTGGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTGACCAGCA 339	ογ
0 7	GlnGlyLeuProGlySerProGlyAla	7 q
Ä	TCCTCTACCCCACTTCCAGCAGCAGGGGGGCAA	δy
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3 E		e è
TELEX: 910 277299 FHT UR INFORMATION FOR SEQ ID NO: 72:	563 AGGACAGTGCCCAGATGAAGGCCGGCGGCGCCATAGCGTCCACGCCAGTGGTCAC 507	δ.
; TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8700 TELEFAX: (415) 494-8771	548 ThrProGlyProglnGlyLeuProGlySerProGlyAlaPro 561	qq
REGISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A55556-3	623 ACAGCAGCCTGCTAGCCAGCCGGCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCA 564	ογ
; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: ROWLAND, Bertram I	683 AGTCCARCACCCAAGATGAGCAGTGCCAGCTCCAGGGGCTTGGGATCCGGGC 624 :::	do do
## PAPELICATION NUMBER: US/08/642,255 FIFTING DATE:	512 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 529	qq
SOFTWARE: Patentin Release #1.0,	740CCGGAAGAGGTCAGAGAGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGA 684	Οy
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible		qq
SIP: 94111-4187	AAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGT	δλ
CITY: San Francisco ; STATE: California ; OTINATE: CALIFORNIA	85/ GGTAGGGGCAGGGCACTGGTGTCCAGTCAATGGCAGGAGGAGGTAGCCAAGGAGC 798 	Å a
ADDRESSEE: FLEHR, HOHBACH, TEST, STREET: 4 Embarcadero Center, Sui	LeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro	අු ,
HILLE OF INVENTION: PROPERTY FOR YOUNGER OF SEQUENCES: 135 CORRESPONDENCE ADDRESS:	902 AGATGAGGTGAGCAAAGAGCAACTCTCCTGGGTGCCCA 858	Qy
; APPLICANT: FERRARI, Franco A. ; TITLE OF INVENTION: High Molecular in the contraction of the contraction o	454 GlyAlaProGlyThrProGlyProGln	qq
GENERAL INFORMATION: APPLICANT: CAPPELLO, Joseph		ογ
US-08-642-255-72 Sequence 72, Application US/08642255	1019 CCCGGCATGGACAGCAGTGGCGCGACAAGGAGGGGCCCAACAGCCTTCTGCTGGC 960	Oy Dp
Db 712 lyThrProGlyProGlnGlyLeuProG	en	qa
Qy 59 CAGATCTGGCCGAGGCGCGCGC		δ
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Qy 105ACACCTGCTGCTG	GCGCAGGGTGCGGGGCATGCGGCAGCACA	ò
Db 674 uProGlySerProGlyAlaProGl	1178 CCTCGCCACGAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATGCAGC	å a
659 164	თ	qq
Db 659 uProGlySerProGlyAlaProGlyTh		i

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GCTCCCCAAAACCCTTCTCTAGGTGTGTCTCAA 2288 | 11 | 11 | 11 | 11 | 11 | 113
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            TGGGGCACCTCAGTGGGACACGTCTCATCACT 60
Weight Collagen-Like
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164 GCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCA- 106	QY	2227 AGTGCATGGAGCCCTTCTGGCTCCCTGTATAAGTCCAGAACTGAAAACCCCCTTGGAAGGC 2168
 	qq	
TCACT	oy Db	2167 CTCCAGTCAGGCAGCCCTAGAGACTGGGGAGGAGGAGGGACGCCCCAGCCCCAGCT 2108
TOSITATARFIOSITATION TO TO TO THE CONTROL OF THE CO	Qy	2107 GTGCAGCTACGCACCTCAGCAGCACAGCAGCAGAGAGCCACATTACTTTGGCAGC 2048 101 ProglnGlyLeuProGlySerProGlyAlaProGlyThrProGlyP 116
	Qy	2047 AACAGAAACTGGCGGCCAGCCCGATGGGGCTAACAGGAGCGGGGACTGGGA 1988
Sequence 50, Application US/U839/b33A Setent No. 5773577 GENERAL INFORMATION: APPLICANT: Cappello, Joseph	dg	1987 CCCAGTGAGGCGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928
ENTION: PRODUCTS COMPRISING SUBSY BYTION: OF ENZYMATIC CROSS-LINKIN QUENCES: 105 CE ADDRESS:	Qy Db	1927 CAAGTCGCTCTTGTCAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCC 1868
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California	Oy Db	TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGGACCAGGACATGGCCCATAAA
COUNTY: USA ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	Qy	1807 CAGGGATGGGCCACCTGGGACGACAGCAAGGCAC
COMPLARS: IDEM PC COMPLIANTE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 SOFTWARE: APPLICATION DATA:	Qy	1769 CAGGATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGC 1721
RELIGIOUS NOMBER: US/US/39/,033A FILING DATE: CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:	Qy	1720 CTCGGTGGGCTCACCCACCACCACGACACGAGACATCACAGGCAG 1674
REGISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1 TELECOMNUICATION INFORMATION: TELECOMNUICATION INFORMATION:	δy	1673 AGCCCCGCAGAGCGCGGTGGAGGGGGAGCAGCTGCCTCCAGCACCCCAGTGTC 1614
(415) 398-3 (277299 (SEQ ID NO	Qy	1613 CATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554
LENGTH: 897 amino acids TYPE: amino acid STRANDENESS: single	Qy	1553 CACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT 1500
<u> </u>	QQ .	1499 CCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGCTGAGAGGTGAACC 1440
Pred. No.: 2.67e-19 Length: 897 Score: 356.50 Matches: 263 Percent Similarity: 35.16% Conservative: 32 Boar foral cimilarity: 37.16% Marches	Qy	1439 CGGTGAGGCGCGCTGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACC 1382
5.73% Instactions: 5.73% Instable: 1 Gaps: 410) v HS-08-397-6338-50 (1-507)	δγ	1381 -GGCAGCCACAGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATGGCT 1323
	Qy	1322 GCACCAGCGGTCCATGACCAGAGAGAGACCAGGGAGATGGCGCACTGCAGGAACA 1266
CTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCC	da Oy	1265
ociyserProGlyAlaProGlyThrProGlyProGlnGly 73	^o	1238 CATCATAGTGTCTCCGGGCCTCGGTGCCCGCTCAGGCTCTGGGCACGCCCTGGTACAGCC 1179

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74 LeuProGlySerproGlyAlaProGlyAlaProGlyAlaPro	3GAGAGAGAGGACGCCCCAGCCCCAGCT		2107 GTGCAGCTACGCACCTCAGCAGCACAGGTGGCAGAGAGCCACATTACTTTGGCAGC 2048	101 ProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyP 116	2047 AACAGAAACTGGCGGCCGGCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGA 1988		1987 CCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928		1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCCAGGCC 1868	145GlyProGlnGlyLeuPro	1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808	155 laProGlyThrProGlyProGlnGlyLeuProGlySerPro 168	1807 CAGGGATGGGGCCACCTGGGACAGCAGGAAGCCACTATC 1769		1768 CAGGATGCCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGC 1721		1720 CTCGGTGGGCTCACCCACCACACGTACGGAGACATCACAGGCAG 1674	euProG	1673 AGGCCCCGCAGAGCGCGGTGGAGGTGGAGCAGGCCACTGCCTCCAGCACCCACGTGTC 1614		1613 CATTAGGGAAGGCACCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554	246 roGlyThrProGlyProGlnGlyLeuProGly-SerProGlyAlaProGlyThrPro 264	1553 CACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT 1500	265 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr 278	1499 CCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACC 1440	:::	SAGGGCGCTGAAGCTGTCACCACGGCCACACTGTGGGA		1381 -GGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 1323		1322 GCACCAGCCGGTCCATGACCAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACA 1266	 320 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 339	1265GRACGCTGCCCAGGCTGCCCTT 1239	340 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 359	1238 CATCATAGIGICICCGGGCCTCGGTCCAGCTCTGGGCACGCCCTGGTACAGCC 1179	
qa	Qy	qq	٥y	đ	QY	đ	Oy	qa	٥y	QQ	οy	QQ	ΟŶ	qq	ρŷ	Q	ογ	q	ογ	qq	Qy	đ	Οy	QΩ	٥y	QΩ	Οy	qu	οy	đ	ογ	qa	Οŷ	Ω	Οy	

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178 CCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGC----- 1125
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                                                                                                                                           360 ProGlySerProGlyAlaProGlyThrProGlyPro---GlnGlyLeuProGlySerPro 378
                                                                                                                                                                                         395 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 414
                                                                                                                                                                                                                                                                        -----LeuProGlySerProGly 394
                                                                                                                                                                                                                                                                                                                                          019 CCCGGCATGGACAGCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGTCGG 960
                                                                                                                                                                                                                                                                                                                                                                                435 ProGlySerProGlyAlaProGlyThr---ProGlyProGlyBroGlySerPro 453
                                                                                                                                                                                                                                                                                                                                                                                                                                   959 TGGGGCCCCAGCGCTGCCT---CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGA 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    902 AGATGAGGGTGAGCCAAAGAGGCACTCCT------CCTGGGTGCCCA 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------Gly 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  484 Gly----AlaProGly-----ThrProGlyProGlnGlyLeuProGlySerProGlyAla 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             797 CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGGT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   740 ---CCCGGAAGAGGTCAGAGGAGGCCCTCCAGTGGAGTGAAGCACACTGGCCACAGA 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       683 AGTCCAGCAGCCCCACGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGC 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           623 ACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     506 TGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCA 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 CATAGGTGATGCCTGCGGCCAAACACCCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AGAGCTGGGCTTTCCGGT---GCCGCAGCGGCGCTCACCCACAGCCTCTGGACCATAG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    620 AlabroGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr-Pr 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 AGGACAGTG---CCCAGATGAAGGGCCGGCGGCGATAGCGTCCACGCCAGTGGTCAC 507
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659 uProGlySerProGlyAlaProGlyThrProGly-------ProGlnGlyLe 674
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APPLICANT: Ferrari, Franco A.

ογ	959 TGGGGCCCAGCGCTGCCTCCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGA 903	
Dβ	454 GlyAlaProGlyThrProGlyProGln	
Qy	902 AGATGAGGTGAGCCAGAGGCCACTCCT	
QQ	464 LeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 483	
οy	857 GGTAGGGGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGGCA	
pp	484 GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 500	
Οy	797 CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGT 741	
. qa	501 ProGlyThrProGlyProGlnGlyLeuProGly 511	
٥y	740CCCGGAAGAGGTCAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACGTGGCCACAGA 684	
Db	512 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 529	
Οy	683 AGTCCAGCAGCCCAGGATGAGCAGTGCCAGCTCCAGGGCCTGGGATCCGGGC 624	
QQ	530 AlabroGlyThrproGlyProGlnGlyLeuProGlySerProGlyAlaProGly 547	
٥y	623 ACAGCAGCCCTGCTAGCCAGCĆGGCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCA 564	
Ор	548 ThrProGly	
Qy	563 AGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCAC 507	
qq	562 GlyThrProGlyProGlyLeuProGly571	
٥y	506 TGGCTGAGCCTAGGAGCGGGACACAGACCAGCCCAGCACTGGACCAATGCCCCAGCACCA 447	
Dp	572SerProGlyAlaProGlyThrProGlyProGlnGlyLeuPro 585	
ργ	446 TGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGAGGGGGGA 399	
Ωp	586 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 605	
δy	398 CATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339	
qq	606	
οy	338 AGAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCTCACCCACACACACATAG 282	
qq	620 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr-Pr 639	
Qy	281 TGGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225	
Dp	639 oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLe 659	
Qy	224 CGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAATCA 165	
Dp	659 uProGlySerProGlyAlaProGlyThrProGly	
Qy	164 GCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCGGGTCCAGCTTCTCAGCCCATGCTC- 106	
QQ	674 uProGlySerProGlyAlaProGlyThrProGlyProGlnGly-LeuProGlySerP 693	
Qy	105ACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACT 60	
qa	693 roGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProG 712	
Qy	59 CAGATCCTGGCCGAGGGGGGGGGGTTCACCCGGAGCC 22	
QQ	712 lyThrProGlyProGlnGlyLeuProGlySerProGlyAla 725	
RESULT 39 US-09-444-	SULT 39:-09-444-791A-103 Sequence 103, Application US/09444791A	

Sequence 103, Application US/09444791A Patent No. 6355776 GENERAL INFORMATION:

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TITLE OF INVENTION: NO. 6355776el Peptides Comprising Repetitive Units of Amino Acids and DNA Sequences Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2287 CTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCC 2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2227 AGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGC 2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAA 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GlySerProGly------AlaProGlyThrPro-----GlyProGlnGly 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 LeuProGly------SerProGlyAlaProGlyThrProGlyProGlnGly 73
                                                                                                                                                                                NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
STREEF Flehr Hobbach Test Albritton & Herbert LLP STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: FIOPPY GISK
MEDIUM TYPE: FIOPPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT ABLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/44,791A
FILING DATE: 22-NO: 6355776-1999
CLASSIFICATION: CURNOWN>
PRIOR APPLICATION NUMBER: US 08/482,085
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
APPLICATION NUMBER: US 08/053,049
FILING DATE: 29-APR-1993
APPLICATION NUMBER: US 06/927,258
FILING DATE: 29-OFT-1987
APPLICATION NUMBER: US 06/927,258
FILING DATE: MINCRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-55186-11/RFT/BTC
TELECOMMUTCATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFRAX: 415-398-3249
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263
32
327
218
57
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
Richardson, Charles
Chambers, James
Causey, Stuart
Pollock, Thomas J.
Cappello, Joseph
Crissman, John W.
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 837 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 103: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.61e-19
356.50
35.16%
31.35%
5.73%
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COMPUTER READABLE FORM:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-444-791A-103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
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1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCC 1868 145GlyProGlnGlyLeuPro	1768 CAGGATGGCGAGGTCCAGGCAGATGCCCCGGC	226 lySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaP 246 1613 CATTAGGGAAGGAGGTCCAGGCTTAGGGCTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554 1	1499 CCCGGTGGTAGAGGGGGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACC		340 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 359 1238 CATCATAGTGTCTCGGGGCCTCGGTCGGCTCAGGCACCCTGGGCACCCTTGGGCACGCCTGGGCACGCCTGGGCACGCCTGGGCACGCCTGGGCACGCCTGGGCACGCCTGGGCACGCCTGGGCACGCCTGGGAAAACAGCC 1179 360 ProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 378	1178 CCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCCATGACTGCCATCCAGC 1125	1070 GCTGGTGCAGCGGGAAAGCAGGGCCCCAGGTTCCGGAAAGCCAAGCGGG 1020
6 8 6 8 8		a & a a	40 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 60 6 70 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 6 80 80 6 <td>\text{7} \text{8} \text{8} \text{8} \text{8} \text{8} \text{8} \text{8} \text{8}</td> <td>a va</td> <td>Q Q Q</td> <td>90 OV</td>	\text{7} \text{8} \text{8} \text{8} \text{8} \text{8} \text{8} \text{8} \text{8}	a va	Q Q Q	90 OV
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/482,085B FILING DATE: UO -JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: US 06/927,258 FILING DATE: 04-NOV-1986 PRILING DATE: 04-NOV-1986		DH or to to the second	/ MOLECULE TYPE: peptide // US-08-482-085B-103 Alignment Scores:	3-15 Gaps: 3-110 (1-3410) x US-08-482-085B-103 (1-837) 7 GGGAAACCAGGTGACTGAGTTATTCAGCTCCCAAAAACC	Qy 2287 CTAGGAGGCTAGCTGGTAACCCTGAGCTAATCCACCTGCAGAGTCCCGCATTCC 2228	GGAGAGAGGACGCCCCAGCCCCAGCT	AACAGAAACTGGCGGCCGCGCCCCCTGGGGGTAACAGGGGGGGG

qq		
Qy	1673 AGGCCCCGCAGAGCGCGGGTGGAGCTGGGAGCAGGCCACTCCCAGCACCCACGTGTC 1614	683
qq		530
ογ	1613 CATTAGGGAAGGAAGCTCCAGGCTTAGGGCQTGGCAGGAAGCTGGTCATCAGGCTGTCCT 1554	623
qq		548
δō	1553 CACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT 1500	Oy 563 AGGACACTGCCCAGATGAAC
qa	265 GlyProglnGlyLeuProGlySerProGlyAlaProGlyThr 278	506
δδ d	1499 CCCGGTGGTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAGGTGAACC 1440	
G 6		QY 446 TGGTCATGAACTTCTCCTCTACC
G Q		586
Oy	1381 -GGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 1323	Qy 398 CATAGGTGATGCCTGCGGCCAAA
QQ	309 oGlyProGlnGlyLeuProGlySerPro	
δò	1322 GCACCAGCCGGTCCATGACCAGAGAGAGACCAGGAGATGGCGCACTGCAGGAACA 1266	620
qa	AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro	Qy 281 TGGGCCAGGCGGGTAGGGC
δō ·	1265	Db 639 oGlyProGlnGlyLeuProGlyS
qa	340 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 359	Qy 224 CGGCTCTGCTCCAGAAGCTGCG
δ		
qa	360 ProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 378	Qy 164 GCCAGGCGCCCATTTCTGCCAGG
δo :		674
qq	379 GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 394	Qy 105ACACCTGCI
δλ	1124TGCACAGCTCAGCCACGAAGAGCCGGCGCGGGGGGGGGTGCGGGGGGTGCGGCAGCAGCACA 1071	693 roGlvAlaProGl
qq	395 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 414	9 6
ογ	1070 GCTGGTGCAGCCGGGGAAGCAGGCGCCCCAGGTTCCGGAAAGCCAAAGCGGG 1020	2y 59 CAGAICCIGGCCGAGGCCCC
Db	415 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 434	96
٥y	1019 CCCGGCATGGACAGTGGGGGCGAAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGG 960	US-50L1 36 US-50L4 2-085B-103
qq	435 ProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 453	; Patent No. 6018030
Οy	959 TGGGGCCCAGCGCTGCCTCCTCAGCCACCAGCAGTGGGCTGCTACGCAGGTGAGG 903	APPLICANT: Ferranco A. Applicant, Franco A. Applicant Person Charles
qq	454 GlyAlaProGlyThrProGlyProGln	APPLICANT: Chambers, James
Qy		APPLICANT: Causey, Stuart APPLICANT: Pollock, Thomas J.
qa	464 LeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 483	APPLICANT: Cappello, Joseph , APPLICANT: Crissman, John W. TITIE OF INVENTION: NO 601803
Qy	857 GGTAGGGGCCAGGGCACTGGTGCCCAGTCAATGGCAGGCA	TITE OF INVENTION: Units of An in Instance of An in Instance of Secure of Se
qa	484 GlyAlabroGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 500	CORRESPONDENCE ADDRESS:
δ, d	797 CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGT 741	STREET: Four Embarcadero Cent (CITW: San Francisco (CTATE: California
2	\	COUNTRY: US
δδ	/40 ***-CCCGGAAGAGGICAGAGGCAGGGCCICCAGIGGAGGGAAGCAGACCGGCCACAGA 084	E-3

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30el Peptides Comprising Repetitive
Amino Acids and DNA Sequences Encoding the Same
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oGlyThrProGly------ProGlnGlyLe 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225
                                 GGATGAGCAGTGCCAGCGGGCCTGGGATCCGGGC 624
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GlnGlyLeuProGlySerProGlyAla-----ProGly 547
                                                                                                                                                                                                                                                             CACAGACCAGCCCAGCACTGGACCAATGCCCAGCACCA 447
                                                                                                                                                                                                                                                                                       GlyThrProGlyProGln------GlyLeuPro 585
                                                                                                                                                                                                                                                                                                                                      CCCCCA-----CTTCCAGCAGCAGGCGCGCA 399
                                                                                                                                                                                                                                                                                                                                                               |||| ::: |||||| || ThrProGlyProGlyAla 605
                                                                                                                                                                                                                                                                                                                                                                                                                 AACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCTCTCCTTCCTGCTGCCGCCAACTGCCTAGGAATCA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCA- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ProGlyThrProGlyProGlnGly-LeuProGlySerP 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProGlyProGlnGlyLeuProGlySerProGly----- 529
                                                                                                                                     AGGCCCGCCGCCGCCATAGCCTCCACGCCAGTGGTCAC 507
                                                                                                              CGCCCCTTGGGATGAGAAGAGCCTCAGCAGGATGCCCA 564
                                                                                                                                                                                                                            LeuProGly----- 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Test, Albritton & Herbert
inter, Suite 3400
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398 CATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339
                                       -----ProGlyThrProGlyProGlnGlyLeuProGlySerProGly 619
                                                                                338 AGAGCTGGGCTTTCCGGT---GCCGCAGGGGGGCGCTCACCCACAGCCTCTGGACCATAG 282
                                                                                                           281 TGGGCCAGGCGGG---TAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225
                                                                                                                                                                                                                                                224 CGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAATCA 165
                                                                                                                                                                                                                                                                                       659 uProGlySerProGlyAlaProGlyThrProGly-------ProGlnGlyLe 674
                                                                                                                                                                                                                                                                                                                                 164 GCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCA- 106
                                                                                                                                                                                                                                                                                                                                                             693 roGlyAlaProGlyThrProGlyProGlnGly---LeuProGlySerProGlyAlaProG 712
                                                                                                                                                                                                                                                                                                                                                                                                                    ---ACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACT 60
                                                                                                                                                                                            ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712 lyThrProGlyProGlnGlyLeuProGlySerProGlyAla 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 CAGATCCTGGC----CGAGGCGCGCGGCTGTCACCCGGAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Crissman, John W.
APPLICANT: Crissman, John W.
APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
NUMBER OF SEQUENCES: 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/707,237A
FILING DATE: 03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UMBER: US 07/114,618
29-OCT-1987
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Patent No. 5830713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Atent No. Joseph
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Capello, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-NOV-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-APR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY: United States 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
FILING DATE: 09-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-707-237A-75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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2287 CTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCC 2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2167 CTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGAGGAGGGACGCCCCAGCCCCAGCT 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTTAGGTGTGTCTCAA 2288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2047 AACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGA 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1987 CCCAGTGAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCC 1868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ProGln------GlyLeuProGlySerProGlyAlaProGlyThrProGly--P 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA 1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1807 CAGGGATGGGGCCACCTGGGACAGCAGGAAGGCAC--------TATC 1769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 Leu---ProGlySerPro------GlyAlaProGlyThrProGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1720 CTCGGTG------GGCTCACCCACCACCACGTACGGAGACATCACAGGCA-----G 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 laProGlyThrProGlyProGlnGlyLeuProGly------SerPro---- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 GlySerProGly-----GlyProGlyThrPro----GlyProGlnGly 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 LeuProGlySerPro---GlyAlaPro------GlyThrProGlyPro---GlnGly 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 LeuproGly------SerProGlyAlaProGlyThrProGlyProGlnGly 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-759-143-110 (1-3410) x US-08-707-237A-75 (1-837)
                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                  NAME: Trecartin, Richard F.
REGISTRATION UNMBER: 31,801
REFERENGE/DOCKET NUMBER: A-55186-10/WHD
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
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                                                                                                      TELEPHONE: (415) 781-1989
TELEFAX: (415) 388-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                           2.61e-19
356.50
35.16%
31.35%
FILING DATE: 04-NOV-1986 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 837 amino acids
                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                  amino acid
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Best I Query DB:	Best Local Sin Query Match: DB:	Similarity: :	31.35% 5.73% 1	Mismatches: Indels: Gaps:	32/ 218 57	
-60-sn	-759-143-	-110 (1-34	410) x US-08-642	-255-101 (1-837)		
οy	2347	GGGAAACCA	GGTGACTGAGTTTAT	GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCT	CCTTCTCTAGGTGTGTCTCAA	2288
. qa	46	GlySerPro	G1y	AlaProGlyThr	roGlyProGlnGly	5.8
٥y	2287	CTAGGAGGCT	TAGCTGTTAACCCTG	AGCCTGGGTAATCCAC	CTAGGAGGCTAGCTGTTAACCCTGAGCTAGTAATCCACCTGCAGAGTCCCCGCATTCC	2228
qq	L)	LeuProGly		SerProGlyAlaPro(SlyThrProGlyProGlnGly	
δλ		AGTGCATGG	AGCCCTTCTGGCCTC	CCTGTATAAGTCCAG	AGTGCATGGAGCCCTTCTGGCCTCCCTGTATAAGTCCAGACTGAAAGCCCCTTGGAAGGC	2168
gg	4	Leurrogiy	serproGlyalapro-	VIDOIA	III.FIOGLYFIO GINGLY	
λ d	2167	CTCCAGTCA 	TCAGGCAGCCCTAGAGAC	TGGGGAGAGGAGGAG	CTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGAGAGA	100
a (1 A	חבתיים	ALYSEL PIONOPHOROR		CENTAIN TANK TANK TANK TANK TANK TANK TANK TAN	2048
<u> </u>	101	ProGln	cocaccicaccaccaccaccaccaccaccaccaccaccacca	 ProGlySerProGly	-GlyLeuProGlySerProGlyAlaProGlyThrProGlyP	16
λO	2047		TGGCGGCCAGCCCGG	CAGCCCCATGGGGCT	AACAGGAGCGGGGAGCTGGGA	1988
_ qa	116		 euProGlySerProG	 yAlaProGlyThrP	roglnglyhrProglyProglnGlyLeuProg	136
٥y	1987	CCCAGTGAG	GCAGGCCCTCCACC	CAATGTGCTGGAAGT	TTTCTACGCTGAGTATTTGGC	1928
Db	136	l lySerProG	 yAlaProGlyThre	ro		144
٥y	1927	CAAGTCGCT	CTTGTCAAATACTAC	CTGTGTAGCAAAGTA	CAAGTCGCTCTTGTCAAATACTACTGTGTAGCAAAGTAAATGGCGACCAGGCC	1868
QQ	145	9	-GlyProGlnGlyLeuPro	ro	GlySerProGlyA	155
Οy	1867		ACACCATATAGGCAGT	GACAGACTGGCTGAG	TGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAA	1808
Dp	155	_	aProGlyThrProGlyProGlnGlyLeuProGly	lyLeuProGly	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	168 .
οχ	1807		SGCCACCTGGGACAC	CAGGAAGGCAC	CAGGGATGGGGCCACCTGGGACAGCAGGAAGGCACTATC	1769
QQ	169		SlyAlaProGlyThre	roglyProglnGlyL	euProGlySerProGlyAlaP	186
Qy	1768		CAGGATGGCGAGGTCCAGGCAGATGCCCCGGC		CCGGAACCACCCTGGC	1721
qq	186		roglyProglnGlyI	JeuProGlySerProG	roGlyThrProGlyProGlyLeuProGlySerProGlyAlaProGlyThrProGlyP	206
ογ	1720	0 -	GGCTCACCC	ACCACCACACGTACGG	TCGGTGGGCTCACCACCACCACGTGGAGACATCACGGCAG	1674
QQ	206	- 14	LeuProGlySerPro	31yAlaProGlyThrP	roGlyProGlnGlyLeuProG	226
ΟŶ	1673		CAGAGCGCGGGTGGAC	SGTGGGAGCAGGCCAC		1614
qa	226		SlyAlaProGlyThri	ProGlyProGlnGlyL	euproGlySerProGlyAlaP	246
ΟŊ	1613		AAGGGAGCTCCAGGC	TTAGGGCCTGGCAGGA	CATTAGGGAAGGGGGCTCCAGGCTTAGGGCCTGCCAGGAAGCTGGTCATCAGGCTGTCCT	_
qq	246		ProGlyProGlnGly	LeuproGly-Ser	ProGlyAlaProGlyThrPro	264
οy	1553		CACTGCTAGCACCTCCAGTGCCCCTCGGTATT-	CCTCGGTATT	TCCCCTCGGTATTTGGGCAGGAACACCTGCTTCT	1500
qq	265).I.d	oglnglyLeuProgly	SerProGlyAlaProGlyThr	278
Qy	1499		TAGAGGGAGGCCAGT	STGTAGGGCAGGATCT	CCCGGTGGTAGAGGGGGGGGGTGTGTAGGGCAGGATCTGCAGGCTGAGAAGGTGAACC	14
qq	279		ProGlyProGlnGlyLeuPro	Glyser	-GlySerProGlyAla-ProGlyThrPr	294
Οy	1439		GCGGCTGAAGCTGTC	accacgccacactgi 	CGGTGAGGCGGGTGAAGCTGTCACCACGGCCACACTGTGGGACAGGCATGTGGCACCT	
Dp	294		oGlyProGlnGlyLeuProGlySerProGly	erProGly	AlaProGlyThrer	309

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1070 GCT-----GGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGG--- 1020
1381 -GGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 1323
                                                              1322 GCACCAGCCGGTCCATGACCAGAGAAAAGACCAGGGAGATGGCGCACTGCAGGAACA--- 1266
                                                                                                                                -----GCCCCAGGCTGCCCATCC---GAACGCCTT 1239
                                                                                                                                                                                               1238 CATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCC 1179
                                                                                                                                                                                                                                                               1178 CCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGC----- 1125
                                                                                                                                                                                                                                                                                                                                  1124 -----TGCACACGCTCAGCCACGAAGAGCCGGCGCGGGGTGCGGGGCATGCGGCAGCACA 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              572 -----SerProGlyAlaProGlyThrProGlyProGln------GlyLeuPro 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                446 IGGICATGAACTICICCTCTACCCCCA------CTICCAGCAGCAGAGGCGGCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             530 AlabroGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla-----ProGly 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              623 ACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 ThrproGly-------proGlnGly---LeuProGlySerProGlyAlaPro 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 AGGACAGTG---CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCAC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 GlyThrProGlyProGlnGlyLeuProGly------571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     797 CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGT 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            740 --- CCCGGAAGAGGTCAGAGAGCAGGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGA 684
                                                                                        340 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 359
                                                                                                                                                                                                                              360 ProGlySerProGlyAlaProGlyThrProGlyPro---GlnGlyLeuProGlySerPro 378
                                                                                                                                                                                                                                                                                                                                                             395 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 414
                                                                                                                                                                                                                                                                                                                                                                                                                                415 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1019 CCCGGCATGGACAGCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGCTCGG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              435 ProGlySerProGlyAlaProGlyThr -- - ProGlyProGlnGlyLeuProGlySerPro 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               959 TGGGGCCCAGCGCTGCCT---CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGA 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 GlyAlabroGlyThrProGlyProGln-----Gly 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            902 AGATGAGGGTGAGGCGCAAAGAGGCACTCCT------CCTGGGTGCCCA 858
                        683 AGTCCAGCAGCCCCACGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGC
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Db 606Proglythrproglyp	Qy 338 AGAGCTGGGCTTTCCGGTGCCGCAGCGCG	Db 620 AlaProGlyThrProGlyProGlnGlyLeuProG	281	639	224	629	164	Db 674 uProGlySerProGlyAlaProGlyThrProC	Qy 105ACACCTGCTGTGGGGCAC	Db 693 roGlyAlaProGlyThrProGlyProGlnGly	QY 59 CAGATCCTGGCCGAGGCGCGCGCGCTGTCACCC	Db 712 lyThrProGlyProGlnGlyLeuProGlySerPro	RESULT 36	Sequent 101, Application US/08642255	GENERAL INFORMATION:	U, Joseph Franco A.	TITLE OF INVENTION: High Molecular Weight C INTERPLY OF INVENTION: Protein Polymers	NOMBER OF SEQUENCES: 135 CORRESPONDENCE ADDRESS:	n E	STATE: California	_ □ ?	MADITURE TYPE: Floppy disk	OPERATING SYSTEM: PC DOS/MS-DOS COPERATING SYSTEM: PC DOS/MS-DOS COPERANDED DATASET FOR	CURRENT APPLICATION DATA:		ATTOMOSTICATION: #33 ATTOMOSTICATION: NAME: ROWLAND RESTRAIN	REFERENCE/DOCKET MINRER. 20,015	TELECOMMUNICATION: TELEPHONE: (415) 494-8700	; TELEFAX: (415) 494 971 : TELEFAX: (415) 494 11	INFORMATION FOR SEQ ID NO: 101:	LENGTH: 837 amino acids	STRANDEDERSS SINGLE	YPE	Alignment Corres.	
	1322 GCACCAGCCGGTCCATGACCAGAGAGAGACCAGGGAGATGGCGCCACTGCAGGAACA 1266	Pro	1265	340 GlyProGinGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 359	1238 CATCATAGTGTCTCCGGGCCTCGGTCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCC 1179	360 ProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 378	AAAACAGCGTGAAGGTCATGA	379 GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 394	1124TGCACAGGTGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCACA 1071	395 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 414		415 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 434		435 ProGlySerProGlyAlaProGlyThrProGlyProGlyTeuProGlySerPro 453	959 TGGGGCCCAGCGCTGCCTCCTCAGCCACCAGGTGTGGCTGCTACGCAGGTGAGGA 903				CACTEGTCCCAGTCAATGGCAGGCAGGTAGCCCCAGGCAGC				CAGA		683 AGTCCAGCACCCCACGCCCAGGATGAGCAGTCCCAGCTCCAGGGGCCTGGGGATCCGGGC 624	530 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGly 547	TTGGGATGAGAAGAG	548 ThrproGly	563 AGGACAGTG CCCAGATGAAGGGCCGGCGGCCGATAGCGTCCACGCCAGTGGTCAC 507		GCACTGGACCAATGCCCAGCACCA		446 TGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGAGAGGGGGA 399	586 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 605	398 CATAGGTGATGCCTGCGGCCAAACACCCCCAAGGCCAAAGGTTAGCAGGTTGACCAGCA 339
qq	Οy	qa	ð á	gr (δ ά	gg ,	ko	qa _	δλ	ପ୍ର	Qy	qq	ολ	Q O	0y	qq	Οy	qq	Qy	qa	, VO	qq	Ολ	qa	Ολ	qa	Οy	q	δò	QΩ	ογ	qq	Oy	QQ	δλ

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ProGlnGlyLeuProGlySerProGly 619
                                       TTGCTGCCGCCAACTGCCTAGGAATCA 165
                                                                          CGGTCCAGCTTCTCAGCCCATGCTCA-106
                                                                                                                        ACCTCAGTGGGGACACGTCTCATCACT 60
                                                                                                                                                                                                                            Collagen-Like
                                                                                                                                                 TON & HERBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 837
Matches: 263
Conservative: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity: 35.16%
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3 Gaps: 57 US-09-759-143-110 (1-3410) x US-08-477-509B-103 (1-837)	. Qy .	Qy 2287 CTAGGAGGCTAGCTGTTAACCCTGAGCTGGGTAATCCACCTGCAGAGTCCCGCATTCC	OY 2227 AGTGCATGGAGCCCTTCTGGCCTCGTATAAGTCCAGACTGAAACCCCCTTGGAAGGC	Oy 2167 CTCCAGTCAGCCGCTAGAGACTGGGGAGAGAGGAGGACGCCCCAGCT	Same Db 101 profineGlyLeuProGlySerProGlyAlaProGlyThrProGlyP	Qy 2047 AACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGAGTTGGGAGTTGGGAGTTGGGAGTTGGGAGTTGGAGTGGAGTTGGAGTGGAGTTGGAGGA	Qy 1987 CCCAGTGAGGCGGCCTCCACCCCAATGTGCTGGAAGTTTCTACGCTGAGTATTTGGC	1927 CAAGTGGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGC	Db 145GlyProGlnGlyLeuProGlySerProGlyA	OY 1867 TGCGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCAGTGAACAATGGAGCCCATAAA	1807	169	Qy 1/88 CAGANIGCGAGGGCCCAGGCCCAGGCCAGGCCAGGCCAGG	Oy 1720 CTCGGTGGCCTCACCACCACCACGTACGGAGACATCACAGGCAG	1673	1613		Db 265 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr	Qy 1499 CCCGGTGGTAGAGGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACC		Db 294 OGLyProGluGlyLeuProGlySerFroely
	Oy 105ACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACT 60	Qy 59 CAGATCCTGGCCGAGGGGGGGGGTGTCACCCGGAGCC 22	RESULT 35 US-08-477-509B-103 Sequence 103, Application US/08477509B	; Patent No. 3/1005. ; GENERAL INFORMATION: APPLICANT: Cappello, Joseph , APPLICANT: Cappello, Joseph	553	NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400	CITY: San Francisco STATE: California COUNTRY: US ZIP: 94111	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC Compatible	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30	CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/477,509B ; FILING DATE: 07-JUN-1995	CLASSIFICATION: 435 FRIOR APPLICATION NUMBER: US 08/175,155 APPLICATION NUMBER: US 08/175,155	FILING DATE: 29-DEC-1993 PRIOR APPLICATION DATE: 08/053.049	FILING DATE: 22-APR-1993 PRIOR APPLICATION DATE: 70 07 111 619	APPLICATION NUMBER: US 0//114,010 FILING DATE: 29-0CT-1987 PRIOR APPLICATION NUMBER: US 06/927,258	ຸ ໆ 🖔	; REFERENCE/DOCKET NUMBER: A-55186-7/RET/MTK ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 415-781-1989 ; TELEPEXX: 415-388-3249	INFORMATION FOR SEQ ID NO: 103: ; SEQUENCE CHARACTERISTICS: . LENGTH: 837 amino acids		9 2	ent Scores: No.:	Conservative:

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2167 CTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGGAGGGACGCCCCAGCCCCAGCT 2108	2107 GIGCAGCIACGCACCICAGCACAGGGTGGCAGCAGCAGAGAGCCACATTACTTTGGCAGC	2047	116	1987 CCCAGTGAGGAGGCCCTCCACCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGC 1928 136 lySerProGlyAlaProGlyThrPro	1927 CAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCC	145	1867 TGCGGCAGACACCATATAGGCAGTGACAGACTGGGTGAGCTGGACAATGGAGCCCATAAA	1807 CAGGGATGGGGCCACCTGGGACAGGAGGCAC		1768 CAGGATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCTGGC	186 roGlyThr	1720 CTCGGTGGGCTCACCACCACCACGACGAGGACATCACAGGCAG	1673 AGGCCCGGAGAGCGCGGGTGGAGGAGCAGGCAATAGCAACAACAACAACAACAACAACAACAACAACAACAACA	226 lySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaP	15	246 roGlyThrProGlyProGlnGlyLeuProGly-SerProGlyAlaProGlyThrPro 2	1553 CACTGCTAGCACCTCCA	265 Gly		CGGTGAGGCGGGTGAAGCTGTCACCACCACACACACACAC	294 oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrpr 309	CAAATAGACTGCTCGAGTGCCGAATCGCT			320 AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 339	12651239		1238 CATCATATGTCTCCGGGCCTCGGTGCCGGCTCAGCTCTGGGGCACGCCCTGGTACAGCC 1179 360 Proglégipnoglvalaproglyahrbr	
Qy Dp	O D	οy	<u>අ</u>	c c	ογ	qq	Oy Dp	Qy	qq	δŏ	QQ ·	Oy Dp	Qγ	qq	Οy	QQ	٥y	QQ ·	Oy Dp	οy	q	δλ	Q C	Οy	qq	ð	අ දි	e 5	

ΟŸ	1178	TAAAACAGCGTGAAGGTCATGAGTGCCATCCAGC 11	125
qu	379	lyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 39	94
Οy	1124	7	071
Dp	395	::: AlaProGlyThrProGlyProGlyCeuProGlySerProGlyAlaProGlyThrPro 414	14
Οy	1070	10	020
Dþ	415	GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 434	34
Qγ	1019	96	90
QQ	435		53
Qy	926	90	33
Д	454	 Gly 46	93
Qy	805	AGATGAGGGTGAGCCAAAGAGGCACTCCTCCTGGGTGCCCA 858	8
qq	464		33
ΟŊ	7	GGTAGGGGCCCAGGGCACTGGTGTCCAATGGCAGGCAGGAGGTAGCCCAGGAGC 798	8
qq	84	31yAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 500	0
οy	97	CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGT 741	-
qq	501	oro	
Qy	740	CCCGGAAGAGGTCAGAGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGA 684	4
QQ	512		,6
Qy	683 1	NGTCCAGCAGCCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCGGGG 624	4
QQ	530 7	AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGly 547	7
Qy	623 #		4
Db	548 1		÷.
Qy	563 4	AGGACAGTGCCCAGATGAAGGGCCGGCGGCGCCATAGCGTCCACGCCAGTGGTCAC 507	7
Db	562 0		1
Qy	506 T	TGGCTGAGCCTAAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCCAGCACCA 447	7
Dp	572 -		S
Qy	446 T		6
qq	586 G		2
Qy	398 C	CATAGGTGATGCCTGCGGCCAAACACGTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339	6
QQ	- 909	ly 61	6
Qy	338 A	GAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCTCACCCACAGCCTCTGGACCATAG 282	7
Dp	620 A	AlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr-Pr 639	σ.
Οy	281 T	GGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCT 225	10
Db	639 0	odlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlyLe 659	•
Οy	224 C	GGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAATCA 165	.0
Db	n 659	ProGlySerProGlyAlaProGlyThrProGly	
Qy	164 G	GCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCA- 106	

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US-08-175-155-68
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                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    659 oGlyThrProGlyProGlnGly-LeuProGlySerProGlyAlaProGlyThrProGlyP 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           317 GCAGCAGGCGCTCACCCACAGCCTCTGGACCATAGTGGGCCAGGCGGG---TAGGGCTC 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               556 ThrProGlyProGln-----GlyLeuProGlySerProGlyAlaProGlyThr 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        374 ACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGT---GCC 318
.106 AGAGCCGGCGCAGGGTGCGGGCATGCGGCACCACCT----GGTGCAGCCGGGGAA 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                 498 GlyProGlnGlyLeuProGlySerProGly-----AlaProGlyThrProGlyProGln 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 GCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACAC 483
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                                                                                                                                                                                                                                                                                                                                           833 CCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCAT 774
                                                                                                                                                                                                                                                                                                                                                                                                                 773 AGACAGAGTAGGCCTGGCGACAGTGGT --- CCGGGAAGAGGTCAGAGAGCA 720
                             381 GlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySer 400
                                                                                                                                                                                                      938 CAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAGA 879
                                                                                                                                                                                                                                         ------GlyLeuProGlySerProGlyAlaPro 449
                                                                                                                                                                                                                                                                                                           450 GlyrhrProGlyProGlnGlyLeuProGlySerProGly---AlaProGly----Thr 466
                                                                 .052 GCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGG---CCCGGCATGGACAGCAGTGGGGCG 996
                                                                                         995 ACAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCCT---CCT 939
                                                                                                                                                                     421 Thr -- - ProglyProglnGlyLeuProGlySerProglyAlaProGlyThrProglyPro 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645 yThrProGly------ProGlnGlyLeuProGlySerProGlyAla---Pr
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                                                                                                                                                                                                                                                                                                                                                                                467 ProGlyProGlnGlyLeuProGlySerProGlyAlaPro-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      719 GGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGCAGCACCACGCCCAGGA
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2347 GGGAAACCAGGTGACTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAA 2288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2287 CTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCGGCATTCC 2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 LeuProGly-----SerProGlyAlaProGlyThrProGlyProGlnGly 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 LeuproGlySerPro---GlyAlaPro-------GlyThrProGlyPro---GlnGly 88
                        95 CTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGC---CGAGGCGCGC 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Flehr, Hohbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                             Sequence 68 Application US/08175155
Patent No. 5641648
GENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
APPLICANT: Cappello, Joseph
APPLICANT: Cappello, John W.
APPLICANT: Cappello, Wary A.
TITLE OF INVENTION: Methods for Preparing Synthetic
TITLE OF INVENTION: Repetitive DNA
NUMBER OF SEQUENCES: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAEENTIN Release #1.0, Version #1.30
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-55186-5/BIR
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FILING DATE: 29-DEC-1993
CLASSIFICATION: 435
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TELEPHONE: 415-781-1989
TELEPAX: 415-389-3249
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I.
REGISTRATION UNMBER: 20015
REFERENCE/DOCKET NUMBER: 015
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356.50
35.16%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94111
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72GlyalaProGlyThrProGlyProGlnGlyLeu 82 2083 CAGGGTGGCAGCAGAGAGCCACATTACTTTGGCAGCAAAACTGGCGGCCAGCCGG 2024	2023 CAGCCCCATGGGGCTAACAGGAGCGGGAGCTGGGACCCAGGCCGCCCCCCCC		212 rodlyProdlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyL 232 1589 TAGGGCCTGGCAGGAAGCTGCTCACGGCTGCTCAGCCCCCCGTGTCCC 1530 1	1415 CCACGGCCACACTGTGGGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCA 1359	1265GCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGG 1215 326 ProGlyAlaProGlyProGlnGlyLeuProGlySerProGlyAlaProGly 345 1214 TGCCCGGCTCAGCTCTGGCACCCCTGCTACAATCCCTCGCCACGAATCCGTAAA 1155 1214 TGCCCGGCTCAGCTCTGGCCCTGCTACACCCCTCGCCCACGAATCCGTAAA 1155 146 ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 364 1154 ACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACACGCTCAGCCACGA 1107 :::
Db Qy Db	40 40 40 40 40 40 40 40 40 40 40 40 40 4	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 6 6 6 6 6 6	0 O O O O O O O O O O O O O O O O O O O	40 60 60 60 60 60 60 60 60 60 60 60 60 60
Db 679 roGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuP 698 Qy 38 GGCTGTCACCCGGAGCC 22 Db 698 roGlyCarProGlyAla 703	SULT 33 -08-397-633A-53 -68-397-633A-53 GENERAL INFORMATION: APPLICANT: Cappello, Josep TITLE OF INVENTION: PRODUC TITLE OF INVENTION: OF ENZ NUMBER OF SEQUENCES: 105 CORRESPONDENCE ADDRESS: ADDRESSEE: FLEHR, HOHBAC STREET: 4 Embarcadero Ce CITY. San Francisco	STATE: California COUNTRY: USA ZIP: 94111-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBW PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/397,633A FILING DATE: CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: ROALING BEFTIAM I RESISTRATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: 2,0015	TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 398-3249 TELEFAX: (415) 398-3249 TELEX: 910 277599 INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: TENGTH: amino acid STRANDEDNESS: single STRANDEDNESS: single STRANDEDNESS: single MOLECULE TYPE: protein Wolecule TYPE: protein STRANDEDNESS: SINGle STRANDEDNESS: Alignent SOCKES: SOCCES: SOCKES: SOCKES: SOCKES: SOCCES:	Pred. No.: 2.38e-19 Length: 829 Score: 357.00 Matches: 356 Percent Similarity: 34.78% Conservative: 33 Best Local Similarity: 30.81% Mismatches: 324 Query Match: 5.73% Mismatches: 219 DB: Gaps: 53 US-09-759-143-110 (1-3410) x US-08-397-633A-53 (1-829) QY 2320 GCTCCCAAAAACCCTTCTTAGGTGTCTCAACTAGGAGGCTAACCTGTTAACCCTG 2264 DD 32 AlaProflyWhrProflyGlughalbisHistorians.columnistics.	2263 AGCCTGGGTAATCCACTGCAGAGTCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTC ::: :::

CAGGGTGGCAGCAGCACTTACTTGGCAGCAACAGAAACTGGCGGCCAGCCCGG 2024	CTGTGTAGCAAAGTAAATGGCGACCAGGCCTGCGGCAGACACCATATAGGCAGT 1844	ACARIGAGECCATAAACAGGGATGGGGCCACCIGGGACAG 170:SerPro	CT 00	212	GTGGGAGCAGCCACCTCCAGCACCACGTGTCCATTAGGGAAGGGAGCTCCAGGCT 1590 ::: :::	TAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCC 1530 	CTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGCCCAGTG 1476 ::: :::	TGTAGGGCAGGATCTGCAGGGCTGAGAGGTGAACCCGGTGAGGCGGGTGAAGCTGTCA 1416 	CCAGGGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAACCTGCCA 1359 	CACTGGCCAAATAGACTGCTCGAGTGCCGAATGCTGCACCGGTCCATGACCAGAG 1299 	AGAAGACCAGGGAGATGGCGCACTGCAGGAACA	GCCCCAGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGG 1215	TGCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAA 1155 	AGTGCCATCCAGCTGCACAGCTCAGCCAGA 1107 :::
CAGGGTGGCAGAGAGCCACP 1 1 1 1 1 1 1 1 1 1	CTGTGTAGCAAAGTAAATGGCGA ro	GACAGACTGGCTGAGCTGGGCACAT 1yLeuProG1y CAGGAAGGCAC roG1yProG1nG1yLeuProG1y	GCCCCGGCCCC uproGlySerProGlyAlaPro	CCACCACACGIACGAGACAILACAGGCA 1yalaproglyThrproglyProglnGlyLe	GTGGGAGCACACTGCCTCC?	TAGGGCCTGGCAGGAAGCTGGT(: euProGly-SerProGlyA	CTCGGTATTTGGGCAGG :: : GlnGlyLeuProGlySerProG	TGTAGGGCAGGATCTGCAGGGC' GlySerProGlyA	CCACGGCCACACTGTGGGACAG	CACTGGCCAAATAGACTGCTCG	AGAAGACCAGGAGATGGCGCACTGCAGGAACA- GlyLeuProGlySerProGlyAlaProGlyThrP	GCCCCAGGCTGCCCAT ProGlyAlaProGlyThrProG	TGCCCGGCTCAGCTCTGGGCAC ThrProGlyProGlnGlyL	ACAGCGTGAAGGTCATGAGTGCCATCCAGC A::
2083 83 2023 102 1963	1903	84 14 78 15	1744	1/03	1649	1589	1529	1475 264	1415	1358	1298	1265 326	1214	1154 365
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	o o o	6 6 6	oy Dp	oy Db	Oy Dp	Ογ Db	Oy Dp	Qy Dp	Oy Db	Qy Dp	Qy Dp	Oy Dp	Oy Dp	Qy

QY	1106	AGAGCCGGCGCAGGGTGCGGCATGCGGCAGCACAGCTGGTGCAGCCGGGGAA 1053
QQ	381	GlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySer 400
Qy	1052	GCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGCCCGGCATGGACAGAGAGGGGGG 996
qq	401	ProdlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGly 420
Qy	995	co.
QQ	421	43
Qγ	938	MGCCACCAGGAGTGTGGCTGCTACGCAGGTGAGGATGAGGGTGAGGAGGCCAAAGA 87
Db	440	
Οy	878	CCTGGGTGCCCAGGTAGGGGCCCAGGGCACTGGTGT 83
Db	450	
Οy	833	SATCATGAAGGCAT
Db	467	ProGlyProGlnGlyLeuProGlySerProGlyAlaPro479
QY	773	AGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCA 720
qq	480	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 497
QY	719	GGGCCTCCAGTGGAGGACACACGGCCACAGAAGTCCAGCAGCCCCAGGA 660
QQ	498	GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln 515
Qy	629	TGAGCAGTGCCAGGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC
ДD	516	GlyLeuProGlySerProGlyAla528
Qy	599	54
qq	529	ProGlndlyLeuProdlySerProGlyAlaProGlyThrProGlyProGlnGlyLeu 547
Qy	542	GGGGCCATAGCGTCCACGCCAGTGGTCACT
qq	548	ProGlySerProGlyAlaProGly 555
Qy	482	AGACCAGGCCCAGCACTGGACCAATGCCCAGCACCATGGACTTCTCCTCTACCC 423
qq	556	ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThr 571
Qy	422	CCACITCCAGCAGCAGAGGGGGCACAIAGGIGAIGCCIGGGGCCCAAAC 375
QQ	572	ProGlyProGlnGlyLeuProGlySerProGlyAla
Qy	374	ACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTCGGCTTTCCGGTGCC 318
Db	286	ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln 605
QY	317	GCAGCAGCGGCTCACCCACAGCTCTGGACCATAGTCGGCCAGGCGGGTAGGGCTC 261
Db	909	GlyLeuProGlySerProGlyAlaProGlyThr-ProGlyProGlnGlyLeuProGlySe 625
Oy	260	-
Db	625	GlyalaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGl 6
Qy	200	CTCTCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGGC 141
Db	645	ΥŢ
٥y	140	CTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTG 96
QQ	629	oGlyThrProGlyProGlnGly-LeuProGlySerProGlyAla
Qy	95	CTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGCCGAGGCGCGC 39

693 ArgGlyAspProGly 697

qq

39 CGCTGTCACCCGGA 25

1) YPTOPTOGIYAL APPTOGIY PROALAGIY PROPROGIYS ETALGG CGGCCCTTCTGCTGGCTGGGTGGGCCCGGCGCTGCCT	GGLYProProGlyAlaProGlyPoGlyPoGlyPalaProGlyPoGlyAlaProGlyGCGCGCGCGTGGCGCGCGGGGGGGGGGGGGGGGGGGG	OProGlySerArgGlyAspProGlyPr 410	GGGGCCCAGGCTGCCT		: 8 :		Programmer 465 CCGGGTCCGGAAGAGGTCAG 7.26	 ProProGlySerArgGlyAspProGl 481	GTGGAGTGAAGCACACGCCACAG 685 GlySerArgGlyAspProGly 499			ProLysG1yAlaHisG1yFroAlaG1 535 GGCGGCCATAGCGTCCACGCCAGTGG 511	::: ProLysGlyAlaHisGlyProAlaGlyProLysGlyAlaHisGl 550	GGCCCAGCACTGGACCAATGCCCAGC 451	AGAGGCGGCACATAG	ALARKOGIY577 AAGGTTAGCAGGTTGACCAGCAAGAGC 334		GCGGGTCACCCACGC 295 ArgGlyAspProGlyProProGlyA1 611	AGGGGCCGTTCAGGCACTCCAGAAC 235		yProProGlyS 638	CCAGCCCTTGGTGCCGGTCCAGCTTCTCAGC 115		laproglyproAlaglypropro 672
		oGlyProProGlyAlaProGlyProAlaGlyProProGlySerArgGlyAspProGly	CTGGCTCGGT	CAGTGTGGCTGC	GCACT	CTGGTGTCCCAGTCAATGCCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCATG	GGCATAGACAGAGTAGGCCTGGCGACAGTGGTGGTCCGG	::: GlyAlaProGlyProAlaGlyProF	AGAGCAGGCCTCCAGTGGAGTGAAGCACCTGGCCACAG	AAGTCCAGCACCCCACGCCCAGGATGAGCAGTCCCAGCTCCAGGGGCCTGGGATCCGGG 	CACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGG	YFIOPFOGLYALAHISGIYPTOALAGLYPTOLYSGIYALAHISGIYPFOALAGI ATGCCCAAGGACAGTGCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGG	1	TCACTGGCTGAGCCTAGGAGCGGGGCACGAGCCCAGCACTGGACCAATGCCCAGC	ACCATGGTCATGAACTICTCCTCTACCCCCACTTCCAGCAGAGGGGGGCACATAG	rosiyətimiyətiymspiriosiyrioriosiyalar SATGCCTGCGGCCAAACACACCTCCAGGCCAAAGGT		GGCTTTCCGGTGCCCCAGCA	CTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGG ::: roGlyPro-AlaGlyProProGlySerArg	CTTCGTCTCGCTCTGCTCCAGAAGCTGCGCCTCT	GlyAlaProGlyProAlaGlyPro	CTAGGAATCAGCCAGGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGC	CCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACG	

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2320 GCTCCCAAAAACCCTTCTCTAGGTGTGTCT---CAACTAGGAGGCTAGCTGTTAACCCTG 2264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2143 TGGGGAGAGAGGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCA 2084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AspValGlySerProGlyAlaProGlyThrPro------GlyProGlnGlyLeu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: EPRRARI, Franco A.
APPLICANT: EPRRARI, Franco A.
APPLICANT: EPRRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
CONNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
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256
33
324
219
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Matches:
Conservative:
Mismatches:
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REGISTRATION NUMBER: 20,015
REGISTRATION NUMBER: 20,015
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 494-8700
TELEFAX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 829 amino acids
TYPE: amino acid
STRANDEDNESS: single
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RESULT 32
US-08-642-255-132
; Sequence 132, Application US/08642255
; Patent No. 5773249
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357.00
34.78%
30.81%
5.73%
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-642-255-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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1554 TCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGG 1495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .068 T-------GGTGCAGCCGGGGAAGCAGGCGCCCCAGGTTCC------ 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                               1668 CCGCAGAGCGCGGGTGGAGGTGGGAGCAGCCACTGCCTCCAGCACCCACGTGTCCATTA 1609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1608 GGGAAGGGAGCTCCAGGCTTA----GGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCC 1555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1353 GCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCGGT---CCATGACCAGAGAG 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1296 AAGACCAGGGAGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCA 1237
                                                                                                                                   1876 AC-------CCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGA 1830
                                                                                                                                                                                                              1829 GCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGA---AGGCAC 1773
                                                                                                                                                                                                                                                                                           --CCGGAACCACCC 1725
                                                                                                                                                                                                                                                                                                                                                                    1724 TGG----CCTCGGTGGGCTCACCCACCACC-ACACGTACGGAGACATCACAGGCAGAGGCC 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1494 TGGTAGAGGGAGGCCAGTGTGT-----AGGGCAGGATCTGCAGGGCTGAGAAGGTGAAC 1441
                                                        GTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAG 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 --GlyProAlaGlyProLysGlyAlaHis-GlyProAlaGlyProLysGlyAla-HisGl 298
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                                                                                             121 GlyProProGlyAlaProGlyProAlaGlyProProGlySerArgGlyAspProGlyPro 140
                                                                                                                                                                                                                                    158 ProProGlyAlaProGlyProAlaGlyProProGlySerArgGlyAspProGlyProPro 177
                                                                                                                                                                                                                                                                                                                                                                                                         178 GlyAlaProGlyProAlaGlyProProGlySerArgGlyAspProGlyProProGlyAla 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 yAspProGlyProProGlyAlaProGlyProAlaGlyProProGlySerArg-GlyAspP
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                      -----GlySer--
                                                                                                                                                                                                                                                                                           1772 TATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGC
340 yAlaProGlyProAlaGlyPro-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2254 AATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGTATAA 2195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: High Molecular Weight Collagen-Like TITLE OF INVENTION: Protein Polymers NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                                 E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1064
265
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296
286
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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Matches:
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NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 455556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/642,255
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TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 1064 amino acids
                      FERRARI, Franco A.
  CAPPELLO, Joseph
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33.26%
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CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                          California
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STRANDEDNESS: sin
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Best Local Similarity:
                                                                                                                                                                                                USA
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                                                                                                                 ADDRESSEE:
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  APPLICANT:
                                                                                                                                                                                                COUNTRY:
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uProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGl	15
TCTIGCTGGTCAACCTGTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGCATCACCT	395
GCCCTCTGCTGGTAGAGTGGGGTAGAGAGAAGTTCATGACCATGGTGCTGG 	455
3TCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACT	515
GGCGTGGACGCTATGGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGC	575
TGAGCCTCTTTCTCATCCCAAGGCCGGCTGGCTAGCAGGCTGCTGTGCC	526
GCCCCTGGAGCTGGCACTGCTCA: ::: GlyLeuProGlySerProGlyAlaProGlyThr	671
. H	719
22	755
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ACTG	291
AGGAGTGCCTCTTTGGCCTGCTCCTCACCTCTCCTCACCTGCGTAGCAGCCACACTGC	929
TGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCTT	989
CCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGCGG	1046
CCCIGCTTCCCCGGCTGCACCAGCTGTGCCGCATGCCCCGCACCCTGCGGCTGT	1106
TCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTT	1155 387
-TTACACGGATTTCGTGGGCGAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGC 11	1208
6 0 0 5 0 7 0 1 6 5 6 5 6 7 7 8 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8	TCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCCGCAGGCATCACCT yalaProGlyThrProGlyGlu

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1209 CGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCCAGCCTGGGGCT-- 1266
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                     519
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                                                                               480 oGlyProGlnGlyLeuProGlySerProGly-AlaProGlyThrProGly---ProGlnG 499
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559 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 578
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                                                           1267 ----GITCCIGCAGIGCGCCAICTCCCIGGICTICTCICTGGICAIGGACCGGCIGGIGC
                                                                                                                                                                                                                                                                                                                           539 GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGly
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                        406 oGlyThrProGlyProGlnGlyLeu-----
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Patent No. 5773249
GENERAL INFORMATION:
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349 Db 657 1106 Qy 1969 367 Ob 676	- 1155 QY e 387 Db	1208 US-(- 1266 r 421	1322 CORRESPONDENCES:	1382	- 1436 ; COMPUTER: KEJADELE FUKA:	1480 CURRENT APPLICATION APPLICATION FILING DATE	1515 CARSERICATION: 530 TATORNEY/AGENT INFORMATION: NAME: ROwland, Bertram I REGISTRARION NUMBER: 20,01	1570 ; TE	1624 ; 558 ;	1672 ; STRANDE TOPOLOG 578 ; MOLECULE	1687 Alignment Scores: 597 Pred. No.:	CC 1747 Secont Similarity: 33.95% Secont Similarity: 29.69% Court Match: 1.00 Co	1792 US-09-759-143- 632 US-09-759-143-	1852 646	1912	
331 rProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAl 1047 CCCTGCTTCCCCGGCTGCACCAGCTGCCGCATGCCCGCACCCTGCGCCGGTCT ::	1107 TCGTGGCTGAGCTGTGGAGCTGGATGGCACTCATGACCTTCACGCTGTT	1156TTACACGGATTTCGTGGGGGGGGGGGTGTACCAGGGCGTGCCCAGAGCTGTGAC 1111 111	1209 CGGGCACCGGGGGCCCGGGGCACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCT	1267GTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGCTGGTGC	1323 AGCGATTCGGCACTCGAGCATTTTGGCCAGTGTGCGGGTTTCCČTGTGGCTGCCG :::	1383 GTGCCACATGCCCACAGTGTGGCCGTGGTGACACCTTCAGCCGCCCTCA 11	1437	1481 GCCTCCCTCTACCACCGGAGAGCAGGTGTTCCT	1516GCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACC	1571 AGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCT	1625 GCTGGAGGCAGTGGCCTGCTCCCACCTCGCGGCGCTCTGCGGGGCC	1673TCTGCCTGTGATGTCC 111 111	1688 TCCGTACGTGGTGGTGGGTGACCCCACCGAGGCCCAGGTGGTTCCGGGCCGGGCATC	1748 TGCCTGGA	1793 GTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTAT	1853 ATGGTGTCGCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTT	1913 GACAAGAGCGACTTGGCCAAATACTCAGGGTAGAAAACTTCCAGCACATTGGGGTG
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ArgGlnAlaGlyAspValGlySerProGlyAlaProG 676
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C CROSS-LINKING
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.0, Version #1.25
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DB: US-09-759-143-110 (1-3410) x US-08-642-255-120 (1-762)	SCAGGTGTTG	Db 52 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro 71			Qy 171 CTAGGCAGTTGCCGGCAGCAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGA 230	AGCAGTTCTGGAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGT	Db 111 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyPro-GlnGlyLe 130	289	130	Qy 336 TCTTGCTGGTCAACCTGCTAGGCCTGGAGGTGTTTGGCCGCAGGCATCACCT 395	396 ATGRECOCTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTO	163 uGlyGlyAlaArgGlnAlaGlyAspValGly	Qy 456 GCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGGTCCTAGGCTCAGCCAGTGACCACT 515	Db 174SerProGlyAlaProGlyThrProGlyProGln 184	Qy 516 GGCGTGGACGCTATGGCCGCCGCCCTTCATCTGGGCACTTGGGCATCCTGC 575	TOT TOTAL TO	Oy 19 19 19 19 19 19 19 19 19 19 19 19 19	627 CGGATCCCAGGCCCCTGGAGCTGGCACTGCTCGGGCGTGG	211 OG1YPrOGING1yLeuPrOG1ySerProG1yAlaProG1yThrProG1yG1uG1	UY 6/2 GGCTGCTGGACTTCTGTGGCCAGGTTCACTCGTGGAGGCCC 719	Qy 720 TGCTCTCTGACCTCTTCCGGGACCC	Db 249.0GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyTh 266	QY 756 GCCAGGCCTACTCTATGCCTTCATGATCAGTCTTGGGGGCTGCTTGCT	Db 266 rProGly	816 TGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGG	Db 277 yAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro- 291	870	292	QY 930 TGGTGGCTGAGGGCAGCAGCTGGGCCCCAGCAGAGAGGCTGTCGGCCCCCT 989	066
Oy 269 GTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGGCTCTGGCTCCA 212 	Qy 211GAAGCTGCGGCCTCTTGCTGCCG 183	798	182 CCAACTGCCTAGGAATCAGCCAGGCGCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGC	818 OG1yProArgGlySerProGlyProGlnGlyValLySGlyGluSerGlyLysProGl	OY 122 TTCTCAG	Oy 92 TGGGGCACCTCAGTGGGACACGTCTCATCACTCAGATCCTGGC	ω	Oy 48	6	NESULY 29 US-08-642-255-120 ; Sequence 120, Application US/08642255	; Patent No. 5773249 ; GENERAL INFORMATION:	; APPLICANT: CAPPELLO, Joseph ; APPLICANT: FERRARI, Franco : : TTMTR OF INVERFIGUE. High Molecular Engight Collegent 1950	TITLE OF INVENTION: Protein Polymers , NUMBER OF SEQUENCES: 135	5 E	; STREET: 4 Embarcadero Center, Suite 3400 ; CITY: San Francisco ; STATE: California	210	88	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: Patentin Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA	APPLICATION NUMBER: US/08/642,255	CLASSIFICATION: 435 ATTORNY/AGENT INFORMATION: AMARE: PONTAND BOTTERM	RETERENCE/DOCKET NUMBER: 20,015; REFERENCE/DOCKET NUMBER: A55556-3/BIR	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (415) 494-8700	; TELEFAX: (415) 494-8771 ; TELEX: 910 277299 FHT UR	; INFORMATION FOR SEQ ID NO: 120; ; SEQUENCE CHARACTERISTICS:	; LENGTH: 762 amino acids ; TYPE: amino acid	EDNESS: GY: lir	MOLECULE TYPE: protein US-08-642-255-120	Scores:	FIGU. NO.: 0./e-20 Lengin: /62 Score: 364.00 Matches: 223 Percent Similarity: 33.95% COnservative: 32	ity: 29.69% Mismatches: 5.67% Indels:

QQ	214GlyGlnAr 221	ë	
٥y	2129 AGGACGCCCCAGCCCCCAGCTGCAGCTACGCACCTCAGCAGAGCACAGGGTGGCAGCAG 2070	δō	
qq		qa	513 GlyPr
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5 d		qa	564 GlyPr
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5 5		qa	584 ArgG1
3 3	orychy arakinatych y metartych	Qy	1013 ATGG
S &	1829 CC.1GGACCART GGAGCCCCATARACAGGGATIGGGGCCACCTGGGGCCAGCCAGCCAGGAGGCACCTT 1/3 284 A - - - - - - - - - - - - - - - - - -	qq	604 AlaAs
3 8		δō	959 TGGG
5 1		qu	618GJ
3 4	GLUMIAGGIYLIEKIOGIYVAIKIOGIYALALYSGIYGLUMSPGIYLYSMSPGIYLOGI	δ	899 TGAGO
Š á	1/51 GGCACATGCCCCGGCCCGGAACCACCTGGCTGGGCTCACCCACC	, qa	629 ProG
}	CHECOCOCOCC	δλ	842 CACTO
÷ 6		Db	647
3 3	GGIJAIGEGGGIJOGIVI GGIJVI GGIGGGIJVI GGGGGGIJVI TEGELGGIJGGEGGIJVI GGIJGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Qy	782 TGAAC
ζ d	GAGGIGGGAGCAGCCACIGCCICCACCACCACIATAGGGGTTTAGGGGTTCTATAGGGGTTCTATAGGGGTTCTATAGGGGTTCTATAGGGGTTCTATAGGGGTTCTAGGGTTCTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGTTGTAGGGGGG	qa	653A1
Q C	roalagiygiuarggiyAlarrosiyrroalagiyrroarggiyalaalagiygiur	ζŎ	728 CAGAC
δλ	CAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCAC	qa	672 GlyG]
OG O	377 roGlyArgAspGlyValProGly-GlyProGlyMetArgGlyMetPro 392	δλ	2222 899
θλ	1541 CTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG	: qa	
qa	393	λO	617 GCCC1
οy	1481 CCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAACCCGGTGAGGGCGGCGGTGAGG 1422	qq ·	711 GlyV
qa	404 ProGlyProProGlySer-GlnGlyGluSerGlyArgProGlyProProGlyProSe 422	۸٥	
λo i	CTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCACGGGAAAGCTG	QQ	723
g	<pre>rG1yProArgG1yG1nProG1yVa1MetG1yPneProG1yProLySG1yAsn</pre>	οy	497 CTAG
Qy	CCACACTGGCCAAATAGACTGCTCGAGTGCCTGCACCAGCGGGTCCATGACCA	qa	 728 ProG
QQ ·	AspGlyAlaProGlyLysAsnGlyGluArgGlyGlyProGlyGlyProGlyPro	QY	437 ACTIC
Vo	GAGAGAAGACCAGGGAGATGCCGCACTGCAGGAACAGCC	qa	: . 741 GlyAs
an .	GINGIYPTOPTOGIYLYSASNGIYGLUIYTGIYFTOGINGIYPTOPTOGIYFTOTNIGIY	Qy	377 AACAG
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513	yAlaProGlyAlaProGlyGlyLysGlyAspAlaGlyAla	532
1178	CACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACACACA	1119
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544		563
1058 564		1035
1034	COOCCCGGC	1014
584	LeuGlySerProGlyProLysGlyAspLysGlyGluProGlyGlyProGly	603
1013	CAAGGAGGGCCGACAGCCCTTCTGCTGGCTCGG	960
വ	GGGCCCAGCGCTGCCTCATCAGCCACAGCAGTGTGGGTGCTACGCAGGTGACGAAGA	0
-	GlyProlleGlyProProGlyProAla	~
899	36TGAGCAGGCCAAAGAGGCACTCCTCGGGTGCCCAGGTAGGGGGCCAGGG	843
629		646
842	GGTGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA	783
647	ArgGlySerProGlyGlu	652
782	SGAAGAGGT	
653	SlyGlnAsn	671
728	CCAGCAGCCCCA	699
672	31yGlyPro	691
668	GCACAGCA	61.8
692	lyProGln	710
617	CAAGGACA	558
711	ro	722
557	GGCTGAGC	498
723		727
497	CTAGGAGCGGGACACAGACCAGCACCAGCACTGGACCAATGCCCAGCACCATGATGA 4	438
728	ProGlyAlaArgGlyLeuProGlyProProGlySerAsn 7	740
437	ACTICICITACCCCCACTICCAGCAGCAGAGGCGGCACAIAGGIGAIGCCIGCGGCCA 3	378
741	GlyAsnProGlyProProSerGlySer7	751
377	AACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAAGGTTGGGGTTTCGGGTGC 31:	318
, ,	C CCCCTA DESCRIPTION OF THE CONTROL	
317	GCAGCAGCAGCCCACCCACACACTCTGGACCATACTGGGCCAGGCGG Z 	270

 roAlaGlyAsnThrGlyAla	767 Pro	GTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCCACA		211GAAGCTGCGGCCTCTCCTTGCTGCCG 183		CCCTTTGGTGCCGGT	818 oGlyProArgGlySerProGlyGlyGluGlyValLysGlyGluSerGlyLysProGl 837	TTCTCAG		92 FGGGGCACCTCAGTGGGGACACGTCTCATCACACGTCCTGGC	48		PRESURE 28 105-09-548-608-21 105-09-548-608-21 105-09-548-608-21 105-09-548-608-21 105-09-548-608-21 105-09-548-608-21 105-09-548-608-21 105-09-548-608-21 105-09-548-608-21 105-09-548-608 105-09-548-608 105-09-58-69-	INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 1078 amino acids
qa .	3 8	δý	qa	٥y	qq	οy	qq	Oy da	gr ·	Oy Dp	οy	qq	Pacquell Pac	INI ;

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2939 GGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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                                                                                                                                                                                                                                                                                                                                            73 ---AlaIleGlyProSerGlyProAlaGlyLysAspGlyGluSerGlyArgProGlyArg 91
                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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       TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                    364.50
30.79%
25.73%
                                                                                                                                                                                                                                     5.868
amino acid
                                                                                                                                                                                                                       Best Local Similarity:
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		Qy	1262 CCAGGCTGCCCATCC
δý	2249 ACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCTGTATAAGTCCA 2190	qu	
qa	200 oGlyAlaLysGlyGluValGlyProAlaGlySerProGly 213	ÀC	1202 CTCTGGGCACGCCCT
Qy	2189 GACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAG 2130	7 40	
qa	214GlyGlnAr 221	a :	
δλ	2129 AGGGACGCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAG 2070	δ :	
qa	:::	qq	
ò	2069 AGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC 2010	λō	1178 CCTCGCCCACGAAAT
; f	vProPro6 vI eAsn6 vSer	qq	533 ProGlyGluArgGly
3 8	TAACAGGAGGAGGAGCTGGGACCCAGTGAGGCAGGCCTCCACCCCAATGTGCTGGAAG	δλ	1118 GCTCAGCCACGAAGA
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ò	1889 AAATGGCGACCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGA 1830	λŏ	
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۸O		Qy	1013 ATGGACAGCAGTGGG
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δÿ		qa	618GlyProileGly
qq	304 GluAlaGlyIleProGlyValProGlyAlaLysGlyGluAspGlyLySAspGlySerPro 323	Ολ	899 TGAGGGTGAGCAGGC
Qy	1751 GGCAGATGCCCGGGCCCGGAACCACCTGGCTCGGTGGGCTCACCCACC	qa	 629 ProGlyAspLysGly
QQ	324 Gly-AspProGlyAlaAsnGlyLeuProGlyAlaAlaGlyGluAr 338	^0	
Οy	1691 CGGAGACATCACAGGCAGAGGCCCGCA	G qq	
qa	338 gGlyAlaLeuGlySerArgGlyProAlaGlyProAsnGlyIleProGlyGluLys-GlyP 358	3	782 TGAAGGCATAGACAG
Qy	1652 GAGGTGGGAGCACTGCCTCCAGCACCACGTGTCATTAGGGAAGGGAGCTC 1596	G	
ФФ	358 roAlaGlyGluArgGlyAlaProGlyProAlaGlyProArgGlyAlaAlaGlyGluP 377	3 8	
δý	1595 CAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCCTCACTAGCAC 1542	7 6	
QQ	 377 roGlyArgAspGlyValProGly-GlyProGlyMetArgGlyMetPro 392	20 5	
Qy	1541 CTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG	Š d	
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g O	IGIYRIOAIGGIYGIHRIOGIYVAIMECGIYFHERIOGIYFIODIYSGIYASH	Qy	497 CTAGGAGCGGGACAC
δ í	CCACACTGGCCAAATAGACTGCTCGAGTG	qa	 728 ProGlyAlaArgGly
aa	Aspelyalarrociylysasnelyetuargelyetyrtociyetyrlociyrto	٥٧	437 ACTTCTCCTCTACC
δλ	GAGAGAAGACCAGGGAGATGGCGCACTGCAGGA	Db	741 GlyAsnProGlyPro
qa	458 GlnGlyProProGlyLysAsnGlyGluTyrGlyProGlnGlyProProGlyProThrGly 477	٥٧	377 AACACACCTCCAGG

	1262	GAACGCCTTCATCATAGTGTCTCCGGGCCTCGGT
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	1202	CTCTGGGCACGCCCTGGTACA1182
	493	GlyProProGlyGluAsnGl
	1181	
	513	GlyproLysGlyGluAlaGlyAlaProGlyAlaProGlyGlyLysGlyAspAlaGlyAla 532
	1178	AACAGCGTGAAGGTCAT
	533	ProGlyGluArgGlyPro
	1118	GCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCCAGC
	1058	GGGGAAGCAGGCCCCAGGTTCC1035
	564	
	584	lyGluProGlyGlyProGly
	1013	ATGGACAGCAGTGGGGCGACAAGGAGGGGCCGACAGCCCTTCTGCTGGCTGGG 960
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	959 618	TGGGGCCCAGCGCTGCCTCCTCAGCACCAGCAGTGTGCTGCTACGCAGGTGAGGAAGA 900
	899	TGAGGGTGAGCAGGCCAAAGAGGCACTCCTGGGTGCCCAGGTAGGGGGCCAGGG 843
	629	ProGlyAspLysGlyGluGlyGlyAlaProGlyLeuProGlyIleAlaGlyPro 646
	842	CACTEGTCTCCCAGTCAATGGCAGGCAGGAAGTAGCCCAGGCAGCCCCCAAGACTGATCA 783
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	2	ArgGlyGluThrGlyProProGlyProAlaGlyPheProGlyAlaProGlyGlnAsn 6/
	728	CAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACAGGCCACAAAAGTCCAGCAGCCCCA 669
	692	ProGlyValAlaValProProGlyGlySerGlyProAlaGlyProGlyProGln 71
	617	
_	711	GlyvalLysGly722
	557	GTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGC 4
_	723	
	497	CTAGGAGGGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCCAGCACCATGGTCATGA 4
	728	ProGlyAlaArgGlyLeuProGlyPro
	437	ACTICICITIACCCCCACTICCAGCAGAGGGGGGCACATAGGTGATGCCTGGGGCA 37
	741	GlyAsnProGlyProProSerGlySer
	377	AACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCC 318

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1939 GGAAGTGGGGGGAACCAGGCTGGGCCAAGAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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290
57
354
426
62
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                               GANISM: Homo sapiens
DIATE SOURCE:
ONE: COLLAGEN ALPHA 1 (III)
-573-21
DECOMMUNICATION INFORMATION:
PELEPHONE: 212-527-7700
PELEFAX: 212-753-6237
PELEX: 236687
WATION FOR SEQ ID NO: 21:
QUENCE CHARACTERISTICS:
ENGTH: 1078 amino acids
YPE: amino acid
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364.50
30.79%
25.73%
5.86%
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ECULE TYPE: protein
GINAL SOURCE:
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3 TAAGGGGCTTAGAGATGGGAAACCAGGTGACTTGAGTTTATTCAGCTCCCAAAAA 2310 	CCCTTCTCTAGGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCC		9 ACCTGCAGAGTCCCCGCATTCCAGTGCATGCAGCCCTTCTGGCCTCCCTGTATAAGTCCA 21		9 GACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGGGG 2130		1 gGlyGluProGlyProGlnGlyHisAlaGlyAlaGlyProProGl 237	AGAGCCACATTACTTTGGCAGCAACAACAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC	YELOFIOGLY LICENSHIGHYDGI TAACAGGAGGAGGAGAACCAACTAAGGAAGCAAGCCTTCACCCAA	:: ::	TTTTCTACGCT	1:: 		3 GlyAlaAsnGlyAlaProGlyLeuArg		4 AlaGiyGluProGlyLysAsnGlyAlaLysGlyGluProGlyProArgGlyGluArgGly 303	2	GluAlaGlyIleProGlyValProGlyAlaLysGlyGluAspGlyLysAspGlySer			1 CGGAGACATCACAGGCAGAGGCCCGCA		GAGGTGGGAGCACTGCCTCCAGGACCCACGTGTCCATTAGGGAAGGGAGCTC		5 CAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCAC 1542		1 CTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG			4 ProGlyproProGlySer-GlnGlyGluSerGlyArgProGlyProProGlyProSe 422	1 CTGTCACCACGCCACACTGTGGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTG 1362		1 CCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCGGCCGG
2363	2309	18	224	200	2189	2129	221	2069	2009	248	1949	261	1889	273	1829	284	1772	304	1751	324	1691	338	1652	358	1595	377	1541	393	1481	404	1421	422	1361
Qy	Qy	qa	ογ	යි	Qy Db	QY	QQ	6 6	3 8	qa	٥y	qq	δλ	qq	Qy	qa	οy	qq	٥y	qa	Οy	QQ	δλ	ΩQ	Qy	qq	Οy	QQ	٥y	Ωp	δλ	qa	ογ

QQ	440	::: AspGlyAlaProGlyLysAsnGlyGluArgGlyGlyProGlyGlyProGlyPro 457
Qy	1301	GAGAGAAGACCAGGGAGATGGCGCACTGCAGGAACAGCC 1263
Db	458	::: GlnGlyProProGlyLysAsnGlyGluTyrGlyProGlnGlyProProGlyProThrGly 477
Qy Db	1262	CCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTTCTCCGGGCCTCGGTGCCCGGCTCAG 1203
Qy	1202	CTGGGCACGCCTGGTACA11
qq	493	 LeuGlnGlyLeuProGlyThrGlyGlyProProGlyGluAsnGluLysProGlyGluPro 512
Qy	1181	900 1179
qa	513	GlyProLysGlyGluAlaGlyAlaProGlyAlaProGlyGlyLysGlyAspAlaGlyAla 532
0y	1178	CCTCGCCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACA 1119
· qa	533	ProdlyGluArgGlyPro
oy.	-	CTCAGCCACGAAGAGCGGCGCGGGGTGCGGGGCATGCGGCAGC
qq	544	ProGlyLeuArgGlyGlyAlaGlyProProGlyProGluGlyGlyLysGlyAlaAl
0y	in (AAGCAGGCCCAGGTTCC10
an	204	ıyrıor
Qy	1034	GGAAAGCCAAGCCCGGC 1014
Dp	584	ArgGlyGlyLeuGlySerProGlyProLySGlyAspLySGlyGluProGlyGlyProGly 603
Qy	1013	ATGGACAGCAGTGGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGCTCGG 960
QQ	604	
Qy	959	AGCAGTGTGCTGCTACGCAGGTGA
Db	618	GlyProlleGlyProPtoGlyProAla
Qy	899	CCTCCTGGGTGCCCAGGTAGGGGGG
QQ	629	ProGlyAspLysGlyGluGlyGlyAlaProGlyLeuProGlyIleAlaGlyPro 646
٥y	842	CACTGGTGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 783
qa	647	
Οy	782	-cccggy
Db	653	ArgGlyGluThrGlyProProGlyProAlaGlyPheProGlyAlaProGlyGlnAsn 671
Qy	728	CAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGAGTCCAGCAGCGCCCA 669
Db	672	GlyGluProGlyGlyLysGlyGluArgGlyAlaProGlyGluLysGlyGluGlyGlyPro 691
οy	668	CGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCA 618
Db	692	ProGlyValAlaValProProGlyGlySerGlyProAlaGlyProProGlp 710
Οy	617	GCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCAAGGACA 558
Db	711	GlyValLysGly 722
Qy	557	GTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCCAGTGGTCACTGGCTGAGC 498
QQ	723	
Qy	497	CTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATGA 438

49 72 43 74 74 74 74 74	741 GlyAsnProGlyProProGlyProSerGlySer	1 1 1 1 1 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	122 TTCTCAG	13.1-21 21, Application US/09500811 21, Application US/09500811 21, Application US/09500811 22, 6323314 21
6 a 6 a 6	5 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	\$ 6 \$ 6 \$ 6 \$ \$	60 63 69 69 69 69 69 69 69 69 69 69 69 69 69	RESULT 26 US-09-500 (Sequence) Sequence) GENERAL I APPLICANTITLE TITLE TITLE TITLE TITLE TITLE CORRECTOND STRAIN STRAIN STRAIN STRAIN COMPUT MEDI MEDI MEDI MEDI MEDI MEDI MEDI MEDI

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2939 GGAAGTGGGGGAACCAGGCTGGCCCAAGAGAGGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2819 TTATCATTIGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCCAGA 2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2759 CCCCAGGAGAAGAATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGGGGACCT 2700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2603 ATATTTAAATGCCTGTGTCTCTGTGATGGCAACAGAAGGACCAACAGGCCACATCCTGAT 2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2699 GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAACACAGA------ 2651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2543 AAAAGGTAAAGAGGGGGGGGGGGGATCAGCAAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGT 2484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2483 TCTTGTGTGTTGCCCCTCAGGACTCTTCCCCTACAAATAAGTCATATGTTCAAATCCCAT 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 ProGlyAspArgGlyLeu--------ProGlyProProGlyIleLysGlyPro 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 Ala-----Glylle-ProGlyPheProGlyMetLys---GlyHisArgGlyPheAspGl 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2423 GGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT 2364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 yArgAsnGlyGluLySGlyGluThrGlyAlaProGly--------LeuLy 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 sGlyGluAsnGlyLeuProGlyGluAsnGlyAlaProGlyProMetGlyProArgGlyAl 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 GlySerProGlyTyrGlnGlyProProGlyGluProGlyGlnAlaGly---ProSerGly 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 --- AlalleGlyProSerGlyProAlaGlyLysAspGlyGluSerGlyArgProGlyArg 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-759-143-110 (1-3410) x US-09-500-811-21 (1-1078)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
                                                                   NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,319
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                           CLONE: COLLAGEN ALPHA 1 (III) US-09-500-811-21
                                                       ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
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30.79%
25.73%
5.86%
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score:
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		QQ	404 ProGlyProPro
qa	175 175	ò	1421 CTGTCACCACGGCCAC
ογ	2423 GGAGGAGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT 2364	G 6	
qa	175 175	3 3	4 0
Qy	2363 TAAGGGGCTTAGAGATGGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAA 2310	3 E	
qq	176 -AspGlyAlaArgGlySerAspGlyGlnProGly	3 8	
Qy	2309 CCCTTCTCTAGGTGTCTCTCAACTÀGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCC 2250	G Q	458 GlnGlyProProGly
qa	189 yProProGlyThrAlaGlyPhePro	^0	1262 CCAGGCTGCCCATCC
Qy	2249 ACCTGCAGAGTCCCCGCATTCCAGTGCAGGCCCTTCTGGCCTCCTGTATAAGTCCA 2190	g qa	478 ProGlyGlyAspLys
qo	200 oGlyAlaLysGlyGluValGlyProAlaGlySerProGly	٥	1202 CTCTGGGCACGCCCTC
QY	2189 GACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCGCCTAGAGACTGGGGAGAGGAG 2130	QQ	
QO	214GlyGlnAr 221	ò	
ογ	2129 AGGACGCCCCAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAG 2070	7. qq	513 GlyProLysGlyGlu
qa	221 gGlyGluProGlyProGlnGlyHisAlaGlyAlaGlnGlyProProGl 237	۸٥	1178 CCTCGCCCACGAAAT
δ	AGAGCCACATTACTTTGGCAGCAACAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC	- qa	
q	237 yProProGly1leAsnGlySer247	ō,	1118 GCTCAGCCACGAAGA
Qy	2009 TAACAGGGGGGGGGGGGCTGGGACCCAGGGGGGGGGCCCTCCACCCCAATGTGCTGGAAG 1950	- q0	
qq	248LysGlyGluMetGlyProAlaGlyIleProGlyAlaPro 260	ò	
Qy	1949 ITITCTACGCTGAGTATITGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGT 1890	5 2	
qa	261GlyLeuMetGlyAlaArgGlyProProGlyProAla 272	2 6	
Qy	1889 AAATGGCGACCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGA 1830	5 6	584 ArgGlvGlvLenGlv
QQ	273 GlyAlaAsnGlyAlaProGlyLeuArg	2 3	
ογ	1829 GCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAGGCAC 1773	δλ -	
qq	::: 284 AlaGlvGluProGlvLvsAsnGlvAlaLysGlyGluProGlyProArgGlyGluArgGly 303	gg	604 AlaAspulyvalrio
3 8	:	Qy	959 TGGGGCCCAGCGCTG
S 6		qa	618GlyProlleGly
o C	GIUALdelyllerioslyvalrioslynalaryselyslunsperjeyslyslerios	٥٧	899 TGAGGGTGAGCAGGC
δλ	GGCAGATGCCCCGGCCCGGAACCACCTIGGCCTGGTGGGCTCACCACCACCACATA	qa	629 ProGlyAspLysGly
QQ O	Gly-AsperoGlyAlaAsnGlyLeutroGlyAlaAlaGly:GluAl	Oy	842 CACTGGTGTCCCAGT
δλ	CGGAGACATCACAGGCGCGCGCGCA	qq	647
qa	gGlyAlaLeuGlySerArgGlyProAlaGlyProAsnGlyIleProGlyGluLys-GLyP	ΟŊ	782 TGAAGGCATAGACAG
Qy		qq	
qa	roAlaGlyGluArgGlyAlaProGlyProAlaGlyProArgGlyAlaAlaGlyGluP	δδ	728 CAGAGAGCAGGGCCT
δŏ .	CAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCAC	qa	672 GlyGluProGlyGly
qa	roGlyArgAspGlyValProGly-GlyProGlyMetArgGlyMetPro	oy	668 CGCCCAGGATGAGCA
Qy	rccagtgtcccctcggtatttggccaggaaCacctgcttctcccggtggtagagggagg	qa	 692ProGlyValAla
qa	GlySerProGlyGlyProGlySerAspGlyLys	Qy	617 GCCCTGCTAGCCAGC
Οy	1481 CCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAGGTGAACCCGGTGAGGCGGCGGCTGAAG 1422	qa	::: 711 GlyvalLysGly

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CCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACA 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCGGCGCAGGGTGCGGGCATGCGGCAGCACAGCTGGTGCAGCC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GAAAAGCCAAGCGGCCCGGC 1014
                                                                                                                                                                                                AGATGGCGCACTGCAGGA-------ACAGCC 1263
                                                                                                                                                                                                                                                                               SAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAG 1203
                                                                                                                                                                                                                                                                                                                                                              3GTACA----- 1182
                                       CACTGTGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTG 1362
                                                                                                                    AGACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGTCCATGACCA 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |||
| AlaGlyAlaProGlyAlaProGlyGlyLy8GlyAspAlaGlyAla 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||||
|GlyGlyAlaGlyProProGlyProGluGlyGlyLySGlyAlaAla 563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerProGlyProLysGlyAspLysGlyGluProGlyGlyProGly 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCGACA----AGGAGGGGCCGACAGCCCTTCTGCTGGCTCGG 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAAGAGGCACTCCTGGGTGCCCAGGT---AGGGGGCCAGGG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATGGCAGGCAGGAAGCCCAGGCAGCCCCCAAAGACTGATCA 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTAGGCCTGGCGACAGTGGT---CCGGGT---CCCGGAAGAGGT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCCAGCTCCAGGG------GCCTGGGATCCGGGCACAGCA 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValProProGlyGlySerGlyProAlaGlyProProGlyProGln 710
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                                                                                                                                                                                                                                                                                                        GlyThrGlyGlyProProGlyGluAsnGluLysProGlyGluPro 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlySer-GlnGlyGluSerGlyArgProGlyProProGlyProSe 422
                                                                    SInProGlyVal---MetGlyPheProGlyProLysGlyAsn--- 439
                                                                                                                                        LysAsnGlyGluTyrGlyProGlnGlyProProGlyProThrGly 477
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A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
1409 GCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTG 1468
                                                                                                                                                             1516 ------GCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGAG
                                                                                                                                                                                                                                           1559 AGCCIGAIGACCAGCTICCIGCCAGGCCCT----AAGCCIGGAGCICCCTICCCTAAT 1612
                                                                                                                                                                                                                                                                                                                           1613 GGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCACCTCCACCGGGGCTCTGCGGGGCC 1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCGGGGCATCTGCCTGGA------CCTCGCCATCCTGGA---TAGTGCCTTC 1780
                                                                                                                                                                                                                                                                                                                                                                                                                        ----TCT 1675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1676 GCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCG 1735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1781 CTGCTGTCCCAGGTGGCCCCATCCCTGTTATGGGCTCCATTGTCCAGGTCAGCTCAGTCT 1840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      841 GICACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGC-----CATTTACTTT 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .895 GCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCC 1954
                                  481 yPro-----GlnGlyLeuProGlySerProGlyAlaProGly-ThrProGlyPro---- 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1955 AGCACATIGGGGIGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGGCTCCTGTIAGCCCC 2014
                                                                                                                                                                                                                                                                                  535 ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln 554
                                                                                                                                                                                                                                                                                                                                                       575 ProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaLysGln 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GlyAlaProGlyThrProGlyGluGlyGlnGlnHisHisLeu---- 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              498 ------GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnG
                                                                                                                                                                                     515 lnHisHisLeuGlyGlyAla-LysGlnAlaGlyAspValGlySerProGlyAlaProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               628 roGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 ------GlyGly-----AlaLysGlnAlaGlyAspValGlySerProGlyAlaProG
                                                                             1469 CCCTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/08963825
Fatent No. 6110689
GENERAL INFORMATION:
APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: in Body Fluids,
TITLE OF INVENTION: in Body Fluids,
TITLE OF INVENTION: in Body Fluids,
TITLE OF INVENTION: in Body Fluids,
TITLE OF INVENTION: Disorders Associated the companies of SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2015 ATGGGGCTGCCGGGCTGGCCG 2035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696 GlnGlyLeuProGlySerPro 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Darby & Darby PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 805 Third Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10022
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2939 GGAAGTGGGGGAACCAGGCTGGGCCAAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 ProGlyAspArgGlyLeu-------ProGlyProProGlyIleLysGlyPro 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 GlySerProGlyTyrGlnGlyProProGlyGluProGlyGlnAlaGly---ProSerGly 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 --- AlalleGlyProSerGlyProAlaGlyLysAspGlyGluSerGlyArgProGlyArg 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 yArgAsnGlyGluLysGlyGluThrGlyAlaProGly--------LeuLy 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 ProProGlyProProGly------
                                SOFTWARE: Patentin Release #1.0, Version #1.25
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Matches:
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                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
                                                                                                                CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                             US/08/963,825
IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
CLONE: COLLAGEN ALPHA 1 (III)
                                                                                                                                                                                                                                           29,714
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INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
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30.79%
25.73%
5.86%
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                                                                                                                                                                                                                       NAME: Gogoris, Adda C
REGISTRATION NUMBER: 2
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                                                                         APPLICATION NUMBER: FILING DATE:
                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity:
Query Match:
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TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING NUMBER OF SEQUENCES: 105
                         STREET: 4 EMDARCAGE SOLIE 3400 CITY: San Francisco STATE: California
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                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 4-58448-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELERAX: (415) 788-3249
TELEX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 26:
SEQUIBCE CHARACTERISTICS:
                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
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Indels:
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Matches:
                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,633A
                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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365.00
35.02%
30.09%
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                               NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
                                                                                                                          Y: USA
94111-4187
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Best Local Similarity:
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1209 CGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGCT-- 1266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 yAla------ProGlyThrProGlyProGlnGlyLeuProGlySerPro- 291
                                                                                                                                                                                   ......GlyLeuProGlySerProGl 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1107 TCGTGGCTGAGCTGTGCAG-----CTGGATGGCACTCATGACCTTCACGCTGT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 rProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 rProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla---Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 yGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAlaPr
456 GCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACT
                                 174 -----SerProGlyAlaProGly---ThrProGlyProGln------
                                                                                                                          516 GGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                              576 TGAGCCT----CTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCT-----GTGCC
                                                                                                                                                                                                                                                                                                                                                                                627 CGGATCCCAG------GCCCCTGGAGCT---GGCACTGCTCATCCTGGGCGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCC-----
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AGTTCTGGGGCCCCCTGAGCCCTGCCCCCCCTGGCCCCCCTGTGGT-	131 AGCAGTTCTGGAGTGCCTGAACGCCCCTGAGCCCTACCCCCCTGTGGTT-1111 11 11
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qa		
Oy	CTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGC 13	•
QQ	441	
Qy	TCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTT	_
qa	441 uGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAl 461	
Qy	1370 CCTGTGGCTGCCGGTGCCTGTCCCACAGTGTG 1408	
qq	УР-	
Qy	1409 GCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTG 1468	
qq	481 yProGinGlyLeuProGlySerProGlyAlaProGly-ThrProGlyPro 497	
, 0 y	1469 CCCTACACACCACCCCCCTCTACCACGGGAGAAGCAGGTGTTCCT 1515	
qa	498GlndlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnG 515	
ΟŊ	1516	
qq	515 lnHisHisLeuGlyGlyAla-LysGlnAlaGlyAspValGlySerProGlyAlaProGly 534	
Qy	GCCTGATGACCAGCTTCTGCCAGGCCCTAA	
QQ	535 ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGln 554	
QŸ	O	
Ор		
Qy	1673TCT 1675	
QQ	575 ProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaLysGln 594	
δy	1676 GCCTGTGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCG 1735	
qq	595 AlaGlyAspValGly-SerProGlyAlapro-GlyThrProG 608	
Qy	GCCGGGGCATCTGCCTGGACCTCGCCATCCTGGA	
QQ	608 lyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuP 628	
οy	AGCTCAGC	
Dp	GlySerProGlyAlaPr	
Οy	1841 GICACTGCCTATAIGGIGTCTGCCGCAGGCCTGGGTCTGGTCGCCAITTACTIT 1894	
Db	647GlyAlaProGlyThrProGlyGluGlyGlnGlHisHisLeu 660	
Οy	ATTTGACAAGA	
QQ	661GlyGlyAlaLySGlnAlaGlyAspValGlySerProGlyAlaProG 676	
Qy	CACTGGGTCCCAGCTCCCGGCTCCTGT	
qa	676 lyThrProGlyProGlyLeuProGlySerProGlyAla-ProGlyThrProGlyPro 695	
Qy	2015 ATGGGGCTGCCGGCTGGCCG 2035	
qa	696 GlnGlyLeuProGlySerPro 702	
RESULT COS-08-30 Sequence Cost Patent Cost Cost Cost Cost Cost Cost Cost Cos	24 397-633A-26 ence 26, Application US/ 1t No. 5773577 ERAL INPORMATION:	
, AF	Pricant: Cappello, Joseph	

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----TGGCAGAAATGGGCGCCTGGC-----TGATTC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STTGGCGGCAGCAAGGAGGAGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACAGCAGCAGGTGTTG-----AGCATGGGCTGAGAAGCTGGACCGGCACCA 137
PAELLO, Joseph
ARARI, Franco A.
TION: High Molecular Weight Collagen-Like
TION: Protein Polymers
ENCES: 135
ADDRESS:
FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
Pharcadero Center, Suite 3400
Gancisco
                                                                                                                                                                                                                                                                                                      SLE FORM:
Floppy disk
NFC compatible
STEM: PC-DOS/MS-DOS
TEM: PC-DOS/MS-DOS
TEM: Release #1.0, Version #1.30
TION DATA:
UMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  D, Bertram I.
NUMBER: 20,015
KET NUMBER: A55556-3/BIR
ON INFORMATION:
415) 494-8770
77299 FHT UR
EQ ID NO: 114:
                                     GCCGGGCTGGCCG 2035
                                                                                                              ation US/08642255
                                                   5.62e-20
365.00
35.02%
30.09%
5.69%
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990 CCTTGTCGCCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCG---GAACCTGGGCG 1046
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91 LeuGlyGly---AlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPro 109
                                          GGTGCCCCACAGCAGCAGGTGTTG-----AGCATGGGCTGAGAAGCTGGACCGGCACCA 137
                                                                                                                                                                                171 CTAGGCAGTIGGCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGA 230
                                                                                                                                                                                                                                                      231 AGCAGTTCTGGAGTGCCTGAACGGCCCCTGAGCCCTACCCGCCTGGCCCACTATGGT-- 288
                                                                                                                                                                                                                                                                            289 -------CCAGAGGCTGTGGGTGAGCCG---CCTGCTGCGGGCACCGGAAAGCCCAGC 335
                                                                                                                                                                                                                                                                                                                                                  336 TCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCT 395
                                                                                                                                                                                                                                                                                                                                                                                                                   149 yAlaproGlyThrProGlyGlu-------GlyGlnGlnHisHisLe 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 ATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAAGATCATGACCATGGTGCTGG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 aGlyAspValGlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySe 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 GGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGC 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----GlyLeuProGlySerProGl 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 oGly-----ThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyTh 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            756 GCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCC 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                816 TGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCC-----CTACCTGGGCACCCAGG 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        930 TGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCT 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHis 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 GCATTGGTCCAGTGCTGGGCCTGGTCTGTGCCCGCTCCTAGGCTCAGCCAGTGACCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SerProGlyAlaProGly---ThrProGlyProGln-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   672 G------GCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       870 AGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 uGlyGlyAlaLysGlnAlaGlyAspValGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         720 TGCTCTCTGACCTCTTCCGGGACCC----------
     US-09-759-143-110 (1-3410) x US-08-707-237A-84 (1-761)
                                                                                                          138 AAGGCC-----TGCCAGAAATGGGCGCCTGGC-----
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662 erProGlyAlaMet-AspProGlyArg 670
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626

671

191 ySerProGlyAlaProGlyThr: 1041 AGGTTCCGGAAAGCCAAGCG 11	ySerP	### ### ##############################	500 uProGlySerProGlyA 645 TCCAGGGCCTGGGATCCGGGCA :	533 pvaldlySerProdlyAlaProd 528 TAGCGTCCAGGCCAGTGGTCACT 551	408 AGAGGGGCACATAGGTGATGCC 569 a	243 CTCCAGAACTGCTTCGTCTCGGC
9 6 6 9 6	, da 6	00 00 00 00 00 00 00 00 00 00 00 00 00	Db Qd Qy	90 60 60	60 00 00 00 00 00 00 00 00 00 00 00 00 0	9y da 9y da
2045	1880 CCAGACCCAGGCCTGCGGCAGACACCATATAGGCAGACAGA	1772	AlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrProGlyProGlnGly CTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGAGCTCCAGGCTTAGGCCTGGCAGG	rprodiyalaprodiythrProdiy	281 pValG1y	1254 CCCATCCGAACGCCTTCATCATAGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTG 1198
6 6 6 6	99 90 90 90	6 6 6 6	a da da da	5 8 8 8 8		6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6

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	41 NORMOG - CANANGOS, SECTION OF THE	
3 8	4.1 westructors-SevanderdadergegecenegeRegecageGegegegegegegegegegegegegegegegegegeg	
٥y	4 GCCGACAGCCCTTCTGCTGGCTCGGTGGCCCCAGGGCTGCCTGCTCTCAGG	
qa	 Pro 44	
ογ	ATGAGGGTGAGGCCAAAGAGGCACTCCT 87	
qq	442GlyAlaProGlyThrProGlyProGlnGlyLeuProGl 454	
δō i	69CCTGGGTGCCCAGGTAGGGGCCAGGGCACTGGTGTCCCCAGTCAATGGCAGG	
qo ,	54 ySerProGlyAlaProGlyThrProGlyGlyAlaLySGlnAlaG	
ογ γ	13 AGGTAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCATAGACAGAG	
aa a	48	
d d	0	
QY	64	
QQ	51	
٥y	SAGA 58	
Db	53	
Qy	3CCA 52	
QQ	55	
Οy	SGCCCAGC 4	
Dp	56	
Qy	Ω -4	
Dp	9	
Qy Db	34	
ογ	introctyriocinclybeuriot, 5	
qq	80	
ΟY	300 CACAGCCICTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGGCCGTTCAGGCA 244	
QQ	600 oGlyalaProGlyThr-ProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyT 620	
. о	43 CTC	
Q O	0 hrProG	
Qy Dp	GGTGCCGGTCCAG 12	
λo	23 CTTCTCAGCCCAATGCTCAACACCTGCTGCTGCTGCTCCAACACACAC	
· 43	51 roGly	
Ϋ́C	OO CATALOGATICATION 46	
qc	662 erproGlyalaMet-AspProGlyArg 670	

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2314 AAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGT 2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2209 GGCCTCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCT 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2149 AGAGACTGGGGAGAGGAGGACGCCCCAGCCCCCAGCTGTGCAGCTACGCACCTCA 2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2089 GCA-----GCACAGGGTGGCAGCAGAGAGCCACATTACTTTGGCAGCAA----- 2046
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12 GludsnPro-----GlyValThrGlnLeuAsn------ArgLeuAlaAlaHis 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 ProProPheAlaSerAspProMetGlyAlaProGlyThrProGlyProGlnGlyLeuPro 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 ------GlyAlaProGlyThrProGlyBroGlnGlyLeuProGlySerProGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2254 AATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682
249
444
294
246
56
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATE: Patentin RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/397,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-759-143-110 (1-3410) x US-08-397-633A-36 (1-682)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                      FILING DATE: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETLEAM I
REGISTRATION NUMBER: 20,015
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH : 682 amino acids
TYPE: amino acids
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                                                                                                                                                                     CITY: San Francisco
STATE: California
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Best Local Similarity:
Query Match:
DB:
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US-08-397-633A-36
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1095 AGGGTGCGGGGCATGCGGCAGCAGCAGCTGGTGCA-----GCCGGGGAAGCAGGGGGCCC 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1515 AGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGGCCA-----GTGTGTAGGGCAGGATC 1462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1461 TGCAGGGCTGAGGAGGTGAACCCGGTGAGGGGGGGCTGAAGCTGTCACCACGGCCACACTG 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1254 CCCA----TCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTG 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .143 GTCATGAGTGCCATCCAGC-----TGCACACACCTCAGCCACGAAGAGCCGGCGC 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1635 CTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGCAGG 1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1401 TEGGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACT 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1341 GCTCGAGTGCCGAATCGCTGCACCAGCGGTCCATGACCAGAGAAGAAGACCAGGGAGATG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1197 GGCACGC-----CCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAG 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1733 GAACCACCCTGGCCTCGGTG-----GGCTCACCCACCACCACCACGTACG------ 1690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1575 AAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGC 1516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 rProGlyAlaProGlyThrProGly----- 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 SerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 -----ProGlySerProGlyAlaProGlyThrProGlyGlyAlaLySGlnAlaGlyAs 281
100 GlyThrProGlyProGlyDeuProGlySerProGlyAlaProGlyThrProGlyPro 119
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158 ---Serpro------GlyAlaProGlyThrProGlnGlyLeuProGly 172
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                                                                                                          120 GlnGlyLeuProGlySerProGlyAlaProGlyThrPro----
                                                                                                                                                                                             -----GlyProGlnGlyLeuPro----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------CAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAG 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2314 AAAAACCCTTCTTAGGTGTGTTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGT 2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2209 GGCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCCT 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2149 AGAGACTGGGGAGAGGAGGAGGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCA 2090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProproPheAlaSerAspProMetGlyAlaProGlyThrProGlyProGlnGlyLeuPro 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ------GlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGly 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 AlaProGlyThrProGlyGlyAlaLySGlnAlaGlyAspValGlySerProGlyAlaPro 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 GluAsnPro-----GlyValThrGlnLeuAsn------ArgLeuAlaAlaHis 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2254 AATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCT----
                                                                                          APPLICANT: CAPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-759-143-110 (1-3410) x US-08-642-255-126 (1-682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REGERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                             Sequence 126, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFANCE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 126:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.04e-20
370.50
35.26%
29.96%
5.95%
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TYPE: amino acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  RY: USA
94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-642-255-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
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	, do	1061 GCGGGGAAGCAGGGCCCCAGGTTCCGGAAAGCCAAGCGGCCCGGCATGGACAGGAGT 1002 1:	ري دې
74 ACACGTCTCATCACTCAGATCCTC	δŏ	412GlyAlaGlnGlyProAlaGlyBroGlyGly 421	qa
134 TECCESTCLAGCITCTCAGCCAN	අධි	GCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGCATGCGGCAGCACAGCTGGTGCA	0y
	gg :c	406 ArgAspProGlyProPro	qq
	δλ	1178 CCTCGCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACA 1119	Qy
	qq 	:: 386 GlyGlySerArgAspProGlyProProGlyAlaGlnGlyProAlaGlyProGlyGlySer 405	qa
254 CCGTTCAGGCACTCCAGAACTGC	Qy		8 8
 664 AspProGlyProProGlyAlaGlr	ପ	1265 GCC	Š Š
314 GCAGGCGCTCACCCACAGCCTC	Oy	.laG1yProG1yG1ySerArgAspProG1yProProG1yAlaG1nG1yPro	an .
	qa —	GCTGCACCAGCGGTCCATGACCAGAGAAAAACCAGGGAGATGGCGCACTGCAGGAACA	δ 6
033 FIOPIOGIYALGGINGI)	g à	347 347	qa
	Oy	CGAATC	δŏ
613 AspProGlyProProGlyAlaGlr	qa	negociacionadoriairon 	7 a
482 AGACCAGGCCCAGCACTGGACCAA	Oy	szu seraigaspriocijyriokijyalacinkijyrroalacijyriotigkijseralg sss 1445 maaachteemeaneeseemeaaneemeaatestaatestaaneeseeseeseeseeseeseeseeseeseeseeseesees	<u> </u>
	G 90	AGAGGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGACTGAGAAGG	oy.
573 yProGlyGlySerArgAspProGl	g å	310GlyAlaGlnGlyProAlaGlyProGlyGly 319	qa
	δλ	E-I	ον
 554 ProAlaGlyProGlyGlySerArg	qq	1990CLAGGG	<u></u> 6 €
	, vo	sproGlyProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgAspFroGlyPro	ପ୍ର
689 CACAGAAGTCCAGCAGCCCCA	Oy 4	1638ccacreceaecaccacereterer	δλ
	qQ	1b/8 G	do d
	ò		qa
806 CCAGCCCCCCAGACTGATCA	ð f	1730CCACCCTGGCCTCGGTGGCTCACCCACCACCACGTACGGAGACATCACA 1679	Qy
AlaGlyProLysGlyAlaHis	qa		. dd
854 AGGGGCCAGGG	δŏ	GAGGHOLAGARANGCOCOCOCOCAN	ò
	qa	1019 GGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGGAAAGGCACTATCCAGGATGGC 1/00 200 rgAspProGtyProProGlyAlaGlnGly	දි දි
896 GGGTGAGGCCAAAGAGGCACT	δ	AspProGlyProProGlyAlaGlnGlyProAlaGlyProGlyGlySerA	a :
 454 GlyGlySerArgAspProGlyPro	Qa. ──	CAGACCCAGGCCTGCGGCAGACCCATATAGGCAGTGACAGACTGGCTGG	oy oy
941CCTCAGCCA	- Oy		

QY	941		26
qq.	454	4	9
Qy	968		22
Db	466	HisGlyProAlaGlyProLysGlyAlaHisGlyPro 4	85
Qy	854	GGGCACTGGTGTCCCAGTCAATGGCAGGCAGGAGGTAGC 8	07
Db	486	5	02
ΟÝ	908	CCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT 74	47
QQ	206	5	19
Qy	746	GGTCCCGGAAGAGGTCAGAGCAGCGCCTCCAGTGGAGTGAAGCACACTGGC 6	90
Dp	520		33
Qy	689	AGTCCAGCAGCCCCA	51
Dp	534	::: AlaGlnGlyProAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGly 55	53
QY	650	CCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCCGG 60	00
QD	554		73
Qy	599	5	43
qa	573		93
0У	542	GGTCACTGGCTGAGGCGGGGCGGACAC 4	83
qq	593	9	12
Qy	482	TTCTCCTCTA 4	26
qa	613		32
Qy	425	CACTICCAGCAGCAGGGGGGCACATAGGIGATGCCTGCGGCCAAACACACCTCCA 3	99
qq	633		43
Qy	365	3	15
qq	644		63
Oy .	314	7	55
qq	664		83
	254	-	95
Db	683		86
Qy	194	CTIGCIGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGG 1	35
qa	869		60
Qy	134	GCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCTGCTGGGGGCACCTCAGTGGGG 7	2
Db	709	LysGlyAlaHisGlyProAlaGlyProLysGlyAlaHisGlyProAlaGlyProL 7	29
Qy	74	TCATCACTCAGATCCTGGCCGAGGCGCGCGCTGTCACCCGGAGCCA 2	
Db	729	G1ys 7	49
Qy	20	GC 19	
Db	749	l 1 er 749	
C E III			

qq	334	roproglySerargAspProglyProProglyAlaProGlyProAlaglyProProglyS 354
Οy	1036	CGGAAAGCCAAGCC
qq	354	erArgAspProGlyProProGlyAlaPro
Qy	916	CITCIGCIG
qq	364	ySerArgAspProGlyP
Qy	931	TGGCTGCTACGCAGG
qa	377	
Οy	872	;
qq	389	rgaspProGlyProProGlyProAlaGlyProProGlySerArgAspPro- 408
. Уд	829	GTCAATGGCAGGCAGGAGGCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGAC 770
ag	409	
Qy	769	AGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCAGGGCCTC 713
qq	417	G
٥y	712	GTGGAGTGA
qa	437	
Οÿ	655	CAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCCCTGCTAGCCAGCC
qq	451	laGlyProProGlySerArgAspProGlyProProGlyAlaHisGlyProA 468
Qy	6	-AGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGG 54
qq	468	laGlyProLysGlyAlaHisGlyProAlaGlyproLysGlyAlaH 483
Qy	4	4 48
Dp	483	isGlyProAlaGlyProLysGlyAlaHisGlyProAlaGlyProLysGlyAlaProGlyP 503
Qy	481	GACCAGGCCCAGCACTGGACCAATGCCCAGCACGATGATGAACTTCTCCTCTACCCC 422
qq	503	roAlaGlyProProGlySerArgAspProGlyProProGlyAlaProGlyProAlaGlyP 523
Qy	421	CACTICCAGCAGCAGGGGGGCACAIAGGIGAIGCCIGCGGCCAAACACACCICCAGGCC 362
QQ	523	roProGlySerArgAspProGlyProProGlyAlaProGlyProAlaGlyProProGlyS 543
oy.	361	AAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAG 311
οp	543	erArgAspProGlyProProGlyAlaProGlyProAlaGlyProProGlySerArgAspP 563
Qy	310	GCGGCTCACCCACAGCTCTGGACCATGGGCCAGGGGGGTAGGGCTCAGGGGCCGT 251
qq	563	rodlyProProGlyAlaProGlyPro-AlaGlyProProGlySerArgAspProGlyPro 582
Qγ	250	GAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCC
DP	583	ProGlyAlaPro592
Qy	190	TGCTGCCGCCAACTG
QQ	593	GlyProProGlySe
Qy		Η (
1	CTO	ASPRIOGLYFIOFIOGLYALARIOGLYFIOALAGLYFIOFIO 526
RESULT 19 US-09-219	-849-	

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APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOUWSTRA, ANDERSA
APPLICANT: MARC W.T.
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WID, RICHELE, T.
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APPLICANT: WID, AND R.
APPLICANT: WID, APPLICATION WID, APPLICATION AND ALSO THE TILL REFERENCE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PALENT: W.
SFOTTM: STORY TO THE TO THE TILL APPLICATION AND ALSO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO THE TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2302 CTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA 2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2242 GAGTCCCCGCATTCC------2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2212 TCTGGCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGC 2153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2152 CCTAGAGACTGGGGAGAGAGGAGGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACC 2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2092 TCAGCAGCACAGGGTGGCAGCAGCAGCACATTACTTTGGCAGCAAGAAACTGGCGG 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1981 -----GAGGCAGGCCCTCCA------CCCCAATGTGCTGGAAGTTTTCTACGC 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2359 GGGCTTAGAGAT---GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCT 2303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2032 CCA-----GCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTGGGACCCCAGT--- 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1939 TGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGAC 1880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 AlaGly-----ProGlyGly 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 GlnGlyProAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGlyPro 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 SerArgAspProGlyProProGlyAlaGlnGlyProAlaGlyProGly------ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GlyGly-----SerArgAspProGlyProProGlyAla 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Illustrative OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.11e-20
371.00
32.39%
28.78%
5.96%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6
LENGTH: 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-219-849-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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Qy 294 CTCTGGACCATAGTGGGCCAGGGGGTAGGGCTCAGGGGGCCGTTCAGGCACTCCAG 238	OY 2086 GCACAGGGTGGCAGCAGAGAGCCACATTACTTTGGCAGCACAGAGAGAG
237 AACTGCTTCGGCTCTGCTCCAGAAGTGCGGCCTCTCCTCCTTGCTGCCGCCAAC	Oy 2026 CGGCAGCCCCATGGGGGTAACAGGAGGGGGGAGCTGGGACCC 1
Db 694 lyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyThrProGly 709 Ov 177 mccrasccasamraccrasccrasccrasccrasccrasc	QY 1969 CCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAA
710ProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGly	95
117 AGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCA	Qy 1909 TACTACCTGTGTAGCAAAGTAAATGGCGACCAGGCCTGC
728 InHisHisLeuGly	Oy 1849 GGCAGTGACAGACTGGCTGAGCTGGACAATGGAGCCCATAAACAG
OY	Db 105 laProGlyProAlaGlyProProGlySerArgAspPro
SULT 18	
02-02-217-03-4-7-5 Sequence 5, Application US/09219849 ; Patent No. 6150081	UD 121 IYALAFIUGIYFIUMIAGIYFIUFIUGIYSEIALGASPFIUGIYFIUGIYFIUMIYTIMIYFIUMIYFIUMIYFIUMIYFIUMIYFIUMIYFIUMIYFIUMIYFIUMIYFIUMIYFIUM
Ĕ	141 lyProAlaGlyProProGlyS
APPLICANT: VAN KLJN, ALAXIS C. APPLICANT: BOUWSTRA, JAN B. APPLICANT: DE WOLF, FREDERIK A.	1711
	091
	Qy 1651 AGGTGGGAGCAGGCCACTGCCTCCAGCACCACGTGTCCATT
TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE TITLE OF INVENTION: PREPERENCE: 2728-2 FILE REFERENCE: 2728-2	Qy 1605AAGGGAGCTCCAGGCTTAGGGCCTGG
TION NUI	Db 199 rArgAspProGlyProProGlyAlaProGlyProAlaGlyPro-P
NUMBER OF SEQ ID NOS: 50 SOFTWARE: PatentIn Ver. 2.1 SEO ID NO 5	Qy 1564 CAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTGGGTATTT
CLATER 960 TYPE: DRT	1504
ORGANISM: Artificial Sequence FEATURE:	237
OTHER INFORMATION: Description of Artificial Sequence: Illustrative OTHER INFORMATION: amino acid sequence S-09-219-849-5	Oy 1444 GAACCCGGTGAGGGGGGGCTGAAGCTGTCACCACGGCCACACTGTG
ment Scores: 1.14e-20 Length:	1384 ACCGGCAGCC
tive:	Db 271 spProGlyProProGly
. 30.408 6.028 4	н
US-09-759-143-110 (1-3410) x US-09-219-849-5 (1-960)	278
2257 GGTAATCCACCTGCAGAGTCCCGGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCT	Db 291 roProGlyAlaProGlyProAlaGlyF
19 GIYALAKIOGIYPIOATAGIYPIOPTOGIYSETALGASPETOGIYFIOFIOGIYALAFIO	Qy 1204 AGCTCTGGGCACGCCTGGTACAGCCCCTCGCCCACGAAATCCGT
OY	Db 303 erArgAspProGlyProProGlyAlaProGlyProAlaGlyPro
GACTGGGGAGAGGAGGGACGCCCCAGCCCCCAGCTGTGCAGCTACGCACCTCAGCA	1144 GGTCATGAG
	318ProGlySerA
	Qy 1084 CATGCGGCAGCACAGCTGGTGCAGCCGGGAAC

2086	GCACAGGGTGGCAGCAGAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCC 2027
2026	CGGCAGCCCCATGGGGCTAACAGGAGCGGGAGCTGGGACCCAGTGAGGCAGCCCT 1970
1969 95	CCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAA 1910
1909	TAGCAAAGTAA
1849	ACTGGCTGAGCTGGACAATGG alaGlyProProGlySerArg
1789	-AGGCACTATCCAGGATGGCGAGGTCCAGGC
1748	AGATGCCCGGCCCGGAACCACCCTGGCCTGGTGGG 1712
1711	CTCACCCACCACCACCACGTACGGAGACATCACAGGCAGAGGCCCGCAGAGCGCGGGTGG 1652
1651 179	AGGTGGGAGCAGGCCACTGCCTCCAGCACCCACGTGTCCATTAGGG 1606
1605	AAGGGAGCTCCAGGCT roProGlyAlaProGlyProA
1564	CAGGCTGTCCTCACT
1504	CTTCTCCCGGTGCTAGAGGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGT 1445
1444	GAACCCGGTGAGGGCGGCTGTCACCACGGCCACACTGGGGACAGGCATGTGGC 1385
1384	ACCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCG 1325
 1324	CTGCACCAGCCGGTCCATGACCAGAGAAGACCAGGGAGATGGCGCAC'
 1264	CCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTC 1205
 1204	AGCTCTGGGCACGCCTGGTACAGCCCCTCGCCACGAAATCCGTGTAAAACAGCGTGAA 1145
 1144	GGTCATGAGTGCCATCCAGCTGCACACGCACGAAGAGCCGCGCGCG
1084	CATGCGGCAGCACAGCTGGTGCAGCCGGGAAGCAGGGGCGCCCA

HisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPro 110 TCCCCGCATTCCAGTGCAGCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAACC 2180 TCCCCGCATTCCAGTGCAGCCCTTCTGGCCTCCTGTATAAGTCCAGACTGAAACC 2180 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 126 CCCTTGGAAGGCCTCCAGTCAGGCACCTAGAGAGAGAGAG	2006 167 1946 181	AAAGTAAAT 1886 187 GCTGAGCTG 1826 199 ACTATCCAG -1766		CCAGAGCGGGGGGGGGGGGCACTGCCTCCAGCACCGCGTGTCCATTAGG 1607 Compared to the com	42 00 33 33 33	JULIAN CONTROLLA DE CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DE LA CONTROLLA DEL
			and the second s			GGAACA
Db 91 Qy 2239 Db 111 Qy 2179 Db 127 Qy 2119 Db 141 Db 141	Qy 2065 Db 160 Qy 2005 Db 168	Oy 1945 Db 182 Qy 188 Db 188 Oy 188	Db 200 Qy 1765 Db 209 Qy 1717 Db 229	Qy 1666 Db 246 Qy 1606 Db 262 Qy 1546 Db 277	0y 1486 0b 286 0y 1426 0y 301 0y 1376 0b 320 0v 1331	

Dp	351 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGlu 370
Qy	1244 CGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGC 1191
qa .	371 GlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAla 390
Qy	1190 CCTGGTACAGGCCCTCGCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131
qq	391 ProGlyThrProGlyProGlnGly
Qy	
qq	401 GlySerProGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 420
Qy	1070 GCTGGTGCAGCCGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAGCGGCCCGGC 1014
QQ	421 ProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 440
Qy	1013 AT-GGACAGCAGTGGGGCGACAAGGAGGGGGCCGACACCCTTGTGCTGC 964
q	441 GluGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGly 460
δŏ	963 TCGGTGGGG
qa	461 AlabroGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla-ProGlyThrPr 480
Qy	·933 ACCAGCAGTGTGGCTACGCAGGTGAGGAAGATGAGGTGAGGCGAGGCCAAAGAGGCAC 874
qq	480 oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGlnGlyLe 500
Qy	873 TCCTCCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGGTGTCCCAG 829
qa	500 uProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHisLeuGlyGl 520
Qy	828 TCAATGGCAGGCAGGCAGGAGGTAGCCCAGGCAGGCCCCAAGACTGATGAAGGCA 775
qq	520 yAlaLysGlnAlaGlyAspValGlySerProGlyAlaPro533
Οy	774 TAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCGGGAAGAGGTCAGAGAG 721
qq	534GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPr 551
Qy	720 AGGCCTCCAGTGGAGTGAAGCACACTGGCCACAGAAGTCCAGCAGCAGCCCCAGG 661
qa	551 oGlyProGlnGlyLeuProGlySerProGly····-AlaProGlyThrProGlyProGl 569
Qy	660 ATGAGCAGTGCCAGGTCCAGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCCAGCC
qq	
QY	600 GCCCTTGGGATGAGAAAGAGCTCAGCAGGATGCCCAAGGACAGT 556
qa	587 sHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPr 607
Qy	STCCACGCCAGTGGTCACTGGCTGA
Qa	607 oGlyProGlnGlyLeuProGlySe 615
Qy	SACCAATGCCCAG
qa	615 rProGlyAlaProGlyThrProGlyPro624
Qy	כיז
qa	
Qy	378 AAACACCTCCAGCCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGT 321
qq	634 oGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGl 654
Οy	320
qq	654 uGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAl 674

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2290 CAACTAGGAGGCTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCA-----GAG 2240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCT--- 2291
237 AACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGGCTCTCCTCCTTGCTGCTGCCGCAAC 178
                                                                                      177 TGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTC 118
                                                                                                                                   117 AGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCA---- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AlaProGlyThrProGlyGluGlyGlnGlnHis 90
                                694 lyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly----
                                                                                                                                                                                                                                                                                     US-08-397-633A-26
Sequence 26, Application US/08397633A
Sequence 2733577
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 762 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762
259
41
296
259
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-759-143-110 (1-3410) x US-08-397-633A-26 (1-762)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/397,633A
                                                                                                                                                                                                                                          744 lyAlaMet-AspProGlyArg 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                                                      ----CTCAGATCCTGGCCGA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,(
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
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              CCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 1131
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Db 709ProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnG 727	qq	111 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 126
Qy 117 AGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCA 62	Qy da	2179 CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGGAGAGAGA
Oy 61CTCAGATCCTGGCCGA 46 :::	QY	2119 CAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGGGTGGCAGCAGAGAG 2066
RESULT 16 US-08-642-255-114 : Sequence 114, Application US/08642255	, y 4	CCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCATGGGGCTAAC
; Patent No. 5773249 ; GENERAL INFORMATION: ; APPLICANT: CAPPELLO, Joseph ; APPLICANT: FERRARI, Franco A.	à và d	AGGAGGGGGAGCTGGACCCAGTGAGGCAGCCCTCCACCCCAATGTGCTGGAAGTTTT ::::: :::::
NVENTION: NVENTION: SEQUENCES: ENCE ADDRES	, yo d	CTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAAT
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT; STREET: 4 Embarcadero Center, Suite 3400; CITY: San Francisco; STATE: California	Oy Op	GCGACCAGGCCTGCGCCAGACACATATAGGCAGTGACAGGCTGAGCTG
(; U M4111 READ TYPE	Qy	CAGGAAGGCACTATCCAG roGlyAlaProG
P P P	Qy	1765 GATGGCGAGGTCCAGGCAGATGCCCGGCCCGGAACCACCCTGGCCTC 1718
K H C F	Qy	1717 GGTGGGCTCACCACCACCACGGGGGACATCACAGGCAGAGGCCCC 1667
4 Z S F	Qy	1666 GCAGAGCGCGGGTGGAGGTGGGAGCAGCGCTGCCTCCAGCACCCACGTGTCCATTAGG 1607 ::
TELEFANE: (4.15) 494-8771 TELEX: 910 277299 FHT UR INFORMATION FOR SEO ID NO: 114:	ζζ	1606 GAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCT 1547
SQUENCE CHARACTERISILES:	φ	1546 AGCACCTCCAGTGTCCCCTCGGTATTTGGCAGGAACACCTGCTTCTCCCGGTGGTAGAG 1487 [1 1 1 1 1 1 1 1 1 1
YPE 14	Qy Db	1486 GGAGGCCAGTGTGAGGGCAGGATCTGCAGGCCTGAGAAGGTGAACCCGGTGAGGGGGG 1427
5.68e-22 Length: 391.00 Matches: [Gimilarity: 35.17% Conservati	QY	1426 TGAAGCTGTCACCACGGCCACACTGTGGGACAGGCATGTGGCACCGCAG 1377
0.28% MISHALCHES. 1. Gaps: Gaps: Gaps: A10. Y HG-08-KA2-25E-114 (1-762)	Qy	1376
AAACCAGGTGACTGAGTTTATTCAGCTCCC	Qy Db	1331 CGÄÄTGGCTGCACCAGCGGTCCATGACCAGAGAAGACCAGGGAGATGGCGCACTGCA 1272
2290 CAACTAGGAGGCTAGCTGTTAACCCTGGGGTAATCCACCTGCAGAG 11111111 11 91 HisleuGlYGLYAlaLvSGlnAlaGLYASVAIGLYSPFOGLYALAPFOGLYTHPFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	QQ QD	1271 GGAACA
TCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGTATAAGTCCAGACTGAAACC	Oy Db	1244 CGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGGCCACGC 1191

2119 CAGCCCCAGCTGTGCAGCTACGCACCTCAGCACAGGGTGGCAGCAGAGAG 2066 	GCCCCATGGGGCTAAC 20	OS AGGACIGAGAGCTIGAGACCCAGTAACACAACACAACAACAAACAAAAAAAAAA	167 GlnAlaGlyAspValGlySerPro; -GlyAlaProGlyThrPro 180	1945 CTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAAT 1886	181	85 GG	187GlySerProGlyAlaProGlyThrProGlyProGln 198	25 G		1765 GATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCTGGCCTC 1718	GAGGCCCC 1	yAspValGlySerPr 2	1666 GCAGAGCGCGGGTGGAGGTGGGAGCAGGCCACTCCAGCACCCACGTGTCCATTAGG 1607	245 oGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 260	1606 GAAGGGAGCTCCAGGCTTAGGGCCTGCAGAAGCTGGTCATCAGGCTGTCTCACTGCT 1547 [46 AGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAG 14	::: ::: 276	1486 GGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGC 1427	285 lyLeuProGlySerProGlyAla-ProGlyThrProGlyGluGly 299	5 TGAAGCTGTCACCACCACACTGTGGAACAGCATGTGGCACCGGCAG	300GlnGlnHisHisL	1376	1331 CGAATCGCTGCACCAGCCGGTCCATGACCAGAGAAGAAGACCAGGGAGATGGCGCACTGCA 1272	 332GlyalaproGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 349	GCCCCAGGCTGCCATCCG	350 GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGlu 369	\bar{c}	370 GlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAla 389	90 CCTGGTACAGCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 11	390	1130 TCCAGCTGCACAGCTCAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCACA 1071
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qq	400 G	 GlySerProGlyAalaProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAla 419
٥٨	1070 G	GCTGGTGCAGCCGGGGAAGCAGGGCGCCCAGGTTCCGGAAAGCCAAAGCGGGCCCGGC 1014
QQ	420 P	
0y	13	-GGACAGCAGTGGGGCGACAAGGAGGGGCCGACAGCCCTTCTGCTGCC
DB	40	nHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGly 45
Qy	963 T : 460 A	TCGGTGGGGCCCAGCGCTGCCTCCTCAGCC 934 :::
Qy	933 A	CCAGCAGTGTGGCTGCTACGCAGGTGAGGAGGTGAGGGTGAGGCAGGC
Db	479 0	
Οy	873 T	
Db	499 u	
Qy	828 T	CAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCA 775
Dp	519 y	AlaLysGlnAlaGlyAspValGlySerProGlyAlaPro532
Qy	774 T	AGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGG 721
Db	533 -	GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrPr 550
Qy	720 A	GGGCCTCCAGTGGAGGACACACGCCACAGAAGTCCAGCAGCCCCAGG 661
Db	550 0	oGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyProGl 568
Qy	660 A	ATGAGCAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCC
Db	568 n	GlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHi 586
Qy	600 G	GCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGT 556
Db	586 sl	HisLeuGlyGlyAlaLySGlnAlaGlyAspValGlySerProGlyAlaProGlyTh
Οy	555 G	CCCAGATGAAGGGCCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGA
Db	909	GlyP
Qy	498 C	CTAGGAGGGACACAGACCAGGCCCAGCACTGG
qa	614 r	ProGlyA
Οy	438 A	CTTCTCCTCTACCCCCACTTCCAGCAGAGGCGGC
qq	624 -	GlnGlyLeuProGlySerProGlyAla
Qy		AAACACATCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGT 321
Dp	633 00	oGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGl 653
Qy	320 -	GCGCAGCAGGCGGCTCACCACGC 295
QQ	653 u(uGlyGlnGlnHisHisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAl 673
Οy	294 C	TCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGGCCGTTCAGGCACTCCAG 238
qa	673 al	aProGlyThr-ProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProG 693
Οy	237 A	AACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGGCTCTCCTTGCTGCCGCCAAC 178
qq	693 13	yProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 708
Qy	177 TC	GCCTAGGAATCAGCCAGGCGCCCATTCTGCCAGCCTTTGGTGCCGGTCCAGCTTCTC 118

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782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGT---CCCGGAAGAGGT 729
                                                                                                                                        549 GlyThrProGlyProGlnGlyLeuProGlySerProGly-----AlaProGlyThrPro 566
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                                           534 ------GlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro
                                                                                         728 CAGAGAGCAGGGCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGCCCCA
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Patent No. 5830713
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Capello, Joseph
APPLICANT: Capello, Joseph
APPLICANT: Carsman, John W.
APPLICANT: Dorman, Mary A.
TITLE OF INVENTION: METHODS FOR PREPARING SYNTHETIC
TITLE OF INVENTION: REPETITIVE DNA
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
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San Francisco

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2347 GGGAAACCAGGTGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCT~-- 2291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2239 TCCCCGCATTCCAGTGCATGGAGCCCTTCTGGCCTCCCTGTATAAGTCCAGACTGAAACC 2180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2179 CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGGAGGGGACGCCC 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 HisLeuGlyGlyAlaLysGlnAlaGlyAspValGlySerProGlyAlaProGlyThrPro 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 GlyProGlnGlyLeuProGlySerPro---GlyAlaPro-------GlyThrProGly 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 GlySerProGly------AlaProGlyThrProGlyGluGlyGlnGlnHis
                                                                                                      OPERATING SYSTEM: PC-FOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-759-143-110 (1-3410) x US-08-707-237A-84 (1-761)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: A-55186-10/WHD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                      PAPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-CCT-1987
FRIOR APPLICATION NUMBER: US 06/927,258
FRIOR APPLICATION NUMBER: US 06/927,258
FILING DATE: 04-NOV-1986
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
                                                                                                                                                                     APPLICATION NUMBER: US/08/707,237A FILING DATE: 03-SEP-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,155
FILING DATE: 29-DEC-1993
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/053,049
FILING DATE: 22-APR-1993
PRIOR APPLICATION DATA:
                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Trecartin, Richard F. REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (415) 781-1989
             ZIP: 94111-410,
COMPUTER READABLE FORM:
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TYPE: .amino acid
STRANDEDNESS: unknown
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35.178
30.368
6.318
United States
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                      COMPUTER:
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us-09-759-143-110.rai

Db 209 lyThrProGlyProGlnGlyLe	Qy 1717 GGTGGGCTCACCCACCACACA	Db 229 GlyGlnGlnHisHisL	Oy 1666 GCAGAGCGCGGGTGGAGGTGGG	Db 246 oGlyAlaProGlyThrProGly	QY 1606 GAAGGGAGCTCCAGGCTTAGGG	Db 262GlyAlaProGlyThr	Qy 1546 AGCACCTCCAGTGCCCTCGG	Db 277	Oy 1486 GGAGGCCAGTGTAGGGCAGG	Db 286 lyLeuProGl	QY 1426 TGAAGCTGTCACCACGCCACA	Db 301GlnGlnHisHisLeuGlyG	Oy 1376CCACAGG	Db 320 ProGlyThrProGlyProGlnG	Qy 1331 CGAATCGCTGCACCGGTC	Db 333GlyAlaProGlyThrP	Oy 1271 GGAACA	Db 351 dlyThrProGlyProGlnGlyL	Qy 1244 CGCCTTCATCATAGTGTCTCCG	371	1190	391	1130	401	1070			T 5 5	855	461	941	478		498	OY 836 TGTCCCAGTCAATGGCAGGCAG	1
ນ		ATTORNEY AGENT TONE STATION: NAME: ROWLAND, BETTAM I		TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989				STRANDEDNESS: single	: MOLECULE TYPE: peptide US-08-397-633A-31	Alianment Scores:	2.8e-22 Length: 395.00 Matches:	Percent Similarity: 34.50% Conservative: 38 Best Local Similarity: 30.06% Mismatchee: 298	6.35% Indels:	08-397-633A-31 (1-762)	QY 2347 GGGAAACCAGGTGACTTTATTCAGCTCCCAAAAACCTTTTTAGAGAAAAAAAA	76 GlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHis					OY 2179 CCCTTGGAAGGCCTCCAGTCAGGCAGCCCTAGAGACTGGGGACGAGGAGGGACGCC 2120	Db 127 ProGlnGlyLeuProGlySerProGlyAlaProGlyThrPro 140	Oy 2119 CAGCCCCCAGCTGTGCAGCTACGCACCTCAGCACGCACAGGGTGGCAGCAGGAGAG 2066	Db 141 GlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGln 159	QY 2065 CCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAAC 2006	sLeu(QY 2005 AGGAGCGGGGAGCTGGACCCAGTGAGCCCTCCACCCCAATGTGCTGGAAGTTTT 1946	Db 168 GinAlaGlyAspValGlySerProGlyAlaProGlyThrPro 181	QY 1945 CTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTGCTGTGTAGCAAAGTAAAT 1886	Db 182 187	PATAGG	Db 188GlySerProGlyAlaProGlyThrProGlyProGln 199	QY 1825 GACAATGGAGCCCATAAACAGGGATGGGGCCCTGGGACAGGAAGGCACTATCCAG 1766	Db 200	Oy 1765 GATGGCGAGGTCCAGGCAGATGCCCCGGC	

q	209	lyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro-GlyThrProGlyGlu 22	28
λλ	1717	GAGGCCCC 16	299
q	229	GlnGlnHisHisLeuGlyGly-AlaArgGlnAlaGlyAspValGlySerPr 24	91
λλ	1666	16	507
ą	246		51
<u></u>	1606	GAAGGGACTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCT	547
	4	AGAG 14	
ą	7		9
	.1486	STGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGC 14	127
ą	78	GlySerProGlyAla-ProGlyThrProGlyGluGly 30	00
<u>۸</u>	Č Č	GAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCCACGGCAG 13	
g ;	301	-GINGINHISHISLEUGIYGIYAIAARGGINAIAGIYASPVALGIYSErPrOGIYAla 31	σ
₂ 9	32		33.2
>	~	4ATTCCTGCACTAGCACTAGACAGACAACAACAAGAGAAAAAACAAAAAAAA	
	33	aProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaPro 3	
Á	1271	ST	245
- ₄ 2	S	GlyLeuProGlySerProGlyAlaProGlyThrProGlyGlu 37	0
Āζ	1244	CTCGGTGCCCGGCTCAGCTCTGGGCACGC 11	191
q	371		90
Δį	1190	TCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCA 11	131
q	391	roglyThrProglyProglngly	00
λί	1130	GGCAGCACA 1	071
ą	401	42	20
λi	1070	GCTGGTGCAGCCGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGC 101	014
q	421	odlyProglnglyLeuProglySerProglyAlaProglyThrProgly 44	0
λi	1013	GTGGG 99	99
ð	441	InGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGly	09
Δi	966	CTCGGTGGGCCCCAGCGCTGCCT 94	2
ą	461		11
	941	SCAGGCCAA 88	32
	478	GlyProGlnGl	7
Ā	881		78
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¥ .	m -	80	<u>m</u>
Ω	518	alGlySerProGlyAlaPro 53	<u>ლ</u>

		Qy 728 C
ογ	1666 GCAGAGCGCGGGTGGAGGTGGGACGGCCACTGCCTCCAGCACCCACGTGTCCATTAGG 1607	Db 549 G
ОС	246 oGlyAlaProGlyThrProGlyProGlnGlyLeuProGlySerPro 261	668
ογ	1606 GAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCT 1547	
qq .	262GlyAlaProGlyThrProGlyProGlnGlyLeu-ProGlySerPro 276	
ΟY	1546 AGCACCTCCAGTGCCCCTCGGTATTTGGCCAGGAACACCTGCTTCTCCCGGTGGTAGAG 1487	
QQ		
ΟŸ	GGAGGCCAGTGTAGGGCAGGATCTCCAGGGCTGAGAGGTGAACCCGGTGAGGGCGGC	
QQ	lyLeuProGlySerProGlyAla-ProGlyThrProGlyGluGly	Qy 506 T
δλ	TGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACGGCAG	Db 615 -
qq	GInGinHisHisLeuGlyGlyAlaArgGinAlaGlyAspValGlySerProGlyAla	Qy 446 1
δ	1376CCACAGGAAAGCTGCCACACTGGCCAAATAGACTGCTGGGTGC 1332 1111111111111111111111111111111111	Db 625 -
3 3	ricely in ricely from the recent of the rece	Qy 386 C
à É	CGANICOCIOCACCAGCCOGICCAIGNOCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Db 634
2 (Caryonactodary interocary todary bear todary delications and the construction of the c	Qy 326 T
δδ	12/1 GGACG	Db 652 F
		Qy 302 C
දි සි	COCCITICALENTAGICALCOGGGCCCCGGGGCCCGGGCTCAGGGCA	Db 672 F
8	oryonnernnraneactiveryonastychnaractyastyvareryna 	Qy 245 C
oy 1	CCTGGTACAGCCCCTGGCGCAAATCCGTGTAAAACAGCGTGAAGGTCATG	Db 691 3
2 .	FrociyingFrociyFrocinciy	Qy 185 C
δλ	TCCAGCTGCACAGCTCAGCCACGAAGAGCCGGCGCGGGTGCGGGGCATGCGGCAGCACA 111	Db 710
q ₀		0y 125 #
Qy	1070 GCTGGTGCAGCGGGAAGCAGGCCCCCAGGTTCCGGAAAGCCAAGCGGCCCGGC 1014	Db 725 u
QQ	421 ProGlyThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly 440	
У	1013ATGGACAGCAGCAGGG 999	ſ
qa	:::	DD /41 }
ò	998 GCGACAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCCAGCGCTGCCT 942	RESULT 14 US-08-397-633A-
QQ		; Sequence 31, ; Patent No. 57
٥y	941 CCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAA 882	; GENERAL INFO ; APPLICANT:
οQΩ		; TITLE OF 1
. 6	AGAGGCACTCTCCTGGGTGCCCAGGTAGGGGCCAGGGCCAGG	, NUMBER OF
7 名	GlnGlyLeuProGlySerProGlyAlaProGlyThrProGlyGluGlyGlnGlnHisHis	; ADDRESSE ; STREET:
ογ	836 TGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCA 783	; CITY: 5 ; STATE:
' ପ୍ର	518 LeuGlyGlyAlaArgGlnAlaGlyAspValGlySerProGlyAlaPro 533	; COUNTRY: ; ZIP: 94
Qy	782 TGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGACCCGGAAGAGGT 729	; COMPUTER F ; MEDIUM T
qq		; COMPUTER ; OPERATIN SOFTWARE

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------proGlnGlyLeuProGlySerProGlyAla---ProGlyThrProGlyGl 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCGGT-----GCGCAGCAGCGGGGCTCA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProGlyGluGlyGlnGlnHisHisLeuGlyGlyAlaArgGlnAlaGlyAspValGlySer 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCACAGCCTCTGGACCATAGTGGGCCAGGCGGG---TAGGGCTCAGGGGCCGTTCAGG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGGCCTCTCCTCCTTGCTG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yThrProGlyProGlnGlyLeuProGlySerProGlyAlaProGlyThrProGly---- 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCCTGCTA 609
                                                                                                                                                                                                                               TGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGAGGGGGCACATAGGTGATGC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGAGAGCAGGCCTCCAGTGGAGTGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCA 669
                                              GlyThrProGlyProGlnGlyLeuProGlySerProGly-----AlaProGlyThrPro 566
                                                                                                                            GCCAGCCGGCCCTTGGGATGAGAAAGA---------GGCTCAGCAGGATGCCCA 564
                                                                                                                                                                                                                                                                                                  AGGACAGTG---CCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCAC 507
                                                                                                                                                                                                                                                                                                                                    TGGCTGAGCCTAGGAGCGGGACACAGACCAGCCCAGCACTGGACCAATGCCCAGCACCA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SerProGlyAlaProGlyThrProGlyPro------ 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----- 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCTTCTCAGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITE CAPPELLO, JOSEPH
TINVERTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
TINVERTION: OF ENZYMATIC CROSS-LINKING
PREQUENCES: 105
SINDENCE ADDRESSS:
SISEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
TESTS: A Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        READABLE FORM:
TYPE: Floppy disk
ER: IBM PC compatible
ING SYSTEM: PC-DOS/MS-DOS
RE: PatentIn Release #1.0, Version #1.25
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5773577
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILIAG DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1490 TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATAC 1525
                                                                                                                                                                                                                                                                                                                                             US-09-759-143-110 (1-3410) x US-09-605-785-706 (1-123)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
                                                                                                                                                                                                                                                                                           Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                           Indels:
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Patent No. 5773249
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426.00
97.83%
94.57%
6.64%
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ATTORNEY/AGENT INFORMATION:
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Wang, Aijun
                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-605-785-706
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Best Local Similarit
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                                                                                                                                         SEQ ID NO 706
LENGTH: 123
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2065 CCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGGCTAAC 2006
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Indels:
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Matches:
                     REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
                                                                                            TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-871
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 762 mmino acids
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ROWLAND, Bertram I.
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34.50%
30.06%
6.35%
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Best Local Similarity:
Query Match:
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APPLICANT:
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                                                                                                               Conservative:
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Indels:
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Matches:
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; Sequence 571, Application US/09439313;
; Patent No. 6329505
                      TOPOLOGY: linear MOLECULE TYPE: No. 6252047e
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1287.00
100.00%
100.00%
20.05%
           STRANDEDNESS: single
amino acid
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1673 TCTGCCTGTGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTT 1732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C9
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Mismatches:
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 571
LENGTH: 84
Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan Louise
Jiang Yuqui
Reed, Steven G.
Kalos, Michael
Fanger, Gary
Retter, Mark
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel
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                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                              Solk, John
Day, Craig
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DB:
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1672

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1BM Compatible
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Mismatches:
                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASLEDO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
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                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PPLICATION UNBER:

FILING DATE: 02-MAY-1997
ATTORNEY AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.P1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: No. 6130043e
                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER; IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
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60064-3500
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                                                                                                                                                                                   FILING DATE:
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                                           COUNTRY:
                                STATE:
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1658 GCGCTCTGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGTGGTGGTGGTGAGCCCACC 1717
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APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEDENCE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS: 41
                                                                                                                                                                                                                                                                                                                                                                                                       241 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/09525397
Patent No. 6252047
GENERAL INFORMATION:
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GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
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1127 TGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCCTGTAC 1186
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RESULT 7 US-09-23 ; Sequer	7 32-1492 113 100 113	ILT 7 19-232-149A-113 quence 113, Application Us	ation US/0923:	2149A			a ò
GENER!	AL INFO	ORMATION: Xu, Jiane	gebun				qa
; APPL]	CANT:	Dillon, Mitcham,	Davin C. , Jennifer Lyr	g			οy
; TITLE	S OF IN	VENTION:	COMPOUNDS FOI	; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY O. TITLE OF INVENTION: CANCER AND METHODS FOR THEIR	OF PROSTATE R USE		qa
CURRE	REFERI	SNCE: 210.	121.427C6 NUMBER: US/09	1/232,149A			QY
NUMBE	SNT FIL	SEQ ID NO	: 1999-01-15 S: 338				qa
SEQ IE	SOFTWARE: F	astSEQ fo 13	or Windows Ve	sion 3.0			Qy
r's	TYPE: PRT ORGANISM: 1 9-232-149A	Homo sapie	ien				qa Xo
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Pred. No.:			1.61e-211	Length:	553		δō
Percent Best Loc	Simila al Sin	int Similarity: Local Similarity:	100.008 100.008	<pre>Matches: Conservative: Mismatches:</pre>	55 3 0 0		qa —
Query Ma DB:	матсп:		44.58%	Indels: Gaps:	00		Qy
US-09-75	9-143-110	(1-	3410) x US-09-2	32-149A-113 (1-5	53)		qa
Qy	284	ATGGTCCAG	GAGGCTGTGGGTGA	GCCGCCTGCTGCGGCA	CCGGAAAGCCCAGCTCTTGCTG	343	QY
Db	1	MetValGln				1 20	Db
Oy	344	GTCAACCTG	SCTAACCTTTGGCC	TGGAGGTGTGTTTGGCC	CGCAGGCATCACCTATGTGCCG	403	Οy
Db	21	ValAsnLeu	uLeuThrPheGlyL		ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	40	qq
Qy	404	CCTCTGCTG	SCTGGAAGTGGGGG	TAGAGGAGAAGTTCAT	SACCATGGTGCTGGGCATTGGT	463	Qy
qq	41	ProLeuLeu	uLeuGluValGlyV	alGluGluLysPheMet	ProLeuLeuLeuGluValGlyValGluLySPheMetThrMetValLeuGlyIleGly	. 60	qq
Oy	464	CCAGTGCTG	366CCT6GTCTGT6	TCCCGCTCCTAGGCTC	AGCCAGTGACCACTGGCGTGGA	. 523	Oy
qq	61	Provalleu	ıGlyLeuValCysV	alProLeuLeuGlySer	ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly	80	qa
Oy		CGCTATGGC	CGCCGCCGGCCT	TCATCTGGGCACTGTCC	CGCTATGGCCGCCGCCGCCGTCATCTGGGCACTGTCCTTGGGCATCCTGAGCCTC	583	Qy
qq	81	ArgTyrGly	ArgArgArgProP	helleTrpAlaLeuSe	rLeuGlylleLeuLeuSerLeu	100	ar .
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1004 TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1063
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GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
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                                                               824 ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 883
                                                                                                                   GGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 943
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                                          CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1843
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APPLICANT: Reed, Steven G.
APPLICANT: X. Jiangchun
APPLICANT: X., Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.44652
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 1107
                                                                                                                             1904 GTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
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Matches:
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47 1/14 AGGSTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	VS dd	644 GAGCTGGCACTGCTCAT
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1844 ACTGCCTATATATATATATATATATATATATATATATATA	q _Q	141 ThrProLeuGluAla
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RESULT 5 US-09-352-616A-113	Qy	884 GGCCTGCTCACCCTC
Sequence 113, Application US/09352616A Patent No. 6395278	qa	201 GlyLeuLeuThrLeuIle
GENERAL INFORMATION: APPLICANT: Dillon, Davin C.	Qy	944 GCAGCGCTGGGCCCCACC
; APPLICANT: natlocker, Susan Louise ; APPLICANT: Jiang, Tiang, Applicant: APPLICANT: Y. Tianghin	qa	221 AlaAlaLeuGlyProThr
; APPLICANT: Mitcham Jennifer Lynn TTHE OF INVENTION COMPONING CON TAXABLE	δλ	1004 TGCTGTCCATGCCGGGCC
; TITE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS ; FILE REFERENCE: 210121 42200	q	241 CYSCYSProCysArgAla
CURRENT APPLICATION NUMBER: US/09/352,616A	٥y	1064 CACCAGCTGTGCTGCCGC
NUMBER OF SECTION OF 472	qa	261 HisGlnLeuCysCys
SOFTWARE: FastSEQ for Windows Version 3.0	Qy	1124 AGCTGGATGGCACTCATG
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US-09-352-616A-113	Qy	1184 TACCAGGCGTGCCCAGA
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Qy 284 ATGGTCCAGAGGTGTGGGTGAGCCGCCTGCTGCGGAAAGCCCAGCTCTTGCTG 343	0y	1364 GCTTTCCTGTGGCTGCC
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Oy 404 CCICTGCTGCTGGAAGTGGGGGTAGAGAGAGATCATGACCATGCTGGGGATTGGT 463	δy	1484 TCCCTCTACCACCGGGAG
Db 41 ProLeuLeuCluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60	QQ	401 SerLeuTyrHisArg
Qy 464 CCAGIGCIGGECIGGICIGCICCICCIAGGCICAAGCCAGIGACCACIGGCGIGGA 523	δy	1544 GCTAGCAGTGAGGACAGC
Db 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80	qq	421 AlaSerSerGluAsp
QY 524 CGCTATGGCCGCCCCGGCCCTTCATCTGGCCACGTTCTTGGCCATCCTGCTGAGCCTC 583	Qy E	1604 TTCCCTAATGGACACGTGC
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Qy 584 TTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGGCCGGATCCCAGGCCCCTG 643	Š t	1994 TGCGGGGCCTCTGCCTGTG
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APPLICANT: Millon, Davin C.
APPLICANT: Millon, Millon, Davin C.
APPLICANT: Fanger, Steven G.
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Solk, John DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: UNMBER: US/09/439,313
CURRENT FILIKG DATE: 1999-11-12
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                                  ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 763
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Renger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: U., Samuel
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Walliam
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Wasir A.W.
APPLICANT: Bepler, Walliam
TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
TILE REFERENCE: 210121.427216
CURRENT APPLICATION NUMBER: US/09/605, 785
541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 113
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                                                   Sequence 113, Application US/09605785 Patent No. 6321716
                                                                         GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                     -09-605-785-113
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TYPE: PRT
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1004 TGCTGTCCATGCCGGGCCCGGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG
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    MEDIUM TYPE: Floppy disk
COMBUTER: IBN PC Compatible
COMBUTER: IBN PC Compatible
OPERATING 'SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                   210121.427C3
                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 anino acids
TYPE: amino acid
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Best Local Similarity:
Query Match:
                                                                                              CLASSIFICATION:
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Pred. No.:
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Indels:
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Matches:
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100.00%
44.58%
                               ORGANISM: Homo sapiens
               MOLECULE TYPE: protein ORIGINAL SOURCE:
STRANDEDNESS: single
        linear
                                                                              Percent Similarity:
Best Local Similarity:
                                      US-09-020-956-113
                                                       Alignment Scores:
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STREET: 6300 Columbia Center, 701 Fifth
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Patent No. 6262245
GENERAL INFORMATION:
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(without alignments) 6802.181 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                            OM nucleic - protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
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Maximum DB seq length: 200000000
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Command line parameters:

-MODEL-frame+_n2p.model -DEV=xlp
-Q=-Cgn2_1/USPTO_spool/US09759143/runat_05062003_111320_23081/app_guery.fasta_1.3591
-Q=-Cgn2_1/USPTO_spool/US09759143/runat_05062003_111320_23081/app_guery.fasta_1.3591
-DB=Issued_partente_A -OFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LIOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALICN=45
-MODE=LCOAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USFR=US09759143_eCGN_1_1.25_efunat_05062003_111320_23081 -NCPU=6 -ICPU=3
-NO_MMAP -LARCEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREDUTS=1 -XORAPDF=10 -XGAPEXT=0.5 -FCAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELDP=6 -DELEXT=7

Database :

/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/pcTuS_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:* /cgn2_6/ptodata/2/laa/5A_COMB.pep:*/cgn2_6/ptodata/2/laa/5B_COMB.pep:* Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Out Score Ma No. Score Ma 2 2 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 8 6 1 4 4 2 0 2 8 6 1 4 4 2 0 2 8 6 1 4 4 2 0 2 8 6 1 4 4 2 0 2 8 6 1 4 4 2 0 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	% % % % % % % % % % % % % % % % % % %	Query Query Query Autor Length DB Autor S53 4 8861 44.6 553 4 8861 44.6 553 4 8861 44.6 553 4 8861 44.6 553 4 8861 44.6 553 4 8861 44.6 553 4 8861 22.1 255 4 22.1 255 4 452 20.1		US-09-020-956-113 US-09-030-607-113 US-09-030-607-113 US-09-05-785-113 US-09-439-313-113 US-09-352-616A-113 US-09-233-149A-113 US-09-605-785-708 US-09-523-397-36 US-09-523-397-36 US-09-523-397-36	Description Sequence 113, App Sequence 113, App Sequence 113, App Sequence 113, App Sequence 111, App Sequence 111, App Sequence 111, App Sequence 101, App Sequence 708, App Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl
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Segmence 120 App	1 (7)	84	114,	26	Sequence 5, Appli	Sequence 6, Appli	Sequence 126, App	Sequence 36, Appl	Sequence 84, Appl	Sequence 114, App	26	21,	21,	21	21,	120	31,	62	132	53,	9	103,	101,	75, A	103	103,	50, A	72,	4 , A	Sequence 49, Appl	٦,	Sequence 73, Appl
US-08-642-255-120	-08-397		õ	õ	US-09-219-849-5	US-09-219-849-6	US-08-642-255-126	US-08-397-633A-36	US-08-707-237A-84	US-08-642-255-114	US-08-397-633A-26	US-08-963-825-21	US-09-500-811-21	US-09-570-573-21	US-09-548-608-21	US-08-642-255-120	US-08-397-633A-31	US-08-642-255-62	US-08-642-255-132	US-08-397-633A-53	US-08-175-155-68	US-08-477-509B-103	US-08-642-255-101	US-08-707-237A-75	US-08-482-085B-103	US-09-444-791A-103	US-08-397-633A-50	US-08-642-255-72	US-08-931-820-4	US-09-219-849-49	82	US-08-642-255-73
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ALIGNMENTS

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APPLICANT: XL, Jiangchun
APPLICANT: XL, Jiangchun
APPLICANT: Dillin, Davin C,
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  E: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Maki, David J.
REGISTRATION UNBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     us/09/020,956
                 Sequence 113, Application US/09020956 Patent No. 6261562 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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Hayatsu, N., Hiramoto, K., Hiracoka, T., Imotani, K., Ishii
Nakamura, M., Kawai, J., Koʻjima, Y., Konno, H., Kouda, M., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Taqawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Towardiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                     2171 TICCAAGGGGTIICAGICIGGACTIAIACAGGGAGGCCAGAAGGGCICCAIGCACIGGA 2230
2111 TGGGGGCTGGGGGGTCCCTCTCTCCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCC 2170
                                                                                                                                                                                                               ATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCTCCTAGTTG 2290
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
'Mormalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNA-libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikewa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                            Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suebliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
181-45-503-922
                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                               BB701488
BB701488 RIKEN full-length enriched, in vitro fertilized eggs Musmusculus cDNA clone 7420429L15 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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BB701488
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                          Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" GAGAGAGAGGACCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    940 GGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCC 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 GGAGGCAGTACTGGGCCCACCCGAGCCGGCAGAGGGTTGTTGGTCTCTGCCGTGTCGCG 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 AGCCTTCTCTTTTTAACGCCTTCATGATCAGCCGTGGGGGCTGCCTGGGCTACCTCTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      582 TCTTTCTCATCCCAAGGGCCGGCTGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      642 TGGAGCTGGCACTGCTCATCCT - - GGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            700 CTTCACTCCACTGGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  760 GGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cap-trapper. Second strand cDNA was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        820 TGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                           /note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                 /clone_lib="RIKEN full-length enriched, in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ж
Э,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Indels
                                                                                                                              /tissue_type="in vitro fertilized eggs"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
/db_xref="taxon:10090"
/clone="7420429L15"
                                                                                                                                                       /dev_stage="egg"
/lab_host="DH10B"
                                                                               fertilized eggs"
                                                                                                     /sex="female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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41

9, 2003, 19:43:37

Job time : 4214 secs

/organism="Mus musculus"

source

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AW135465
UI-H-BII-aca-e-07-0-UI.sl NCI_CGAP_Sub3 Homo sapiens cDNA clone
IMAGE:2713812 3', mRNA sequence.
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                                                                                                                    TGATGAGACGTGTCCCCACTGAGGTGCCCCACAGCA-GCAGGTGTTGAGCATGGGCTGAG 120
                                                                                                                                                                                                                                                                                  289
                                                                                                                                                                                                                                                                                                                                                   CAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCC--AGCTCTTGCTGGTCA 347
                                                                                                                                                                                                                                                                                                                                                                                                                      348 ACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTGCTAACCTTTGGCCTGGAGGTGTGTGTGGCGCGCAGGCATCAACCTATGTGCCGCCTC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        461
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                                                                                                                                        121 AAGCTGGACC-GGCACCAAAGGGCTGGCAGAAATGGGCGCCTG-GCTGATTCCTAGGCA- 177
                                                                                                                                                                                                                         136 AAGCTGGACCTGGCACCAAAGGGCTGGCAGAAATGGGCCCCTGTGCTGATTCCTAGGCAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 370)
                                                 61
                                                                                 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  627 CGGATCCCAGGCCCCTGGA-GCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTC
                                                                    16 GGAACCAGCCTGCACGCGTGGCTCCGGGTGACAGCCGCGCCCCGGCCAGGATCTGAG
                                                                                                                                                                                                                                                                                                                               AGTTCTGGAGTGCCT - - - GAACGGCCCCCTGAGCCCTACCCGCC - TGGCCCACTATGGTC
                                                  2 GGAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCCCTCGGCCAGGATCTGAG
                                                                                                                                                                                                                                                            ----GTTGGCGGCAGCAAGGAGGAGGCCCGCAGCTTCTGGAGCAGCCGAGACGAAGC
                  Gaps
                                                                                                                                                                                                       39;
                  Indels
                  0; Mismatches 128;
No. 2.3e-38;
   Pred.
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78.98;
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                  Conservative
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   Best Local Similarity
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REFERENCE

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The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand contained the sequence contained the strand contained the spatial of the strand therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NGI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:
www-bio.llnl.gov/bbtp/image/image.html
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                           Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2713812"
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TAG_SEQ=AAGTG"
109 c 101 g
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/lab_host="bHl0B"
/lab_host="bHl0B"
/lab_host="bHl0B"
/note="vector: pAMPl0; Site_1: Not1; Site_2: EcoRI; lst
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from 5,000-10
,000 microdissected, histologically normal prostate
epithelial cells. Double-stranded cDNA was ligated to
EcoRI adaptors, 5 cycles of PCR applied to the cDNA with
an adaptor-specific primer, and the resulting PCR product
subcloned into pAMPl0 by the UGC-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index.

Unpublished (1997)

Email: cgapbs-rémail.nih.gov

Tissue procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

Tissue procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

Found through the I.M.A.G.E. Consortiun/LLNL at:

Www-blo.llnl.gov/bbrp/image.html

Seq primer: -40ml3 fwd ET from Amersham
                                                                                                                                                                                                                                                                                                                     AA579486 388 bp mRNA linear EST 03-SEP-1997 nf33g07.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:915612 similar to contains element MSR1 repetitive element ;, mRNA
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                     485 GTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_Pr1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:915612"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 343.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Б 66
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AA579486.1 GI:2357670
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Matches 36
                                                                                                                                                                                                                                                                          RESULT 42
AA579486/c
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/Organism="Homo sapiens"
/Ob_xref="taxon:9606"
/Ob_xref="taxon:9606"
/Clone='InbacB:429710"
/Clone='InbacB:429710"
/Clone=InbacB:429710"
/Clone=InbacB:429710"
/Obte="Organ: prostate; Vector: pDNR-LIB (Clontech);
/Obte="Organ: prostate; Vector: pDNR-LIB (Clontech);
/Obte="Organ: prostate; Vector: pDNR-LIB (Clontech);
/Obte="Organ: prostate; Vector: pDNR-LIB (Gorditating)
/Obte="Organ: prostate; Vector: policy and 3' adaptor sequence: 5'-ATTCTAGGGCGGGCGGCGGCATGGTGTGTGGCC]
/Obte B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

Laboratories (Palo Alto, CA)."

1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BF680993 906 bp mRNA linear EST 21-DEC-2000 602156279F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4297170 5',
                                                                                                                                                                                                                      3215 TTTGCAATAATGTCGTCTTATTTATTTAGCGGGGTGAATATTTTATACTGTAAGTGAGCA 3274
                                                                                                                                                                                                                                                                                                                                                                                                                                         3035 GCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAG 3094
                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 906)
                                                                                                                                     261 CCTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTC
                                                                                                                                                                                                                                                   201 AGGAGCACCCCTGCCTGAGCTAAGGGAGGTTTATCTCTCAGGGGGGGTTTAAGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact Capper remail. nih.gov Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                        3095 CCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAAACTC
                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Plate: LLCM1150 row: n column: 19
High quality sequence stop: 564.
Location/Qualifiers
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BF680993
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DB 12; Length 906;

Score 359.2;

10.5%;

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GTAGAGGAGAAGTICATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                    /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
                                                                                                                                                                                                                                                                                        FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 45 row: C column: 12
Seq primer: ATTTAGGGTGACACTATAG.
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1. .537
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                            pig.
Sus scrofa
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                                                 contributed to prepare mouse tissues. 1st strand cDNA was
                                                             primed with a primer [5'
GAGAGAGAAAGGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                        61 GTGATGAGACGTGTCCCCACTGAGGT - - GCCCCACAGCAGGTGTTGAGCATGGGCTG 118
                                                                                                                                                                                                                                                                                                                                                     AGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAG 178
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prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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                                                                                                                                                                                                                                                                                                              37 GGTTCCGACTCGCACGCGCCAGCCCCAGGTGACAGCCGCACGCC-GGGCCAGGATCTGA
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Pred. No. 3.4e-41;
0; Mismatches 118; Indels 12; Gaps
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120845 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
AW787124
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79.2%;
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
     Euteleostomi;
                                                   1 (bases 1 to 537)
Stabrankrugy.S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E.
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
and Keele, J.W.
                                                                                                                                                         pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTGAACGGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGTG
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                 Design and use of two pooled tissue normalized EST discovery in swine Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Fax: 402 762 4366
                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.8%; Score 369.4; DB 10; ilarity 85.0%; Pred. No. 1.3e-39; Conservative 0; Mismatches 76;
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L motholished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih;gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11137 row: n column: 24
High quality sequence store: 2
High quality sequence store: 2
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 TIGAGCAIGGGCIGAAAGCIGGACCGGCACCAAAGGGCIGGCAGAAAIGGGCGCCIGGC 164
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/lab_host="DHIOB (T1 phage-resistant)"
/note="Organ: liver: Vector: pCMv-SpORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 CAGTGCTGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGAC
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%; Score 389.4; DB 13; Length 630; 79.4%; Pred. No. 2.9e-42; Live 0; Mismatches 116; Indels 11; Gaps
                                                                                                                                                                                                                                                                          1. .630
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                               /clone-"IMAGE:5050583"
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibagawa, A., Shiragawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M. and Hayashizaki, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS, (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

(2000) FIXEN integrated Sequencer. Genome Res. Y. and Hayashizaki, Y. Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinaqawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa Hayashizaki, Y. Shibata, K. and
                                                                                                                                                                                                                                   BB627844 RIKEN full-length enriched, adult male ufinary bladder Musmusculus cDNA clone 9530042b02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome-gsc.riken.go.jp,
Carninci.P., Shibata.Y., Hayasu.N., Sugahara.Y., Shibata.K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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/clone_lib="RIKEN full-length enriched, adult male urinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-2 Suebiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/dev_stage="adult"
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/organism="Mus musculus"
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                                        612 AGTAGGCCCTGCTGATC 628
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645 AGCTGGCACTGCTCATC 661
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/note="Site_1: Sall; Site_2: BamHI; cDNA library was

Page 27

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BI145201 630 bp mRNA linear EST 05-JUL-2001 602909395F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5050583 5',
                                                                                                                                                                                                                                                                                                                                       /note="multiple clone assembly from multiple libraries and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 CCTATGTGCCGCCTCTG--TGCTGGAATGGGGGTAGAGGAGAAGTTCATGACGACATGGTGC 417
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Mammalla; Eutherla; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CAGCAGCAGGTGTTGAGCATGGGCTGAGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ACAGCCGCGCCCTCGGCCAGGATCTGAGTGATGAGACGTGTCCCCACTGAGGTGCCCCA 60
Walker,M.G., Volkmuth,W., Sprinzak,E., Hodgson,D. and Klingler,T.
Prediction of gene function by genome-scale expression analysis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 AGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCA
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                                                                                                                                                                                                                                                                               /clone_lib="Homo sapiens prostate adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 11.5%; Score 391; DB 9; Local Similarity 97.0%; Pred. No. 2.1e-42; les 420; Conservative 0; Mismatches 10
                                                                                                                     Incyte Pharmaceuticals
3174 Porter Drive, Palo Alto, CA 94304,
co-expressed with known prostate-cancer
Location/Qualiflers
                                           prostate cancer-associated genes
Genome Res. 9 (12), 1198-1203 (1999)
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/db_xref="taxon:9606"
/clone="IPCA-8"
                                                                                                                                                                                                                                                                                                    /tissue_type="prostate"
/dev_stage="adult"
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Contact: Walker MG
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                                                                                                                                                                                                                                                                                                                                         /note="Organ: nervous_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF109303 Homo sapiens prostate adult Homo sapiens cDNA clone IPCA-8
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                                                                                  Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NT0147-
191100-482-h07&t3=2000-11-19&t4=1)
Seq primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
      Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Pred. No. 5.1e-43;
0; Mismatches 2;
                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                       High quality sequence stop: 418.
Location/Qualifiers
                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone_lib="NT0147"
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                                                 +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=RC3&t2=RC3-BT0046-
310899-002-F07&t3=1999-08-31&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 411.
                                                                                                                                                                                                                177 AAAGGGCTGGCAGAAATGGGAACCTGGCTGCACCCTAGGAGGTTAGTGCTAGTGAGGAGG 236
                              AGAGGCCGCAGCTTCTGGAGCAGAGCC3AGACGAAGCAGTTCTGGAGTGCCTGAACGGCC 256
                                               CGGCACCGGAAAGCCCAGCTCTTGCTG3TCAACCTGCTAACCTTTGGCCTGGAGGTGTGT 376
                                                                                                                                                                                                                                                                                              CCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTG 316
                                                                                                                                                                     464
                                                                                                                                                                                                                                                                                                                                               554
                                                                                                                                                                                                                                                                                                                                                          614
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                               GTTCATGACCATGGTGCTGGCCATTGGTCCAGTGCTGGGCCTGG-TCTGTGTCCCGCTCC
                                                                                                                                                                                                                                                                                                                                           TAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGCCCTTCATCTGGG
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
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AW175665/C
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/note="Organ: breast; Vector: pucl8; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue
                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1855 GGTGTCTGCCGCAGGCCTGGGTCTGGTTTACTTTGCTACACAGGTAGTATTGA 1914
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                           1795 GGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATAT 1854
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                         11.7%; Score 398.6; DB 10; Length 412; 99.0%; Pred. No. 2.2e-43; Live 0; Mismatches 4; Indels 0;
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20202663
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
/organism="Homo sapiens"
                                                                                                                                                                                                                                             stringency conditions.'
                       /db_xref="taxon:9606"
/clone_lib="BT0046"
/dev_stage="Adult"
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BG246497.1 GI:12756312
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Local Similarity 77.4%;
nes 578; Conservative
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BG246497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GTGATGAGACGTGTCCCCACTGAGGT - - GCCCCACAGCAGCAGCAGTTGAGCATGGGCTG
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numan Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAAGCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCTTGGCTGATTCCTAGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.0%; Score 409.4; DB 10; Length 692; 79.1%; Pred. No. 6.5e-45; cive 0; Mismatches 127; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5e-45;
es 127; Indels
                                                                                                                                                                    /tissue_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                       143 t
                                                                                      /organism-"Mus musculus"
                                                                                                    /db_xref="taxon:10090"
/clone="9530024M01"
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BG246497 BY BR BH4 bp MRNA linear EST 13-FEB-2001 602360526F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4488895 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTGAGGT -- GCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGAAGCTGGACCGGCACC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGCGGCAGCAAGGAGG 196
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                           567 AGACCCTTTATCTGGGCTTTGTCCTGGGGGTGCTCTTAGCCTTTTCTCATCCGGGGGG
                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
507 GTTTCTGTTCCACTCCTAGGCTCAGCCAGTGACCAGTGGCGTGGGCGCTATGGCCGCCGG
                                                                CGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGG
                                                                                                                                                                                             GCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGGATCCCAGGCCCCTGGAGCTGGCACTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 9.5e-44;
0; Mismatches 153; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10336 row: c column: 08
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/dlone="IMAGE:448895"
/clone=11b="NG:CGAP_Man1"
/tissue_type="tumor, blopsy samp/dev_stage="10 months, virgin"
/lab_host="DH108"

    .844
    /organism="Mus musculus"

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Location/Qualifiers
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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BB627667
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                                                                                                                                                                   Depublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-Temail.nih.gov
Tissue Procurement: Joffrey F. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
CLone distribution: McC clone distribution information can be informed through the I.M.A.G.E. Consortium/LLNL at:
http://amage.lnl.gov
Plate: LLAM9810 row: 1 column: 07
High quality sequence start: 3
High quality sequence start: 3
High quality sequence stop: 756.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 CIGAACGCCCCCTGAGCCCTACCCGCCTGGCCCACTATGGTCCAGAGGCTGTGGTGAG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      427 AGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGT 486
                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:422998"
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/note="Organ: Kidney: Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library. |"
218 c 243 g 167 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGAGTGC 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 GCTCGCACGCCCAGCCCCAGGTGACAGCCGCACGCC-GGGCCAGGATCTGACCGACGAG 74
                                                                                                               1 (bases 1 to 759)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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    BF789072.1 GI:12094108
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                                        house mouse.
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Dukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (basa 1 to 692)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A. Hiramotto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,H., Kouda,D., Shibata,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,A., Takawanstel,M. and Hayashizaki,Y. RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing pipeline with 384 multicapillary sequencer. Genome Res. . . (0 (11), 1757-171 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BB627667 RIKEN full-length enriched, adult male urinary bladder Mus unsculus CDNA clone 9530024M01 5', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rappd discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                    543
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                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                664 AGTGGGGCTGCTGGACT--TTGTGGCAGGTGTGTCTTTACTCCATTGGAGGGCTTACTCTC 721
                                                                    485 TCCACTCCTAGGCTCAGCCAGTGACCAGTGGCGTGGGCGCTATGGCCG-CGGAGACCCTT
487 CCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTT
                                                                                                                                                    547 CATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCTG
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB627667
BB627667.1 GI:16465271
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667 CCCTCTACCACCGTGAGAAGCCGGTGTCC 695

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BB610495 RIKEN full-length enriched, adult male stomach Mus musculus cDNA clone 2210413P12 5', mRNA sequence.
BB610495 GI:16452013
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rappid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi.K., Fujiwake,S., Inoue,K., Togawa,X., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikuwa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA
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/db_xref="taxon:10090"
/clone="2210413P12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-45-503-9216
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BF789072 759 bp mRNA linear EST 12-JAN-2001
602104930F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:4222998
                 RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" GAGAGAGAGGGGGGGGAACTCGAGTTTTTTTTTTTTTV 3'], CDNA was
                                                                                                                                                                                                                                                                                                                                  1458 TGCAGATCCTGCCCTACACACTGGCCTCCTCTACCACGGGGAGAAGCAGGTGTTCCTGC 1517
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                                                                                          prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                        TGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTG
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                                                                                                                                                                                                                                                           12.3%; Score 419.6; DB 1
78.8%; Pred. No. 2.9e-46;
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Matches 547; Conservative
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      /clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/tlab_host="DH10g="carcinoid"
/note="Organ: lung: Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs la14920-1417991. and 1520904-1522439). Subtraction by Bento
                                                                                                                                                                                                                                                                                                                                                                     2686 GATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATC 2745
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTTTGGCCCAGCCTGG
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                  DB 10; Length 448;
                                                                                                                                                                                                                                                                                1; Indels
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                    Soares and M. Fatima Bonaldo.
142 c 96 g 114 t
                                                                                                                                                                                                                                          Ouery Match
12.8%; Score 435.4; DB
Best Local Similarity 99.6%; Pred. No. 3e-48;
Matches 447; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611
                                                                                                                                                                                                                                                                                               /clone="IMAGE:4220415"
/clone=lib="NOI_CGAP_CO24"
/lab_host="DH10B_(TI_phage-resistant)"
/note="Gran: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9803 row: p column: 16
High quality sequence start: 2
High quality sequence stop: 680.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 12.7%; Score 433.8; DB 12; Length 700; al Similarity 84.5%; Pred. No. 3.9e-48; 582; Conservative 0; Mismatches 97; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
                                                                                                                                                                                        Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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BE674096
BE674096.1 GI:10034637
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Unpublished (1997)
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/note="Neator: psport; Site_1: Sali; Site_2: Noti; This clone is among a rearrayed set of 15,247 clones from 11 embryo. cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E1.5 female mesonephrosygonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT). Not piners. References include: (i) Genome-wide expression profiling of mid-gestation placenta and embryousing a 15,000 mouse developmental cDNA microarray, 2000, proc. Nall. Acad. Sci. U S A, 97: 9127-9132; (2) inage-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the x chromosome, 1998, Hum Mol Genet 7: 1967-1978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute on Aging/National Institutes of Health Mational Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdnadigsun.grc.nia.nih.gov Tris clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Please primer: -21M13 Reverse High quality sequence stop: 549
                                                                                                                                                                                                                                                                                                                                                                                                                 Kargul, G.J., Dudekula, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka, T.S., Carter, M.G. and Ko, M.S.H.
Verification and initial annotation of NIA mouse 15K CDNA clone set
                                                                                                                                                                     EST 26-JAN-2001
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                    H30660045 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone BG081576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="H3066G04"
/clone_lib="NTA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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         3276 TCAGAGTATAATGTTTATGGTGACAAATTAAAGGCTTTCTTATATGTT 3324
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Pred. No. 1e-48;
0; Mismatches 69; Indels 0;
                                 /db_xref="niaEST:H3066G04-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: George J. Kargul
Laboratory of Genetics
                                                                                                                                                                                                                                                            BG081576.1 GI:12564144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
Other_ESTs: H3066G04-3
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Best Local Similarity 87.4%;
Matches 480; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 549)
                                                                                                                                                                                                                                                                                                                                   Mus musculus
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BG081576
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CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BEG74096 448 bp mRNA linear EST 08-SEP-2000 7d74g04.xl NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3278742 3' similar to contains element MER22 repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  1482 CCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAG 1541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1542 GTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTC 1601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1602 CCTTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGC 1661
                                                                                                                                                                                   1242 GCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTC 1301
                                                                                                                                                                                                                                                                                                            1302 TEGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGG 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 CCTCCCTCACCACCGTGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGACGCTGGAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TGGTCATGGACAGGCTGGTACAGAAGTTCGGCACACGGTCAGTCTATCTGGCCAGTGTGA 240
                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
9
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 448)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute; Cancer Genome Anatomy Project (CGAP),
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                                                              1182 TGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCCCCGAGGCCCGGAGACACTATGATGAAG
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Matches 462;
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                                                                               53 GGATCTGAGTGATGAGACGTGTCCCCACTGAG--GTGCCCCACAGCAGCAGGTGTTGAGC 110
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                                                                                                                                         CTAGGCAGTTGGCGGCAGCAAGGAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGA
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                                   Score 453; DB 14; Length 934;
Pred. No. 1e-50;
0; Mismatches 130; Indels 55
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77.5%;
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AI703348 469 bp mRNA linear EST 18-DEC-1999 wd93b09.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2339129 3',

AI703348.1 GI:4991248

human. EST

mRNA sequence. AI703348

DEFINITION AI703348/c

ACCESSION VERSION KEYWORDS SOURCE

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In Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capabb-riemail.ih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.hml
Insert Length: 566 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_LuS was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414921 and 1520904-1524439). Subtraction by Bento Soares and M. Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2857 AAGGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTCTTGGC 2916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2917 CCAGCCTGGTTCCCCCCACTTCCACTCCCCTCTACTCTTAGGACTGGGCTGAAG 2976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 CCAGCCTGGTTCCCCCCACTTCCACTCCTCTACTCTATCAGGGACTGGNCTNATGAAG 350
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          Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 469)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                    Chordata; Craniata; Vertebrata; Euteleostomi;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="carcinoid"
/lab_host="DH10B"
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Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples [Dibert Smith, NIH"]
                                                                                                      1486 CCTCTACCACCGGGAGAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGC 1545
                                                                                                                                                                                                                                                                                                                                                                                     EST 08-FEB-2000
1426 AGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTC 1485
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                             622 CAGTGCCCTCACGGGGTGCATCTC-GGGCTGGAGATACCGGCTTACACGCACTT 679
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                                                                                                                                                                                                                                                                                                                                                                                     AW412402 592 bp mRNA linear EST 08-FEB-20C uo78h02.yl NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2648691 5' similar to TR:Q39231 Q39231 SUCROSE-PROTON SYMPORTER. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 592)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI'CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, blopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
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High quality sequence stop: 421.
Location/Qualifiers
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Mus musculus
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1148 ACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAG 1207
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/clone="IMAGE:6396364"
/clone="IMAGE:6396364"
/lab_host="be"NcICGAP_CO24"
/lab_host="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/note="organ: cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                        907
                         122 GCCCCTACCTGGGTACTCAGGAAGAATGCCTCTTTGGCCTCCTCACCTCATTTTCCTC 181
                                                                                          908 ACCIGCGIAGCAGCACACIGCIGGIGGCIGAGGAGGCAGCGCIGGGCCCCACCGAGCCA 967
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Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
Tobna Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
I.Column: 05
High quality sequence stop: 634.
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AGENCOURT_8881033 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:6396364 5', mRNA sequence.
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946 AGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTG 1005
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Innoyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM9855 row: j column: 10
High quality sequence stop: 610.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /strain="FVB/N"
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/clone="InAGE:1240607"
/clone=lib="NCI_CGAP_Kid14"
/lab_host="DH10B (Ti phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life
a 275 c 262 g 202 t
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                  /note="Organ: prostate; Vector: pT713D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I: oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Sco RI sites of the modified pT713 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491 CAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGGCTTCAGGTCTCAACGGCTTCCCTA 432
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 929)
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                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 4.4e-51;
0; Mismatches 7; Indels
                                                                                                               /tissue_type="normal prostate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                       116 t
                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1158206"
/clone_lib="NCI_CGAP_Pr22"
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98.0%;
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                                                                                                 /sex="male"
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                                                                                                                              1085 CCCGCACCCTGCGCCGCTCTTCGTGGCTGTGCAGCTGGGATGGCACTCATGACC 1144
CCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGC 1024
                                                               TIGGCTITCCGGAACCTGGGGGCGCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCATG 1084
               5;
                                                                                422 CCCGCACCTGCGCCGGCTCTTCGTGGCTGAGCTGGAGCTGGATGGCACTCATGACC 481
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11 (bases 1 ttp://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Plate: LLAM10257 row: e column: 03
High quality sequence stop: 608.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs_remail.nih.gov
Tyssue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 1.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:4458602"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sam/dev_stage="10 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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al Similarity 82.9%;
583; Conservative
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959 ACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCCACTGCTGTCCATGCCGG 1018
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                                                                                                                                                                                                                                                                                   1259 CIGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTG 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1319 GTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCTTTCCCTGTGGCT 1378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emst. Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 919 Std Error: 0.00
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                        241 GGCATGCCTCGCACCCTACGCCGACTCTTTGTGGCTGAGCTGTGCAGCTGGATGGCACTT 300
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NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                      181 GTTGGCCTGGCTTTCCGGAATCTGGGTACCCTGTTTCCCCGGCTGCAGCAGCTGTGCTGC
                                                                                              1019 GCCCGCTTGGCTTTCCGGAACCTGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGC
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High quality sequence stop: 472.
Location/Qualifiers
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Unpublished (1997)
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AA631143
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242 CTCACCTGCGTAGAGCCCACACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAG 301
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/db_xref="taxon:9606"
/clone="IPCA-2"
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99.0%;
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Matches 476; Conservative
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                                                                                                                                                                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGTCCGAGCTCGCACGCCCAGCCCCAGGTGACACCGCCAGGCCAGGATCTGA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGGGIGAGCCGCCIGCTGCGCACCGGAAAGCCCAGCICTTGCTGGTCAACCTGCTAAC 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.6%; Score 463; DB 13; Length 90
78.5%; Pred. No. 5e-52;
Live 0; Mismatches 165; Indels
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                       /strain="1129.CSTBL/61,FVB/N"
/db_xref="taxon:10090"
/clone="twAGE:5337073"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
                                               e: LLAM11855 row: p column: 02 quality sequence stop: 778.
Location/Qualifiers
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                                                                                                                                                         /organism="Mus musculus"
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                      http://image.llnl.gov
Plate: LLAM11855 row:
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AF109299 Homo sapiens prostate adult Homo sapiens cDNA clone IPCA-2
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/note="multiple clone assembly from multiple libraries and
                                                                                                                                                                                716 GCCCTGCTCTCTGA--CCTCTTCCGGGACCCGGACCAC-TGTCGCCAGGCCTACTCTGTC 772
692 GATCTTGGGAGTGGGGCTGCTGGACGT-TGTGGCCAGGTGTGCTTGTACTCCATTTGGAG 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  666 GCGTGGGGCTGCTGGACTTCTGT-GGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTC 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 482) Walker,M.G., Volkmuth,W., Sprinzak,E., Hodgson,D. and Klingler,T. Prediction of gene function by genome-scale expression analysis: prostate cancer associated genes conne Res. 9 (12), 1198-1203 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         725 TCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATG 784
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Pred. No. 7.6e-52;
0; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Homo sapiens prostate adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmaceuticals 3174 Porter Drive, Palo Alto, CA 94304, USA co-expressed with known prostate-cancer genes. Location/Qualifiers
                                                                                                                                                                                                                                                                                                          831 GGGACA-CCAGTGCCCTGGCCCCTACCTGG 860
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901 bp mRNA linear EST 12-SEP-2001
603296208F1 NCI_CGAP_Mám3 Mus musculus cDNA clone IMAGE:5337073 5',
mRNA sequence.
B1650119
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                                                                                                                                                      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
CNA Library Arrayed, by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Lncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                    CCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCA
                  241 GGACACCAGCGTTCTGGCCCCCTACCTGGGTACTCAGGAAGAATGCCTCTTTGGCCTCCT
                                                                                                                                                                                                                                                                                                                                                                                                 361. GGGCCCACCGGAGCGGCAGAAGGGTTGTTGGTCTCTGCCGTGTCGCGCGGATGCTGCCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                              653 CTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTG
                                                                                                                                                                                                                                                                                                                     GGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCCAGGAGGAGTGCCTCTTTGGCCTGCT
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Contact: Robert Strausberg, Ph.D.
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E I (bases 1 to 786)

I (bases 1 to 786)

I Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLMAN10264 row: e column: 05
High quality sequence stop: 666.
I Constinn/Qualifiers
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602334219F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4457452 5',
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                                                                                                                                                                                                                                    GCGTGGGGCTGCTGGACTTCTG - - TGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCT 723
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TCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCT
                                                                              GGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGG
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/dev_stage="10 months, virgin"
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                                                                                                                                                                                                                                                                                                                                                                                                                     840 TGCTGGGCCCCTACCTGGGTAATCAGG 866
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Ste_2: Not!, Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation? 3.31 (1996)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 GGACCGCCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGTTGGCGG 185
13. GAATTGGCACTAAAGGGCTGGCAGAAATGGGAACCTGGCTGCACCCTAGGAGGTTAGTGC 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
                                                                                                                                                                cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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                                                                                                                                              cDNA Library Preparation: Life Technologies, Inc
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                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM10834 row: i column: 18
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/organism="Mus musculus"
                                                                     Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:5473696"
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/tissue_type="amelanotic melanoma, cell line"
/lab_host="PHIOB (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ReoRI; cDNA made by oligo-dT priming Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies). Note: this is a NIH_MGC Library.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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BM912193.1 GI:19362572
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TITLE
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                                                                                                           2843
                                                                                                                                                                                                                                                                                                                                                                                    BG122427 118 bp mRNA linear EST 30-JAN-2001 602353324F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4451572 5',
                                                                                                                                                                                    2844 AGGGTGTTGAA-GGAAGGTAGAGGTGGGGCTTCAGGTCTCAACGGCTTCCCT-AACCAC 2901
                                                                                                                            61 AACAGCTAGCCTCCTAGTTGAGACACACTAGAGAAGGG-TTTTGGGAGCTGAATAAACT 119
                                  CTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCAT 361
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 715)
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/tlosue_lib="NIH_MGC_90"
/tlssue_type="footbase."
/lab_nost="Dell'adenocarcinoma, cell line"
/lab_nost="Dell'adenocarcinoma, cell line"
/lab_nost="Dell'adenocarcinoma, cell line"
/lab_nost="Organ: liver; Vector: pcWv-SpORT6; site_1: Not!;
Site_2: Sall; cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                           2784 CAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAATGCTGTTACCCAAGGTT
                                                                                                                                                                                                                       482 AGGGTGTTGAACGGAAGGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAAACCAC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                           2902 CCCTCTTCTCTTGGCCCAGCCT-GGTTCCCCCCCACTTCCACTCCCCTC 2948
                                                                                                                                                                                                                                                                              15.4%; Score 525; DB 12; Length 715; 94.5%; Pred. No. 3.9e-60;
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Plate: LLAM10238 row: p column: 05
High quality sequence stop: 689.
Location/Qualiflers
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/db_xref="taxon:9606"
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Matches 664; Conservative
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AGNOCORT_6613122 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5473696 BM912193
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1667)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM1985 row: 1 column: 17
High quality sequence stop: 448.
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                             120 CAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCT
                                                                                                                                                         180 TGCATGGGAGTTTCTAGGATGAACACTCCTCCATGGGATTTGAACATATGAAGTTATT
                                                                                                                                                                                                                                                     2450 GTAGGGGAAGAGTCCTGAGGGGCAACACAAGAACCAGGTCCCCTCAGCCCACACTT
                                                                                                                                                                                                                                                                                                                   240 GTAGGGGAAGAGTCCTGAGGGGCAACACAAGAACCAGGTCCCCTCAG-CCACAGCACT
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                                                                                                                            2391 TGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATG-ACTTATTT
                                                                                                                                                                                                                                                                                      2868 TGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCT 2910
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: DCTD/DTP
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Similarity
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JOURNAL
COMMENT
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                         RESULT 16
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/db_xref="rtaxon:gofo"
/clone="IMAGE:4905674"
/clone="IMAGE:4905674"
/clone="IMAGE:4905674"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.8%; Score 538.2; DB 12; Length 1035; 93.1%; Pred. No. 5.9e-62; tive 0; Mismatches 33; Indels 14;
                                                                                                          /organism="Homo sapiens"
High quality sequence start: 3
High quality sequence stop: 602.
Location/Qualifiers
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/ub.tel TrAAGE:4661500"
/clone=TrAAGE:4661500"
/clone=TrAAGE:4661500"
/clone=TrAAGE:4661500"
/lab_host="BH10B (phage=resistant)"
/note="Organ: colon: Vector: porB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oliqo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5 adaptor: GGCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)"
35 a 153 c 133 g 168 t
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                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://image.llnl.gov
Plate: LLCM1460 row: k column: 05
High quality sequence stop: 587.
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BG469586 589 bp mRNA linear EST 21-MAR-602533622F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4661500 5'
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 589)
1 (NHH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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2.2e-61;
2;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                              mRNA sequence.
BG469586
BG469586.1 GI:13401861
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qq	Qy	qq	Qy	qq	δδ	qq	Oy	qq	ολ	QQ	Qy	QQ	δλ	qa	QY	QQ	Qy	QQ	Qy	qa	Qy	qq		RESULT 1 BG828841	DEFINITI	ACCESSIO	KEYWORDS	ORGANI	CNG GEGGG	AUTHOR TITLE	JOURNA			
301 AGTCTGTCACTGCCTATATGGTGTCTCCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTG 3,60	1896 CTACACACGTAGTATTTGACAAGGCGACTTGGCCAAATACTCCAGGTAGAAAACTTCCA 1955	361 CTACACAGGTAGTATTGACAAGAGGGACTTGGCCAAATACTCAGCGTAGAAAACTTCCA 420	1956 GCACATTGGGGTGGAGGGCTGCCTCACTGGGTCCCAGCTCCCGGCTCCTGTTAGCCCCA 2015	421 GCACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCAGCTCCCGCTCCTGTTACCCCCA 480	2016 TGGGGCTGCCGGGCTGGCCGCCAGTTTCTGTTGCTGCCAAGTAATGTGGCTCTCTGCTG 2075	481 IGGGGCTGCCGGCCGGCAGGTTCTGTTGCTGCCAAAGAAATGTGGCTCTCTACTG 540	2076 CCACCCTGTGCTGCTGAGGTGCTGCACAGCTGGGG 2115	541 CCACCTGTGCTGCTGAGGAGCCTAGCTGCAACGGGG 580				BC242597 BC242597 1 GI:12752412		Mus musculus Eukarvota Matazoa Chordata	Mammalla: Ettheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1116)		Unpublished (1999)	Email: cgapbs.refmail.nih.gov Tissue Promirement: Gilbert Smith. Dh.n.	CDNA Library Preparation: Life Technologies, Inc.	DNA Sequencing by: Incyte Genomics, Inc.	found through the I.M.A.G.E. Consortium/LINE at:	hete: LLAM10319 row: c column: 03	high quality sequence stop: bbb. Location/Qualifiers		/Strain= rvb/n /db_xref="taxon:10090" />conseq=rayon=r	/clone_lib="NCICGAP_Mam1" /tions_troot_abs_mam1" /+icon_troot_abs_mam1	/tissue_fype= cumot, biopsy sample: /dev_stage="10 months, virgin" /lab host="nulne"	/inc_nose_final parametry: Vector: pCNV-SPORT6; Site_1: Sall; Site 2: Not1: Cloned unidirectionally. Primer: Olico dr.	Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith. NIH"	209 a 349 c 314 g 244 t	tch al Similarity 84.8%; Pred. No. 1.2e-62; 644; Conservative 0; Mismatches 111; Indels 4; Gaps 3;	1023 GCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCCGCA 1082		1083 TGCCCGGACCTGCGCCGCTCTTCGTGCCTGAGCTGCAGCTGGATGGCACTCATGA 1142
Dp	Qy 1	qq	Oy 1	Op	0y 2	qq	0y 2	qq	RESULT 14		DEFINITION	ACCESSION VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	JOURNAL						FEATURES	aoinos						BASE COUNT ORIGIN	Query Match Best Local Matches 64	0y 1	qa	Oy 1

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                                           1143 CCTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGGGTGTACCAGGGCGTGCCCAGAG 1202
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1035)
                                                               369 CTGCCACCTGCCAGTGCCAGCGTGGTAGTGACAGCCTCAGCTGCCTCACCGGGT
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement. Afroc
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can http://image.lln.gov
Phttp://image.lln.gov
I column: 03
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BG828841
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1836 AGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGCGCATTTACTTTG 1895
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98.3%;
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Best Local Similarity
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                              RESULT 13
BM914562
                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                               ACCESSION
                                                                                                           VERSION
KEYWORDS
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                                                                                                                                                                                            REFERENCE
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                                                             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH 22, 37-43 (1999) " 22, 37-43 (1999) " 215 t
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/dev_stage="10 months"
/lab_host="DH10B"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IxMAGE:5480245"
/clone="IxMAGE:5480245"
/clone=lib="NIH_MGC_113"
/lab_host="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr prining. Dixectionally cloned
into ECORI/XhoI sites using the following 5; daptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
BM914562 1060 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6615475 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480245
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                                                                                                                                                                                                                                                                                                                                                                  L Morbilished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capbs-rémain.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Rlate: LLCM2002 row: m column: 14
High quality sequence stop: 485.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 2.3e-65;
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Ph.D

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BI107873 858 bp mRNA 11near EST 26-JUN-2001 602901816F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5031771 5',
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1510 GTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGAC 1569
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 958)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                         1690 CGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCT-
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                                                                                         1570 CAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTACTCGAATGGACACGTGGGTGCTGG
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Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng i
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng i
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
Cound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMI1088 row. o column: 04
High quality sequence stop: 810.
Location/Qualifiers
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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BI107873
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TITLE
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/lab_host="bullOB (phage-resistant)"
/nab_host="bullOB (phage-resistant)"
/note="oran colon, Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XioI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
73 a 272 c 264 g 185 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: agapba-remail.nih.gov
Email: agapba-remail.nih.gov
Tissue Procurement: Arrayed
Tissue Procurement: Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1458 row: a column: 09
High quality sequence stop: 671.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
NIH-MGC http://mgc.noi.nih.gov/.
Nathonal Institutes of Health, Mammalian Gene Collection (MGC)
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                                                 2998 ACCCCCAACTTTCCCCTACCCCCAACTTTCCCCACAGCTCCACAACCCT-GTTTGGAGC
                                                                    3057 TACTGC--AGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCC
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/db_xref="taxon:9606"
/clone="IMAGE:6202754"
/clone_lib="Lupski_sclatic_nerve"
              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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Mammalia! Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 875)
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NIH-MGC http://mgc of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pcMv-SPORT6 (Life Technologies); Site_1: Not1: Site_2: Sal1; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TGAACCAGGGGGGCGCGGTa, and
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CDNA Library Arayed by: The I.M.A.G.E. CONSORTHUM (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
flound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM13621 row: f column: 03
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1974 CCTGCCTCACTGGGTCCCAGCTCCCGGTTCTTAGCCCCATGGGGGTGCCGGGCTGGC 2033
                                                                                                                                                                                                   2034 CGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCCTCTCTGCTGCCACCCTGTGCTGCTGAG 2093
                                                                                                                                                                                                                                                                                  2154 CTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAA 2213
                                                                   483 GTGCGTAGCTGCACAGCTGGGGGCTGCCTCTCCTCTCTCCCCAGTCTCTAGGG 542
        303 ACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGGTGGAGGG 362
                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1196 row: a column: 08
High quality sequence stop: 675.
Location/Qualifiers
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BF972601
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NotI; Site_2: Sall; cDNA made by oligo-dr priming.
Directionally cloned using the following adaptors:
5. TGGACGAGGGGTCGG-3. and
1 kb for average insert length.187 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
Technologies.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1614 GACACGIGGGIGCIGGAGGCAGIGGCCIGCICCACCICCACCGGGGCTCIGCGGGGCCT 1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1674 CTGCCTGTGATGTCTCCGTACGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTC 1733
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                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Consortium/LLNL at:
High quality sequence start: 2
High quality sequence store: 490.
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                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="IMAGE:6204253"
/sex="male" Lupski_sciatic_nerve"
/sex="male"
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0; Mismatches 13
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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IMAGE: 6204253 5', mRNA sequence.
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                                      BQ950805.1 GI:22366283
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/db_xref="taxon:96pfo"
/clone="IMAGE.4331407"
/clone="IMAGE.4331407"
/clone="IMAGE.4331407"
/clone="IMAGE.4331407"
/clone="IMAGE.4331407"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.88b. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Strategene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
            EST 22-JAN-2001
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebratå; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 850)
BF972601 850 bp mRNA linear EST 22-JAN-20
602243025F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4331407 5',
                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 020)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
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Matches 733; Conserv
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EST 20-0CT-2000
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                                     CTGTGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGG 1737
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                                                                                                                                     181 CCGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGC 240
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                                                        62 GETGGGTGCTGGAGGCAGTGGCTCCCACCTCCACCGCGCGCTCTGCGGGGCCTTTGC 121
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov. a column: 04
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                                                                                                                  CCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGC
                                                                                                                                                                                               CCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AGENCOURT_8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                          1300 TCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGT 1359
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                                                                                                                                                                          Library constructed by Life
                                                                                                           /tissue_type="adenocarcinoma"
/lab_host-"DH10B (phage-resistant)"
/note-"Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.8 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1540 AGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGC
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                                                                                                                                                                                                                                                       19.4%; Score 660.2; DB 12; Length 718; 97.7%; Pred. No. 6.2e-78; tive 0; Mismatches 14; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1958 ACATTGGGGTGGAGGCCTGCCTCACTGGGTCCCAGCTCCCCGCTC 2003
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                                                                                                                                                                                                             1 others
                                                                                                                                                                                                             210 g 168 t
                                               /organism="Homo sapiens
                                                                              /clone="IMAGE:3846411"
/clone_lib="NIH_MGC_65"
High quality sequence stop: 693.
Location/Qualifiers
                                                               /db_xref="taxon:9606
                                                                                                                                                                                               Technologies.
                                                                                                                                                                                                                                                                                           690; Conservative
                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 690; Conserval
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5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCCCGAGCGCCCCCT(15)-3'. Size selected >
1' Ab for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2277 TAGCCTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCA 2336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Gaps
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.6%; Score 703.2; DB 14; Length 916; 98.8%; Pred. No. 1.2e-83;
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                                                                                                                                                                                                                                                                  /clone="IMAGE:6205362"
/clone_lib="Lupski_sciatic_nerve"
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0; Mismatches 3
                                                                                                                                                                                                                                                                                                                        /tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                    http://image.llnl.gov
Plate: LLAM13628 row: b column: 19
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                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                     High quality sequence stop: 579.
Location/Qualifiers
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Matches 751; Conservative
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/db_xref="taxon:gentems"
/db_xref="taxon:gentems"
/clone="INAGE:4660703"
/clone="INAGE:4660703"
/clone="ThAGE:4660703"
/clone="ThAGE:4660703"
/clone="Cype="Nadenccarctnoma cell line"
/lab.host="DH10B (phage=resistant)"
/note="Organ: colon; vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by ollgo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5/ adaptor: GGCACGAG(G). Size=selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life'Technologies)"
35 a 245 c 239 g 181 t
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2992
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                  602532993F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660703 5',
                     2875 TCAGGTCTCAACGC-TTCCCTAACCACCCCTCTTCTCTTGGCCCAG-CCTGGTTCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: ArCc
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                         601 TCAGGTCTCAACGCTTTCCCTAACCACCCTCTTCTTTGGCCCAGCCCTGGTTCCCCC
                                                                                                                                                                2933 CACTTCCACTCCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 800)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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                                                                                                                                                                                                                                                    2993 CCCCTACCCCAAC - TTTCCCCTACCCCAACTTTCCCC 3030
                                                                                                                                                                                                                                                                        19.6%; Score 667.4; DB 12;
97.0%; Pred. No. 6.6e-79;
....matches 16;
                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
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High quality sequence stop: 741.
Location/Qualifiers
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Best Local Similarity
Matches 744; Conserv
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/db_xref="taxon:9606"
/db_xref="Tuxon:9606"
/clone="Inse:5481218"
/clone=lib="NHH_MGC_41"
/tissue_type="amelanotic melanoma, cell line"
/tissue_type="amelanotic melanoma, cell line"
/tasue_type="amelanotic porps: state_1: XhoI; Site_2:
/lab_host="BulloB (phage-resistant)"
/note="Organ: skin; Vector: pOTP7; Site_1: XhoI; Site_2:
Gool: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                        AGENCOORT_6702317 NIH_MGC_41 Homo saplens cDNA clone IMAGE:5481218 5', mRNA sequence.
BM915082
BM915082.1 GI:19365461
EST.
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1022 CGCTTGGCTTTCCGGAA -- CCTGGGCGCCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCC 1079
                                                                1195 GCCCAGAGCTGAGCCGGGCACC-GAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGG 1253
                                                                                                                                   1138 CATGACCTTCACGCTGTTTTACACGG - - ATTTCGTGGGCGAGGGGCTGT - ACCAGGGCGT 1194
                720 GGCATGCCCGGAACCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGCATGGCAACT 779
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1025)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: Rhe I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2005 row: f column: 03
High quality sequence start: 35
High quality sequence stop: 657.
                                                                                                                                                     840 TGCCAGAGCTGAGCCGGGCACCGGAAGCCCGGAGAACCTATGCTGAACGCGTCCGCAT-G
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                                                                                                                                                                                                                                                                         1254 GCAGCCTGGGGCTGTTCCTGCAGTGC 1279
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Contact: Robert Strausberg, Ph.D.
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Subaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 916)
                                                                                                                    72 TCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAG 131
12 CCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTG 71
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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BG469889
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 94). NIH-WGC http://mgc.nci.nih.gov/. NIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                          ACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCAGTT
                                                                    ACTGGGTCCCAGCTCCCCGCTCTGATAGCCCCATGGGGCTGCCGGGCTGGCCGCCAGTT
                                                                                                         2102 CTGCACAGCTGGGGCTGGGGCGTCCCTCTCTCTCCCCAGTCTCTAGGGCTGCCTGA
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Contact: Robert Strausberg, Ph.D.

Unpublished (1999)

TITLE JOURNAL COMMENT

REFERENCE AUTHORS Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC

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/clone_lib="NiH_MGC_15"
/clone_lib="NiH_MGC_15"
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/lab_nost="bH10B (phage-resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis Kit
(Stratagene) and Superscript II RT (Life Technologies)"
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                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4661075"
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/clone_lib="Lupski_sciatic_nerve"
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/organism="Homo sapiens'/db_xref="taxon:9606"
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/organism="Homo sapiens"
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/db xref="taxon:9606"
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/clone_lib="NIH_MGE:441"
/tissue_type="amelanotic melanoma, cell line"
/tab_host="Bull08 (phage-resistant)"
/lab_host="Bull08 (phage-resistant)"
/note="Organ: skin; Vector: pOrB7; Site_1: XhoI; Site_2:
/note="Organ: skin; Vector: porB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Sifatagene) and
Superscript II RT (Life Technologies). Note: this is a
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AGENCOURT_6701857 NIH_MGC_41 Homo sapiens CDNA clone IMAGE:5481717
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NIH-WGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Preparation: Rubin Laboratory
Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.j column: 22
High quality sequence start: 131
High quality sequence stop: 308.
Location/Qualifiers
                             803 CTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTACCTGGGC
745 GGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTC - -TTGGGGGCTGC
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                                                                                                                                                                                                                                                                               863 A -- CCCAGGAGAGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 others
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95.0%; Pred. No. 4.2e-92;
ive 0; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 g
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283 c 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM915527.1 GI:19365906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5', mRNA sequence.
BM915527
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June 9, 2003, 15:13:08; Search time 4204 Seconds (without alignments) 13136.682 Million cell updates/sec
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3410
1 gggaaccagcctgcacgcgc.....aaaaaaaataaaaaaaaa 3410
                                                                                                                                                                                                                                                                                                                                                                                         32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                            16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                            OM nucleic - nucleic search, using sw model
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em_gss_mus:* em_gss_other:* gb_gss:* em_gss_hum:* em_gss_inv:* em_gss_vrt:* em_gss_fun:* em_gss_mam:* gb_est2:*
gb_htc:*
gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:*
em_estfun:* em_gss_pro:* em_gss_rod:* em_gss_pln:* em_estmu:* em_estov:* em_estpl:* em_estro:* em_htc:* gb_est1:* em_estba:* em_esthum:* em_estin:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	SC	% Query Match	- Fe	DB	SUMMARIES	Description
4	7.64.2			14		BO948390 AGENCOURI
7	767.2			14	BM915527	BM915527 AGENCOURT
٣	749.6			12	BG469889	BG469889 60253334
4	748.6	22.0	1025	14	BM915082	BM915082 AGENCOURT
Ŋ	703.2			14	BQ950912	BO950912 AGENCOURT
9	667.4			12	BG469487	BG469487 60253299

BE867241 601442309 BQ950805 AGENCOURT BG942028 AGENCOURT BG469520 602532838 B1107873 602901816 BM914556 AGENCOURT BG242597 602354010 BG88841 60275813 BG124257 60233422 BG124257 60233422 BG12429 AGENCOURT BG884609 602798469 BG184699 BG1843419 BG174136 60233411 AA631143 nq75908 SB17673136 60233411 AA631143 nq75908 SB173348 60233411 AA631143 nq75908 SB174044 xBE674096 G0210444 xBE674096 G0210444 xBE674096 BBC104959	BB627667 BG246497 602360526 AW175665 RC3-B7004 AF109303 AF109303 B1145201 60290395 BB627844 BB627044 AW787124 120845 MA AA579486 nf33407.s BF680993 602156279 AW135465 UI-H-BII-BB701488
BEB67241 B0950805 BF872601 BF872601 BF72601 BF72601 BF72601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601 BF772601	BBC27667 AW175665 AW10303 AF92235 AF109303 BI145201 BB627844 AW787124 AM579486 BF680993 AW135465
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	335 335 335 335 335 444 445 445 455 455
U U	00 00

ALIGNMENTS

		AGENCOURT_8803099 Lupski_sciatic_nerve Homo sapiens	BQ948390	BQ948390.1 GI:22363868	EST.	human.	4 Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 885)	NIH-MGC http://mgc.nc1.n1h.gov/.	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	Contact: Robert Strausberg, Ph.D.	Email: cgapbs-r@mail.nih.gov	Tissue Procurement: Dr. James R. Lupski	CDNA Library Preparation: Life Technologies, Inc.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Agencourt Bioscience Corporation	Clone distribution: MGC clone distribution information can be	found through the I.M.A.G.E. Consortium/LLNL at:	http://image.llnl.gov	Plate: LLAM13611 row: b column: 08	High quality sequence stop: 615.	Location/Qualifiers	
RESULT 1 BQ948390	rocus	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT											FEATORES	

		1106 ACAGCCGCAGGAGGAGCATGCGGGAGCAGCAGCAGGAGCAGGAGCAGAAGCAGAAGCAGAAGCAGG 1047
SGAGCTGGGACCCAGTGAGGCAGGCCCTCCAC 1966	λ'n	
	QQ	
	· 0y	1046 CGCCCAGGTTCC
	qa	567 ProproGlyAlaAlaGlyThrProGlyLeuGlnGlyMetProGlyGluArgGlyGlyLeu 586
	Qy	1034GGAAAAGCCAAGGGGCCCGGCATGGACAGCT 1002
10.1	qq	587 GlySerProGlyProLysGlyAspLysGlyGluProGlyGlyProGlyAlaAspGlyVal 606
	Qy	1001 GGGGCGACAAGGAGGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCCAGCG 948
######################################	qq	607 ProGlyLysAspGlyProArgGlyProThrGlyProIle 619
	Qy	947 CTGCCTCCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCA 888
AGGAAGGCACTATCCAGGATGGCGA 1/58	qa	620 GlyProProGlyProAlaGlyGlnProGlyAspLys 631
	Qy	887 GGCCAAAGGCACTCCTCCTGGGTGCCCAGGTAGGGGGGCCAGGGCACTGGTGTCCC 831
:::	qa	632 GlyGluGlyGlyAlaProGlyLeuProGlyIleAlaGlyPro 645
	٥٧	830 AGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGA 771
	q a	
yGluProGlyArgAspGlyValProGlyGlyP 385	۸٥	770 CAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCAGGG 717
CACGTGTCCATTAGGGAAGGGAGCTCCAGGCT 1590	' qq	ThrGlvProProGlvProAlaGlvPheProGlvAlaProGlvGluProGlv
GlySerAspGlyLys	ò	
SGCTGTCCTCACTGCTAGCACCTCCAGTGTCCC 1530	7 6	
	aa ,	GIYLYSGIYGILARIGETYALARIOGIYGILALYSGIYGILAGIYGIYRIDFIOGIYGAI
CTCCCGGTGGTAGAGGGAGGCCAGTGTGTAGG 1470	Oy	GCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCC
	qq	694 AlaGlyProProGlyGlySerGlyProAlaGlyProProGlyProGlnGlyValLySGly 713
ממטעיטעטע	Qy	605 AGCCGCCCTTGCGATGAGAAGAGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGA 546
	qq	714GluArgGlySerProGlyGlyPro721
	δδ	GGCTGAGCCTA
GGCAGCCACAGGGAAAGCTGCCACACTGGCCA, 1350 	. qa	::: 722
AlaProGlyLys 444	ò	485 CACAGACCAGGCCCAGGACTAGGACCAGGACCATGGTCATGGACTTGAACTTCTCCTCTA 426
SCACCAGCCGGTCCATGACCAGAGAGAAGACCA 1290	do	GlyLeuProGlyPro
slyProGlyGlyProGlyProGlnGlyProPro 460	٥	CCCCCACTTCCAGCAGCAGAGGCGGCACATAGGT
ACAGCCCCAGGCTGCCCA 1251	7 7	
	an	ProproglyProserglyser
GGCCTCGGTGCCCGGCTCTGGGCACGC 1191	δλ	299299
 	qq	752 GlyLysAspGlyProProGlyProAlaGlyAsnThrGlyAlaProGly 767
	δλ	305 TCACCCACAGCCTCTGGACCATAGTGGG
	qa	
	٥٧	257 GGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCA 212
	qa	
	QY	211GAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAG 171
	Dp	
ProGlyLeuAlaGlyAlaProGlyLeu 546	_	

Qy Db	170 GAATCAGCCAGGCGCCATTCTGCCAGCCCTTGGTGCCGGTCCAGCTTCTCAG 116	q a	::: 82 LeuproGlyMetLysGlyHisArgGlyPheSerGlyLeuAspGlyAlaLysGlyAspAla 101
δ	ACCTCA	δδ	1876 ACCCAGGCCTGCGGCAGCACCATATAGGCAGTGACAGACTGCTGAGCTGGACAA 1821
qa	840 uSerGlyGluArgGlyProProGlyProGln-GlyLeuProGlyLeuAlaGlyThra 859	qa —	GlyProAlaGlyProLysGlyGluProGlySerProGlyGluAsnGlyAlaProGlyGln
oy :	GTGGGGACACGTCTCACTCAGATCCTGGC	Oy Db	1820 TGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCA 1782
g ::		Oy	
දු පු	48	qa	
RESULT 43	100 T 100 T	Oy	1721 CCTCGGTGGGCTCACCCACCACACACGTACGGAGACATCACAGGGAGAGGCCCCGC 1665
US-09-219-849-49	849-49 49, Application US/09219849	ପ୍ପ	159 lyProThrGlyProProGlyPheProGlyAlaValGlyAlaLysGlyGluAlaGlyProG 179
Patent	Patent No. 6150081 GENERAL INFORMATION:	· 0y	1664 AGAGCGCGGGTGGAGGTGGGAGGAGGCCACTGCCTCCAGCAC 1623
APPLICANT:	ANT: VAN HERDE, GEORGE V.	qa —	
, APPLICANT:	NYT: BOUWSTRA, JAN B. BOWSTRA, JOHN B. BOWSTRA, JOHN B.	Oy	1622 CCACGTGTCCATTAGGGAAGGGAGCTCCAGGCTTAGGGCCTGGCAGGAAGC 1572
APPLICA	ANT: MODBREK, ANDREAS ANT: WERTEN MARANDEAS	ପ୍	
APPLICA	ANT: WIND, RICHELE D. VAN DEN ROCH, TANTA J.	Qy	1571 TGGTCATCAGGCTGTCGCTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGA 1512
TITLE	DE INVENTION SILVER HALDE EMULSIONS WITH RECOMBINANT COLLAGEN TO INVENTION SILVER HALDE EMULSIONS WITH RECOMBINANT AS COMPANY OF THE PROPERTY	qa	219 GlyAlaAsnGlyAlaPro
; TITLE (JE INVENTION: PREPARATION THEREOF	Qy	1511 ACACCTGCTTCTCCCGGTGGTAGAGGAGGCCAGTGTAGGGCAGGATCTGCAGGGCTG 1452
CURREN	: TILE REFERENCE: 2/20-2 : CILL REPRENT APPLICATION NUMBER: US/09/219,849 : CILL REPRENT PITING NAME. 1000-13-23	qa	
NUMBER SOFTWAR	DE CALLO CAL	٥٨	1451 AGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTGTCACCACGGCCACACTGTGGGACAGGC 1392
SEQ ID NO 49	76.9 70.9 1.823	qa	
TYPE:	Janain Saria ORGANISM Artificial Semiono	Oy	1391 ATGTGGCACCGGCACCACAGGGAAAGGTGCCACACTGGCCAAATAGACTGCTCGAGTGC 1332
FEATURE:	(E. T. T. C. C. C. C. C. C. C. C. C. C. C. C. C.	qa	
) OTHER INFORM US-09-219-849-49	ATION: amino acid sequence	ογ	1331 GGAATGGCAGCAGCAGGGGTGACCAGAGAGAAGACCAGGGAGATGGCGCACTGCA 1272
Alignment Scores		. qa	277valGlnGlyProProGlyProAlaGlyGluGluGlyLysArgGlyAlaArg 293
Pred. No.: Score:	6.84e-19 Length: 351.00 Matches:	QY	1271 GGAACA
Percent S. Best Local	Percent Similarity: 32.94% Conservative: 37 Best Local Similarity: 28.60% Mismatches: 328	qq	294 GlyGluProGlyProSerGlyLeuProGlyProProGlyGluArgGlyGlyProGlySer 313
Query Mato DB:	5.64% Indels:	VO.	1241CTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCA 1194
.03-09-759	19 (1-822)	qa	314 ArgGlyPheProGlyAlaAspGlyValAlaGlyProLysGlyProSerGlyGluArgGly 333
oy 2	2131 AGAGGGACGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGC 2072	O.Y	1193 CGCCCTGGTACAGCCCCTCGCCCAGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTG 1134
qq		qq	334 AlaProGlyProAlaGlyProLysGlySerPro 344
0,		QY	1133 CCATCCAGCTGCACAGCTCAGCAAGAGCGGGGGGAGGGTGCGGGGGATGCGGCAGC 1074
	27 GlyGluProGlyGluProGlyGlySerGlyProMetGlyProArgGlyProProGlyPro 46	qq	345Gly 345
Qy 3		٥y	
ОЪ		QQ	
0y . 1	CAATGI	Oy 40	AGCGGGCCCGGCATGGACAGCAGTGGGGGGGGAGGGGGCCGACAGCCCTTCTGCTG 96
qq	67 ProProGlyProGlnGlyAlaArgGlyLeuProGlyThrAlaGly	g :	GlySerProGlyProAspGlyLysThrGlyProProGlyProAlaGlyGlnAsp
0y 1	1936 GTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAG 1877	оу 	965 GCTCGGTGGGCCCAGGCTGCT942

qq	384 GlyArgProGlyProAlaGlyProProGlyAlaArgGlyGlnAlaGlyValMetGlyPhe 403
γç	941 CCTCAGCCACCAGCAGTGTGGCTACGCAGGTGAGGATGAGGGTGAGGCCAA 882
qo	
ρy	881 AGAGGCACTCCT
qc	419 ArgGlyLeuProGlyProProGlyAlaValGlyProAlaGlyLysAspGlyGluAlaGly 438
λς Op	869CCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGGTGTCCCAGTCATGGCAGGGA 816
} ;	∇
, G	9 GlySerProGlyPheGlnGlyLeuProGlyProAlaGlyProProGlyGluAlaGlyLys
δý	779 AGGCATAGACAGAGTAGGCCTGGGGGGGGGGTCGGGGTCCCGGAAGAGGT 729
Q Q	479 ProGlyGluGlnGlyValProGlyAspLeuGlyAlaProGlyProSerGlyAlaArgGly 498
λς.	728 CAGAGACCAGGGCCTCCAGTGGAGTGAAGCACCCTGGCCACACACA
2	stuniytiyrneriOsiystuniysiyvatsinsiyriOriOsiyriOniasiyriO
Qy Dp	668 CGCCCAGGATGAGCAGTGCCA
Οy	GCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAGAGGGC
_ qa	:: 538 AlaProGlySerGlnGlyAlaProGlyLeuGlnGlyMetProGlyGluArgGly 555
Οy	578 TCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCGCCATAGCGTCCAC 519
qa	:::
Qy	518 GCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACAGGCCCCAGGCCCAGGACCAA 459
qq	
٥y	458 TGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGCAGCGGCA 399
Db	591GlyProProGlyProAlaGlyAlaProGly 600
Qy	398 CATAGGTGATGCCTGCGGCCAAACACACTCCAGGC
Dp	601 AspLysGlyGluAlaGlyProSerGlyProProGlyProThrGlyAlaArgGlyAlaPro 620
٥y	362CAAAGGTTAGCAGGTTGACCAGCAAGAGGTGGGGTTTCCGGTGCCGCAGCA 312
QQ	621 GlyAspArgGlyGluAlaGlyProProGlyProAlaGlyPheAlaGlyProProGlyAla 640
QY	311 GGCGGCTCACCACAGCCTCT
QQ	
Qy	290GGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCC 240
qq	661 ProproGlypro-alaGlyproalaGlyproproGlyprolleGlyAsnValGlyAlapr 680
Qy	GAAGCTGCGGCCTCT
qq	680 oGlyProLysGlyProArgGlyAlaAlaGlyProPro-GlyAlaThr- 695
οy	179 ACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTC 120
qq	696GlyPheProGlyAlaAlaGlyArgValGlyProProGlyProSerGlyAsnA 713
οy	9 TCAGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGT
Db	713 laglyproproglyproproglyprovalGlyLysGluGlyGlyLysGlyProArgGlyG 733

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1966 ------CCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTT 1916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2110 GCTGTGCAGCTACGCACCTCAGCACACAGGGTGGCAGCAGAGAGCCACATTACTTTGGC 2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2050 AGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGCTAACAGGAGCGGGGAGCTG 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1990 GGA----- 1000 TGCAGTGAGGCAGGCCCTCCA----- 1967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 GlyAlaPro---GlyProGlnGlyPheGlnGlyProProGlyGluProGlyGluProGly 51
                                 733 luThrGlyProAlaGlyArgProGlyGluValGlyProProGlyProProGlyProAlaG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 AlaSerGlyProMetGlyProArgGlyProProGlyProProGlyLysAsnGlyAspAsp 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --G 45
                                                                                                                                                                                                                                   TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-759-143-110 (1-3410) x US-08-931-820-1 (1-1057)
   74 ACACGICICATCACTCAGAICCIGGCCGA---
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/931,820 FILING DATE:
                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
FILING DATE:
                                                                   44 GCGCGCGCTGTCACCCGGAGCC 22
                                                                                                                                                 US-08-931-820-1

Sequence 1, Application US/08931820

Patent No. 6010863

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     υκσΑΝΙΣΜ: Homo sapiens
; TISSUE TYPE: Collagen type I
US-08-931-820-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.16e-18
345.00
32.73%
228.01%
5.54%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
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                                                                     δλ
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	415	905	Qy 854Db 849 AlaClyLysAspGlyGluAlaGly	Qy 839 TGGTGTCCCAGTCAATGGCAGGCACACACACACACACACA	Qy 803 GGCAGCCCCAAGACTGATCATGAU 	Qy 746 CCGGGTCCCGGAAGAGGTC 509 ProGlyProSerGlyAlaArgGly	Qy 692 GGCCACAGAAGTCCAGCAGCCCAAC	Qy 647GCTCCAGGGC	Qy 602 CGGCCCTTGGGATGAGAAGGGCT ::: Db 566 GlnGlyMetProGlyGluargGly		Oy 485 CACAGA	Db 619 AspLysGlyGluSerGlyProSerC	Qy 446 TGGTCATGAACTTCTCCTCTACCCC	Qy 386 CTGCGGCCAAACACACCTCCAGGC- Db 655ProProGlyA	Oy 338 AGAGCTGGGCTTTCCGGTGCCGCAG	Qy 278 GCCAGGGGGGTAG	Qy 230 TCGTCTCGGCTCTGCTCCA	Qy 176 GCCTAGGAATCAGCCAGGCGCCCAT
1915 GTCAAATACTACCTGTGGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACAC 1856 ::: 107 ArgGlyPheSerGlyLeuAspGlyAlaLysGlYAspAlaGlyProAlaGlyProLysGly 126	1855 CATATAGGCAGTGACTGGCTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGC 1796 	1795 CACCTGGGACAGCAGGAAGGCACTATCCAGGATGGCGAGGTCCAGGCAGAT 1745	1744 GCCCCGGCCGGAA		1677GCAGAGGCCCGCAGAGCGCGGGTGGAGCAGCCAGGCCACCTGCCTCCAGCAC 1623 1::	SGCTTAG 31yAlaA		1511 ACACCTGCTTCTCCCGGTGGTAGAGGGAGGCCAGTGTGTAGGGGA 1467			1367 AAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCGGTCCA 1308 :::	1307 TGACCAGAGAGACCAGGGAGATGGCGCACTGCAGGAACAGCCCCAGGCTGCCCATCC 1248	GGGCCTCGGTGCCCGGCT 		AGCTGCACAGGTCAGCACGCAGCGCGCGCGGGGCATGCGGCAGCACCTGCTGCAGCAGCTGCGCAGCAGCTGCGGGGCATGCGGCAGCAGCTGCGGGGCAGCAGCTGCGGGGCAGCAGCAGCTGCGACAGCAGCTGCGGGGCATGCGGCAGCAGCAGCTGCAGAAAAAAAA			959 TGGGGCCCAGCG 930
QY Db	oy O	Oy Dp	Qy Dp	. QY	Qy Db	Qy	Ογ Dp	Oy Dp	O _Y	Oy Dp	· Qy	Qy	yo,	Oy Db	Qy	Oy Op	Qy Db	Qy

qa	
Qy	929GCAGTGGCTGCTACGCAGGTGA 906
QΩ	415 GlnAlaGlyValMetGlyPheProGlyProLysGlyAlaAla428
٥y	1
Ор	429 GlyGluProGlyLysalaGlyGluArgGlyValProGlyProProGlyAlaValGlyPro 448
δλ	854AGGGGCCAGGGCAC 840
qq	
Qy	839 IGGICICCCAGICAAIGGCAGGCAGGA
qq	469 GluArgGlyGluGlnGlyProAlaGlySerProGlyPheGlnGlyLeuProGlyProAla 488
Οy	803 GGCAGCCCCAAGACTGATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT 747
qq	489 GlyproProGlyGluAlaGlyLysProGlyGluGlnGlyValProGlyAspLeuGlyAla 508
οy	746 CCGGGTCCCGGAAGAGGTCAGAGGAGCAGGCCTCCAGTGGAGTGAAGCACACCT 693
q	
٥y	692 GGCCACAGAAGTCCAGCCCCCAGGATGAGCAGTGCCA
qq	528 GlyProProGlyProAlaGlyProArgGlyAlaAsnGlyAlaProGlyAsnAspGlyAla 547
Óλ	647GCTCCAGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCCAGC 603
qa	548 LysGlyAspAlaGlyAlaProGlyAlaProGlySerGlnGlyAlaProGlyLeu 565
٥y	602 CGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGG 543
Dp	566 GlnGlyMetProGlyGluArgGlyAlaAlaGlyLeuProGlyProLysGlyAsp 583
Οy	AGGAGCG
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Οy	てつ ー
qq	601 ValArgGlyLeuThrGlyProIleGlyProProGlyProAlaGlyAlaProGly 618
Qy	452GCACCA 447
qq	619 AspLysGlyGluSerGlyProSerGlyProAlaGlyProThrGlyAlaArgGlyAlaPro 638
Qy	446 TGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGAGGCGCCACATAGGTGATGC 387
qq	639 GlyAspArgGlyGluProGlyProProGlyProAlaGlyPheAlaGly 654
Qy	386 CTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCA 339
qq	aAspGlyGlnProGlyAlaLysGlyGluP
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QQ	670 AspAlaGlyAlaLysGlyAspAlaGlyProProGlyProAlaGlyPro-AlaGl 687
٥y	\circ –
Dp	7 yProProGlyProIleGlyAsn
Qy	0 TCGTCTCGCCTCTGCT
qa	4ArgGlySerAlaGlyPro
Qy	176 GCCTAGGAATCAGCCAGCGCCCATTTCTGCCAGCCTTTGGTGCGGGTCCAGCTTCTA 117 ::

Db 25 HisProProPheAlaSerAspProMetGlyAlaHisGlyProAlaGlyProLysGly 43	2194	Qy 2134 AGGAGAGGCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCAGGTGGC 2075	Qy 2074 AGCAGAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGC 2020	Qy 2019	QY 1975 GGCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTTT 1916	OY 1915 GTCAAATACTGTGTAGCAAAGTAAATGGCGACCAGGCCTGCGGCAGACAC 1856	Qy 1855 CATATAGGCAGTGACAGACTGGCTGGACAATGGAGCCCATAAACAGGGATGGGGC 1796	Qy 1795 CACCTGGGACAGCAGCACTATCCAGGATGGCGAGGTCCAGGCAGATGCCCGGCC 1736	Qy 1735 CGGAACCACCTGGCTCGGTGGGCTCACCACCACCACCACGGAGACATCACAG 1678	Oy 1677GCAGAGGCCCGCAGAGGGGGGGG	Qy 1638CCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGAGCTCCAG 1593	Oy 1592 GCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGCTCACTGCTAGCACCTCCAGTGT 1533	Qy 1532 CCCCTCGGTATTTGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGAGGCCAGTGT 1473	Qy 1472 AGGCAGGATCTGCAGGCCTGAGAAGGTGAACCCGGTGAGGCGGCTGAAGCTGTCACCA 1413 Db 257 ProGlyGlySerArgGly	OY 1412 CGGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACACTGG 1353	QY 1352 CCAAATAGACTGCTCGAGTGCCGAATCGCTGCAGCGGTCCATGACCAGAGAGA 1296	2/2AGACCAGGAGATGGCGCACTGCAGGAACAGCCCA	281 AspProGlyProProGlyAlaGlnGlyProAlaGlyGlyGlySerArgGlyAspPro	Qy 1259 GGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGCTC 1200
Db 722 lGlyProProGlyProSerGlyAsnAlaGlyProProGlyProAlaGlyLy 742	OY 116. GCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGACACGTCTCATC 63	Oy 62 ACTCAGATCCTGGCCGAGGCGCGCGCGCTGT 33	Qy 32 CACCCGGAGCC 22	RESULT 45 US-08-642-255-73 ; Sequence 73, Application US/08642255	; Patent No. 5773249; General Information; Applicant: Cappello, Joseph; Applicant: Ferrari, Franco A.	ENTION: High Molecular Weight Colla ENTION: Protein Polymers QUENCES: 135 CE ADDRESS:	; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT ; STREET: 4 Embarcadero Center, Suite 3400 ; CITY: San Francisco ; STATE: California	PE PE	ompatible PC-DOS/MS-DOS Release #1.0, ATA:		4884	8700 71 73:	HAR 63 Min NES	; TOPOLOGY: Inear ; MOLECULE TYPE: protein US-08-642-255-73	Alignment Scores: Pred. No.: 1.97e-18 Length: 633 Score: 344.50 Matches: 245 Percent Similarity: 33.54% Conservative: 32	: 29.66% Mismatches: 5.53% Indels: 1 Gaps:	US-09-759-143-110 (1-3410) x US-08-642-255-73 (1-633)	OY 2314 AAAAACCTICTCTAGGTGTCTCAACTAGGAGGCTAACTGTAACCTGAGCTGGGT 2255 ::: ::! Db 12 GluAshProGlvValThrGlnLeuAshArgLeuAlaAla 24	2254 AATCCACCTGCAGAGTCCAGTGCATGGAGCCTTCTGGCCTCCTGTATA

317	F 4	1140 326
1139		1080 339
1079	GGCAGCACAGCTGGTGCAGCCGGGAAGCAGGCC ::: GlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAspProGlyP	1035 359
1034		975 3.75
974		933 392
932		873 407
872	CCTCCTGGGTGCCCAGGTAGGGGCCAGGGCACTGGTGTCCCAGTCAATGG 	822
821	CAGGCAGGAGGTAGCCCAGGCAGCCCCAAGACTGATCATGAAGGCATAGACGAGTAGG	762
761	CCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGAGCAGGGCCTCCAGTGGAG	705
704	TGAAGCACACGTGGCCACAGAGTCCAGCAGCCCCACGCCCAGGATGAGCAGTGCCAGCT	645 456
644	44 CCAGGGGCCTGGGATCCGGGCACAGCAGCCTGCTAGCCAGCC	585 467
584	AGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCGCCATAGC	525 482
524	GTCCACGCCAGTGGTCACTGGCTGAGCAGCGGGACACAGACCAGGCCCAGCACTG	465
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523	GCGGCACATAGGTGATGCCTGGGGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGA	345 533
344	CCAGCAAGAGCIGGGCTTTCCGGTGCCGCAGCAGCGGGCTCA	303 553
302	CCCACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGCCGTTCAGG	246 571
245	CACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTG	186 584

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	627 lnLeuval 629		qq
	11 GGCTGGTT 4	11	Qγ
627	608 oLysGlyAlaMet-AspProGlyArgTyrGlnLeuSerAlaGlyArgTyrH1sTyrG 627		QQ
12	71 CGTCTCATCACTCAGATCCTGGCCGAGGCGGCGGCTGTCACCCGGAGCCAGGGCGTGCA 12	71	QY
608	603 sGlyProAlaGlyPr 608		QQ
72	CTCAGCCCATGCTCAACACCTGCTGTGGGGGACCTCAGTGG		Ωÿ
603	584 rArgGlyAspProGlyProProGlyAlaHisGlyProAlaGlyProLysGlyAlaH1 603		qq
131	GGAATCAGCCAGGCGCCATTTCTGCCA		ò

US-09-759	1-143-110 (1-3410) x Q9FVL6 (1-604)	
Οy	193 GAGGAGGCCGCAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGAGTGCCTGAAC 252	
qa	SerArgPheAlaGlnLeuGlulleArgSerAspSerSerSerProArgValSer	
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qa	45 GlygluMetAsnAspSerAsnLeu	
Qy	313 GCTGCGGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGT 372	
qa	59 -valArgAsnSerLeuLeuThrLeuIleLeuSerCysThrValAlaAlaGlyValGlnPh 78	
٥y	373 GIGTITGGCCGCAGCCATCACTATGTGCCGCTCTGCTGGAAGTGGGGGTAGAGGA 432	
Db	78 eGlyTrpAlaLeuGlnLeuSerLeuThrProTyrIleGlnThrLeuGlyIleGluHi 98	
Qy	433 GAAGTTCATGACCATGGTGCTGGGCATTGGTCTGGGCCTGGTCTGTGTCCCGCT 492	
Dp	98 sAlaPheSerSerPheIleTrpLeuCysGlyProIleThrGlyLeuValValGlnProCy 118	
Qy	493 CCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCGCCCTTCATCTG 552	
qq	118 svalGlyIleTrpSerAspLysCysHisSerLysTyrGlyArgArgArgProPheIlePh 138	
QY.	553 GGCACTGTCCTTGGCTATCCTGTGTGAGCCTCTTTCTCATCCCAAGGCCCGGCTGGCT	
qq	138 eIleGlyAlaValMetIleSerIleAlaValIleIleIleGlyPheSerAl 155	
οy	613 AGGGCTGCTGTCCCGGAT	
qq		
Qy	637 GCCCCTGGAGCTGGCACTGCTGATCCTGGGGCTGGGGCTGGACTTCTGTGGCCAGGT 696	
q	175 gSerArgAlaAlaIleValPheValValGlyPheTrpWetLeuAspLeuAlaAsnAsnTh 195	
Qy	697 GIGCITCACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCG 756	
qq	195 rValGlnGlyProAlaArgAlaLeuLeuAlaAspLeuSerGlyProAspGlnArgAs 214	
οy	TACTCTGTCTATGCCTTCATGAT	
qq	Asnile	
Qy	817 GCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTAGGCAC 864	
qq		
Οy	865 CCAGGAGGAGTGC	
QQ	249 nArgAlaCysCysGluProCysGlyAsnLeuLysAlaAlaPheLeuValAlaValValPh 269	
οy	904 CCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGCAGGCAGCGCTGGGCCCCAC 960	
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qa	289 sGlnTyrLysArgMetSerAspSerAlaProLeuLeuAspSerProGlnAsnThrGlyPh 309	
Qy	1004TGCTGTCCATGCCGGGCCCGCTTGCCGAACCTG 1042	
qq	309 eAspLeuSerGlnSerLysArgGluLeuGlnTyrArgAsnSerValAlaAsnAsnGluSe 329	
Qy	1042 1042	
QQ	329 rGluMetGlyHisValAlaAspAsnSerProLysAsnGluGluGluGlnArgProAspLysAs 349	
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Db	349	pGlnGlyAspSerPheAlaAspSerProGlyAlaValLeuValAsnLeuLeuThrSerLe 369
Qy	1075	CTGCCGCATGCCCCGCACCCTGCGCCCGCTTCGTGGCTGAGCTGTGCAGCTGGATGGC 1134
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Qy	1135	ACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTGTACCAGGGCGT 1194 :
3 ,	0 0	
yy g	409	CCCACAGGTGAGCCGGGCACCGGACACCGGACACATGAGGAGCATCAGGAGGACGATGGGGGGGG
Qy	1255	CAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTC
Db	427	
Qy	1315	GCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGT1357
qq	447	::: ::: oMetCysLysTrpIleGlySerArgLeuValTrpAlaValSerAsnPheIleValPheVa 467
QΥ	1358	
qq	467	lCysMetAlaCysThrAlaIleIleSerValValSerIleSerAlaAsnThrGlnGlyVa 487
Qy	1396	GGTG
Db	487	
Qy	1450	CTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTACCA 1494
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Oy	1495	CCTGC
qa	525	
6y	1555	GGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAAGCCTGGAGCTCCCTTCCCTAATGG 1614
Db	531	531
о. О	1615	ACACGTGGGGGGGGGGGGGGGGCTGCTCCCACCTCCACCGGGCTCTGCGGGGCCTC 1674
qq	532	111111 11111 11111 11111 11111 11111 1111
Qy	1675	TGCCTGTGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCCAGGGTGGTTCC 1734
. qq	537	
Qy	1735	GCCTGGACCTCGCC
qa	548	oglnMetValValSerLeuGlyAlaGlyProTrpAspAlaLeuPheGlyGlyGlyAsnIl 568
Qy	1795	သ္မ
ДQ	568	laPheAlaLeuAlaSerLeuAlaAlaLeuAl
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Qy	268	ACCGCCTGGCCCACTATGGTCCAGAGGTGTGGGGTGAGCCGCCTGC	315
qq	m	ThrG	22
δλ	316		366
qa	23	AlaProProSerSerAsnLeuLysLy	42
Qy	367	GGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGGGT	4.26
qq	42	IGinPheGlyTrpAlaLeuGlnLeuSerLeuThrProTyrValGlnLeuLeuGlyII	62
Qy	427	AGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGT	486
Dβ	62	eroHisThrTrpAlaAlaPhelleTrpLeuCysGlyProIleSerGlyMetLeuValGl	82
Qy	487	ည	546
Dp	82	::::: ProlleValGlyTyrHisSerAspArgCysThrSerArgPheGlyArgArgArgProPh	102
Οy	547	CATCTGGGCACTGTGGGCATCCTGGAGCCTCTTTCTCATCCCAAGGGCC	601
qq	102	ellealaalaGlyalaalaServalalavalPheLeuIleGlyTyrAlaAlaAs	122
Qy	602	GGATCCCAGGCCCCTGGAGCT	654
Db	122	Asp	142
Οy	655	GCTCATCCTGGGCGTGGGGCTGCTGCTGCTGGCCAGGTGTGCTTCACTCCACTGGA	714
Dp	142	ephevalvalGlyPheTrpIleLeuAspValAlaAsnAsnAshActLeuGlnGlyProCysAr	162
δŷ	715	CCTGCTCTCTGACCTCTTC CGGGACCGGACCACTGTCGCCAAGGCCTACTCTGT	771
Db	162		182
Oy	772	CTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGCCTGCC	829
Db	182	uPheSerPhePheMetAlaValGlyAsnIleLeuGlyTyrAlaAlaGlyAlaTyrThrHi	202
٥y	830	TGGGACACAGTGCCCTGGCCCTACCTGGGCACCA	. 498
qq	202	ø.	222
٥y	868	CACCCTCATCTTCCTCACCTGCGTAGCAGCCAC	924
qq	222	::: leSerIleAlaLeuLeuLeuValLeuThrValIleAlaLeuTh	242
Qy	925	rGGTGGCTGAGGAGGCTGGGCCCCACCGAGCCAGAAGGGCTGTC	981
qa	242	rValLysGlu-LysGln"rpSerPro-GluIleAlaLysThrValAlaGly	259
Qy	982	ລອອອລລອ	1020
qq	260	ValAspGlyAspAspGluAspGlyProvalGluAlaAlaProLeu	274
Qy	1021	GCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCG	1080
QQ	275		287
οy	1081		1140
Dβ	288	GlnArgProMetArgIleLeuLeuValThrCysLeuAsnTrpIleAlaTrpPh (306
οy	1141		1200
qq	306		326
οy	1201	C.	1260
Dp	326		346
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QQ	26 LeuPheLeuAlaCysMetValAlaGlyGlyValGlnTyrGlyTrpAlaLeuGlnLeuSer 45	1	
οy	395 TATGTGCCGCCTCTGCTGCAAGTGGGGGTAGAGGAAGTTCATGACCATGGTGCTG 454	Qy 1397 TCCCA	CC S
QQ	::: ::: ::: ::: :::	Db 372	;
٥٨	455 GGCATTGGTCCAGTGCTGGGCTGTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC 514	Qy 1457 CTGCA	3CA
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δλ	839 AGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGC	477	_ se
qq	201 HisLysTrpPheProPheLeuMetThrArgAlaCysCysGluAlaCysAlaAsnLeuLys 220		1
δλ	878 CTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG 934	4535 6535	ž
qq	221 AlaAlaPheLeuValAlaValPheLeuGlyLeuSerThrAlaValThrWetValPhe 240	Q9M535;	Ž.
οy	SCAGCGCTGGGCCCCACCGAGCCAG	DT 01-0CT-2000 DT 01-0CT-2000	CC
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Š i	SAGGECEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	Alignment Scores:	
ŝ	31/ ValThrAlaPheGinGiuGiyValArgGinGiyAlaPheGiyLeuLeuLeuAsn 334	Pred. No.: Score:	
δλ	1277 TGCGCCATCTCCCGGTCTTCTCTCGGTCATGGACCGGCTGGTGCAGCGATTCGGCACT 1336	Percent Similarity Best Local Similar	ty: ari
qa	335 SerileValLeuGlyileSerSerPheLeuIleGluProMetCysArgArgLeuGlyAla 354	Query Match: DB:	
Qy	1337 CGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCATGCCTG 1396	US-09-759-143-110	0
qa ,	355 ArgalaValTrpValMetSerSerAlaValValCysValAlaMetAlaAla 371	1	

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ATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTC 1576
CAGTGTGGCCGTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCC 1456
                                                                              GATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCTG 1516
                                                                                                                                                                                                                                                 AGGCCCTAAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGT 1636
                                                                                                                                                                                                                                                                                                                                                                                                                  CGTACGTGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGCCGGGGC 1744
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yalaGlyProTrpAspGluLeuPheGlyGluGlyAsnIleProAlaPheAlaMet 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                         rValProPheAlaValThrAlaGlnLeuAlaAlaSerArgGlyGlyGlyGlnGly 438
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on of mRNAs expressed in underground adventitious buds of la (leafy spurge).";
la (leafy spurge).";
R.2000) to the EMBL/GenBank/DDBJ databases.
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003662; sub_transporter.
8 sugar_tr; 1.
8 sugar_tr; 1.
8 R01301; GPH_sucrose; 1.
8 AA; 55843 MW; 059C1ED3BB02D356 CRC64;
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ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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------GlyAspPheGlyGly---SerValGlnAspAlaAlaArg------
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327.50
40.64%
24.42%
5.10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELIMINARY;
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772 laAspGlyGlnProGlyAlaLysGlyGluGlnGlyGluAlaGlyGlnLysGlyAspAlaG 792	1181GCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCT 112	792 lyAlaProGlyProGinGlyProSerGlyAlaProGlyProGlnGlyProThrGlyV 811	1123 GCACAGCCACGAAGAGCCGGCGCGGGGGGGGGGGGGCGCGCGCACGCT 1068		830 roGlyAlaAlaGlyArgValGlyProProGlySerAsnGlyAsnProGlyProProGlyP 850	1012 TGGACAGCAGTGGGGCGA 995	850 roProGlyProSerGlyLysAspGlyProLysGlyAlaArgGlyAspSerGlyProProG 870	994 CAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCTCT 939	870 lyargaladlyAspProGlyLeuGlnGlyProAlaGlyProProGlyG 886	938CAGCCACCAGCAGTGTGGGC 920	886 luLysGlyGluProGlyAspAspGlyProSerGlyProAspGlyProPro 902	919 IGCTACGCAGGIGAAGAAGAGTGAGCAGCCAAAGAGGCACTCCTCCTGGGIGCC 860	903GlyProGlnGlyLeuAlaGlyGlnArgGlyIleValGlyLeuP 917	859 CAGGTAGGGGGCCAGGGCACTGGTGTCCAGTCAATGGCAGGCAG 815	917 rodlyGlnArgGlyGluArgGlyPheProGlyLeuProGlyProSer 932	814 GAGGTAGCCCAGGCCCCCAAGACTGATCATGAAGGCATAGACAGTAGGCCTGGCG 755		ACAGTGGTCCGGGTCCGGGAGAGAGGTCAGAGAGCAG			- rydruriodaryniydaudaryiiirriodarynaanspolyrio	659TGAGCAGTGCCAGGTGCCAG 641 979 rgAspGlyAlaAlaGlyValLysGlyAspArgGlyGluAlaGlyAlaEuGlyAlaProG 999		1yAlaProGlyProProGlySerProGlyProAlaGlyProThrG	592 GATGAGAAAGGCCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCG 539	1014 lyLysGlnGlyAspArgGlyGluAlaGly-AlaGlnGlyProMetGlyProAlaGlyPro 1033	538 GCGGCGGCCATAGCGTC 522	1034 AlaGlyAlaArgGlyLeuProGlyProGlnGlyProArgGlyAspLysGlyGluAlaGly 1053	521 CACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACAGA	1054 GlualaglygluargglyLeuLysGlyHisargglyPheThrGlyLeuGln 107	479TGCCCAGCACTAGACCAATGCCCAGCACCA 447	109	446 TGGTCATGACTTCTCTCTACCCCACTTCCAGCAGCAGGGGGGCACATAGGTGA 390
Db	δy	QQ	oy Op	٥y	Dp	Qy	QQ	οy	Dþ	οy	QQ	δý	Dp	٥ý	qq	οy	QQ	oy .	qq	ky fa	3 6	දු පු	è	5 q	Οy	Dp	Qy	qq	οy	qq	οy	QQ	Qy Db

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1111 IleProGlyProIleGlyProProGlyProArg------GlyArgSerGly 1125
                                                                                     1145 oGlyProGlyIleAspMetSerAlaPheAlaGlyLeuGlyProArgGluLysGlyProAs 1165
                                                                                                                                                                                                                                  71177
                                                                                                                                                                                                                                                                                                ------GlyLeuArgProHisAspGl 1184
                                                                                                                                                                                                                                                                                                                                                                                                                     329 CTTTCCGGT---GCCGCAGCAGCGGCTCACCCACAGCCTCTGGACCATAGTGGGCCAGG 273
                                                                                                                               272 CGGG--------TAGGGCTCAGGGGCCGTTCAGGCACTCCAGA 237
                                                                                                                                                                                                236 ACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGGCCTCTCCTTGCTGCTGCCGCCAACT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 CTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACC 394
                                                                                                                                                                                                                                                                                                                                124 ------GCTTCTCAGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGG 75
                                                                                                                                                                                                                                                                                                                                                                                                74 ACACGTCTCATCACTCAGATCCTGGCCGAGGCGCGCGGCTGTCACCCGGAGCCAGCGCGT 15
389 TGCCTGCGGCCAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGG
                                                                                                                                                                                                                                                               176 GCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGTGCCGGTCCA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orgza sativa (Rice).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. NIPPONBARE: TISSUE-PANICLE;
Hirose T., Scoffeld G.N., Whitfeld P.R., Aoki N., Furbank R.T.,
Terao T.;
                                                                                                                                                                                                                                                                                                                                                   |||:::
|1184 uGluValGluAlaThrLeuLysSerLeuAsn------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and characterisation of a cDNA for a novel sucrose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transporter, OsSTT3, from rice.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB071809; BAB68368.1; -.
Interpro; IPR0365; sub_transporter.
Pfam; PF00081; sugar_tr; 1.
TIGRFAMS; TIGR01301; GPH_sucrose; 1.
SEQUENCE 506 AA; 52776 MW; 0844DC10E1E63E75 CRC64;
                                                                                                                                                                                                                   : |||:::
1165 pProLeuGlnTyrMetArgAlaAspGluAlaAlaGly------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                506
143
77
207
129
21
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Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q948L0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
Sucrose transporter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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327.50
39.57%
25.72%
5.10%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Best Local Similarity:
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Οy	AAGCCGTTGAGACCTGAAGCC	đ	
Db	162 GlyGluProGlyValSerGlyProMetGlyProArgGlyProProGly-ProProGl 180	a a	
Οy	2852 CAACACCCTAACCTTGGGTAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCC 2793	टें ट	1934 A111
QQ	180 yLysPro 182	3 8	
Qy	2792 AAGGTCCTGGGTTAGGCATTTTGGGGGCCCAGACAGAAGAAGAAGATTCTGGCAATG 2733	3 6	168 VIOL
qq	183 190	3 6	
δy	2732 ATCAGCCCAATGACCAGCTATCTCAGGGGACCTGATTGTTGGGGATCCCCCCACCCTACCC 2673	, 45 10	
Dp	191	a è	1818 GAGG
Qy	2672 AAATAITAGACACCAACACAGAAAGCIAGCAATGGATTCCCTTCTACTTTGTTAAATAA 2613	7 E	
Dp	203GinglyAlaArgGlyPheProGlyThrProGlyLeuPr 215	ì ò	
٥y	2612 ATAAGTTAAATATTTAAATGCCTGTGTCTCTGTGATGGCAACAGAAGACCAACAGCCA 2553	r qa	520 oPro
Dp	215 oGlyValLysGlyHisArgGlyTyrProGlyLeuAspGlyAlaLysGlyGluAlaGlyAl 235	δò	1755 TCC
δÿ	2552 CATCCTGATAAAAGGTAAGAGGGGGGGGGGTGGATCAGCAAAAAGACAGTGCTGTGGGCTGAGG 2493	. qa	 540 yAla
qq		. Oy	1716 GTG
δλ T	ACCTGGTTCTTGTGTGTT	qa	1 560 rgG
gg		QY	1656 GGT
Qý		qq	 579 Gly
Ор	260	Qy	1638 CCA
οy	2372 GCTGCAGGTTAAGGGGGTTAGAGATGGGAAACCAGGTGACTTGAGTTTATTCAGC 2319	ପ୍ର	 599 Pro
QQ	268 oalaGlyalaAlaAlaArgGlyAsnAspGlyGlnProGly 282	۸٥	1602
Qy	2318 TCCCAAAAACCCTTCTCTAGGTGTCTCACTAGGAGGCTAGCTGTTAACCCTGAGCCT 2259	qd	619 Glu
qq	283 -ProalaglyProProGlyProValGlyProAlaglyGly	2 5	
Qy	2258 GGGTAATCCACCTGCAGAGTCCCCGCAITCCAGTGCATGGAGCCCTTCTGGCCTCCCTGT 2199	Z 2	
Db	296 oGlypheproGlyAlaProGlyAlaLysGlyGluAlaGlyProThrGly 312	3 8	
οy	2198 ATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCA	Š Š	
QO		an ,	nry /ea
, VQ	2158GGCAGCCCTAGAGACTGGGGAGAGAGG	δλ O	
Op		on io	100 //0
٥y	2131 2120	à á	
q		a :	Aye 160
Qy	2119 -CAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAGA 2067	8 d	
qa	368 gGlyProFroGlyProGlnGlyAlaThrGlyProLeuGlyProLysGlyGlnThrGlyGl 388	3 8	267 27/
6y	2066 GCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGGCTAA 2007	ž ž	_
qa	388 uproglyllealadlypheLysGlyGluGlnGlyProLysGlyGlubroGlyProAlag1 408	3 &	
Qy	2006 CAGGAGCGGGGACCCGGCCCAGT	; a	755 rg-
qa	. 408 yProGlnGlyAlaProGlyProAlaGlyGluGluGlyLysArgGlyAlaArgGlyGluPr 428	3 8	
οy	1981GAGGCAGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGT 1935	13	

428	 AlaProGlyAsnArgGlyP	
1934	3CCAAGTCGCTCTTGTC	
448	 eProGlyGlnAspGlyLeuAlaGlyProLysGlyAlaProGlyGluArgGlyProSerG	
1912	GTAGCAAAG	
468		•
- 0	-GACCCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGACTGGCTGAGCTGGACAATG 18 :::	•
φ ,	yGIUPTOGLYLEUFIOGLYALaALGGLYLEUIHGGLYRIGHTOGLYRSPAL JO	
1818	GAGCCCATAAACAGGGATIGGGGCCA	_
1775	T. CACTATCCAGGATGGCGAGG I	
520	oProG	
2	TCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGCCTCG 17	_
24	yAlaAsnGlyGluProGlyLysAlaGlyGluLysGlyLeuPro-GlyAlaProGlyLeuA >>>0	
1716	GTGGGGTCACCCACCACACACATACGBAAACATCACAGGGAGGGGGGGGCCCGGGA TILIII	
	91	o.
57	GlyproAlaGlyGluArgGlyGluGlnGlyAlaProGlyProSerGlyPheGlnGlyLeu 598	
1638	CCACTGCCTCCACGTCTCCATTAGGGAAG	m
599	ProGlyProProGlyProProGlyGluGlyGlyLysProGlyAspGlnGl	
1602	GGAGCTCCAGGCTTAGGGCCTGGCAGGAGGCTGGTCATC 15	₹*
619	GlualaGlyAlaProGlyLeuValGlyPro-ArgGlyGluArgGlyPheProGlyGluAr 63	
1563	AGGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGG	
1503	TTCTCCCGGTGGTAGAGGGAGGCCAGTGTGTAGC	
'n	::: ::: yThrAspGlyProLysGlyAlaSerGlyProAlaGlyProProGly	
1458	AGGCTGAGAAGGTGAACCGGTGAGGGCGGCTGAAGCTGTCACCACGCCAC 14	
229	oGlyLeu-GlnGlyMetProGlyGluArgGlyAlaAlaGlyIleAlaGlyProLysG	
	ACTGGCCAA	
697	spargGlyaspValGlyGluLySGlyProGluGlyAlaProGlyLysAspGlyGlyA 7	
4	-GCACCAGCCGGTCCATGACCAGAGAGA 12	
716	/LeuThrGlyProileGlyProProGlyProAlaGlyAlaAsnGlyGluLysGlyG 736	
6 6		
າ	IUVAIGIYPIOPIJETONIAGIYIIIAAIAN TATATATATATATATATATATATATATATATATATAT	
1243	3 GCCTTCATCATAGTGTTCTCGGGCCTCGGTCGGGTCAGCTCTGGGCAGGCCTGGTA 1184	
00	CA	

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ολ	442 ·
qq	79 LeuGlnLeuSerLeuLeuThrProTyrIleGlnThrLeuGlyIleSerHisAlaPheSer 98
Qy	502
qa	99 SerPhelleTrpLeuCysGlyProlleThrGlyLeuValValGlnProPheValGlylle 118
Qy	503 GCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGGCCCTTCATCTGGGCACTGTCC 562
qq	138
Οy	CAAGGGCCGGCTGGCTAGCAGGG 616
qq	139 PheMetileSerileAlaValileIleIleIleGlyPheSerAlaAspileGly 155
Οy	617 CTGCTGTGCCCGGAT
qq	156 TyrLeuLeuGlyAspSerLysGluHisCysSerThrPheLysGlyThrArgThrArgAla 175
٥y	706
Db	176 AlaValValPheIleIleGlyPheTrpLeuLeuAspLeuAlaAsnAsnThrValGlnGly 195
οy	707 CCACTGGAGGCCCTGCTCTTTCCGGGACCACGCACCACTGTCGCCAGGCCTAC 766 Q28
Ор	214
οy	826
QQ	215 AlavalPheCysLeuTrpMetAlaIleGlyAsnIleLeuGlyPheSerAlaGlyAlaSer 234 DE
Qy	CAGTGCCCTGGCCTGGGCACCCAGGAGGAG 874
QQ	235 GlyLysTrpGlnGluTrpPheProPheLeuThrSerArgAla 248 OX
Qy	875 TGCCTCTTTGGC
ФФ	268
٥y	911TGCGTAGCAGCCACACTGCTGGTGGTGGGAGGCAGCGCTGGGCCCCCACCGAGCCA 967
qq	288
οy	1024
qq	289 Thrarg1leGlnAspSerAlaProLeuLeuAspAsp300 DR
Qy	GGAACCTG 1042
Db	301 LeuGInSerLysGlyLeuGluHisSerLysLeuAsnAsnGlyThrAlaAsnGlyIleLys 320 DR
Qy	1042 1042 KW
Ob	321 TyrGluArgValGluArgAspThrAspGluGlnPheGlyAsnSerGluAsnGluHisGln 340
Οy	1043
qa	341 AspGluThrTyrValAspGlyProGlySerValLeuValAsnLeuLeuThrSerLeuArg 360 Perce
٥y	TGGCACTC 1138
Dp	380
Οy	1198
Db	381 PheProPhePheLeuPheAspThTASpTrpWetGluValTyrHisGlyAspPro 400
Qy	1258
qq	pSerLeuHisMetGluLeuTyrAspGlnGlyValArgGluGlyAla 418
Οy	1259 CTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTG 1318

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1319 GTGCAGCGATTCGGCACTCGAGCAGTCTAT---TTGGCCAGTGTGGCAGCTTTCCCTGTG 1375
                                                                                                                                                                   1376 GCTGCCGGTGCCACATGCCTGTCC---- 1399
                                                                                                                                                                                                                                                                         ------CACAGTGGCCGTGGTGACAGCTTCAGCCGCC 1432
                                                                                                                                                                                                                                                                                                                                                               439 CysGlnArgMetGlyAlaArgValValTrpAlaLeuSerAsnPheThrValPheAlaCys 458
                                                                                                                                                                                                           459 MetAlaGlyThrAlaValIleSerLeuMetSerLeuSerAspAspLysAsnGlyIleGlu 478
                                                                                                                                                                                                                                                                                                     ::: ||||||::: ||| || || || 479 TyrlleMetArgGlyAsnGluThrThrArgThrAlaAlavalIleVal-----PheAla 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3032 GIGGGGAAAGTIGGGGGTAGGGGAAAGTIGGGGGTAGGGGAAATITIGGGCAGTGCCIIC 2973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2972 ATCAGCCCAGTCCTAGAGAGAGAGAGGGGAGTGGAAGTGGGGGGGAACCAGGCTGGGCCA 2913
                                                                                                                                                                                                                                                                                                                                                                                                     497 LeuLeuGlyPheProLeuAlaIleThrTyrSerValProPheSerValThrAla----- 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSOURCE OF 18-68 FROM N.A.

RAM AGLGOD J.N., Fubini S.L., Gu D.N., Tetreault J.W., Todhunter R.J.;

RAL Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

DR EMBL; U65528; AAB05773.1; --

DR EMBL; Horquo688; AAB05768.1; --

DR InterPro; IPR000087; Collagen_C.

DR InterPro; IPR000087; Fib_collagen_C.

DR Pfam; PF01219; Collagen; 18.

DR ProDom; PD000007; Collagen; 4.

DR ProDom; PD000007; Collagen; 4.

DR ProDom; PD000007; Collagen; 4.

DR ProDom; PD000007; Collagen; 18.

DR SMART; SM00038; COLFI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1493 CACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT 1543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 ------GluValThrAlaAspSerGlyGly 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Richardson D.W., Dodge G.R.; Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
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Indels:
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30.778
26.268
5.278
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Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Type II collagen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       028396
028396;
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Db 59 SerLeuValThrLeuValLeuS	38131yAspPheGlyGlySerValGlnAspAlaAlaArg 392	QQ
QY 347 AACCTGGTAACCTTTGGCCTGG	1517 CCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTC 1576	Qy
US-09-759-143-110 (1-3410) x 080605	378TrpSerLeu380	q
Query Match: 5.12% DB: 10	1457 CIGCAGATCCIGCCCTACACACIGGCCICCCTCTACCACCGGGAGAAGCAGGTGITCCIG 1516	Oy
Percent Similarity: 38.638 Best Local Similarity: 24.148		qa
	1397 TCCCACAGAGGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCC 1456	Qy
Scores:	355 ArgalavalTrpvalMetSerSeralavalvalCysvalalametAlaala 371	qa
KW Transmembrane. SQ SEQUENCE 594 AA; 63972 MW;	1337 CGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTG 1396	δý
	335 SerIleValLeuGlylleSerSerPheLeulleGluProMetCysArgArgLeuGlyAla 354	qq
	1277 IGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACT 1336	Qy
DR EMBL; AC004138; AAC32907.1; -	317 ValThrAlaPheGlnGluGlyValArgGlnGlyAlaPheGlyLeuLeuLeuAsn 334	qa
	1217 GAGGCCCGGAGACACTATGATGATGAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAG 1276	0y
	297 AspThrAspTrpMetGlyArgGluIleTyrHisGlyArgProAspGlySerProAlaGlu 316	qa
	1157 TACACGGATTTCGTGGGCGAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACC 1216	Qy
RA Shen M., Ronning C.M., Fraser C	281IleValThrGlyLeuThrTrpLeuSerTrpPheProPheIleLeuPhe 296	qa
	CTCATGACCTTCACG	δò
RP SEQUENCE FROM N.A.		q
	1046GCCCTGCTTCCCCGGCTGCACCAGCTGCTGCTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	λÕ
OC Eukaryota; Viridiplantae; Strep OC Spermatophyta; Magnoliophyta: e	AlaSer 260	qq
	995 TCGCCCCACTGCTGCTCGATGCCGGGCCCGCTTGCCGGAACCTGGGC 1045	Qy
		qq
DT 01-NOV-1998 (TrEMBLrel. 08, Cre DT 01-NOV-1998 (TrEMBLrel. 08, Las	secceaecca	δ
	221 AlaAlaPheLeuvalAlaValValPheLeuGlyLeuSerThrAlaValThrMetValPhe 240	qa
RESULT 41 080605	878 CICITIGGCCIGCICACCCICAICTICCICACCIGCGIAGCAGCCACACIGCIGGIG 934	δλ
Db 477 AlaSerValPheAlaAlaAla	::: ::: ::	qa
Qy 1835 CAGTCTGTCACTGCCTATATGC	360	Qy
	183 TrpMetalaLeuGlyAsnIleLeuGlyTyrSerSerGlySerThrAsnAspTrp 200	qa
Qy 1805 CTGTTTATGGGCTCCATTGTCC	782 AIGAICAGICIIGGGGGCIGCCIGGCTACCICCTGCCIGCCAIIGACIGGGACACC 838	Qy
Db 439 LeuCysThrGlyVali	 166 AspLeuSerGlyArgHisGlyProSerAlaAlaAsnAlaIlePheCysSer 182	qa
QY 1745 ATCTGCCTGGACCTCGCCATCC	728 GACCICITCCGGGACCCGGACCACIGICGCCAGGCCIACICIGICIAIGCCTIC 781	ΟŽ
Db 420ServalProPheAlaVal1		qa
Qy 1685 GTCTCCGTACGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	TGTGGCCAGGTGTGCTTCACTCCACTGGAG	Qy
Db 406 AlaLeuPheValPheLeuGlyI		qa
Qy 1637 GGCCTGCTCCA	626 CCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGC 667	Qy
393		qa
QY : L577 CTGCCAGGCCCTAAGCCTGGAC	575 CTGAGCCTCTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGC 625	Qy

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SCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGT 1636
                                                                  --- CCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGAT 1684
                                                                                                                                      GGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGC 1744
                                                                                                                                                                                                            PIGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCC 1804
                    |||||||
|AlaProAlaGluGluGlyGlyValArgAlaSerAlaLeu 405
                                                                                        |||::: ::: :::: ||||:::||| :::
                                                                                                                                                                                                                                                                                                      :::|||
|sluLeuPheGlyGluGlyAsnIleProAlaPheAlaMet 476
                                                                                                                                                                         ThralaGlnLeuThralaSerArgGlyGlyGlyGlnGly 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTGTGTTTGGCCGCAGCCATCACCTAT----- 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C., Besenbeck R., Stadler R., Sauer N.; misporter from Arabidopsis."; Sul,GenBank,DDBJ databases. SRAL MEMBRANE PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r cress).
ptophyta: Embryophyta; Tracheophyta;
eudicotyledons; core eudicots; Rosidae;
sicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shea T.P., Fujii C.Y., Mason T.M., C.M., Somerville C.R., Venţer J.C.; me II BAC TI7M13 genomic séquence."; BL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                   Ŋ.
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st annotation update)
(Sucrose transporter).
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120
72
174
131
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Matches:
Conservative:
Mismatches:
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QQ	. 640 nGlyAlaThrGlyGluProGlyLysAlaGlyGluGlnGlyGlyProGlyGluValGly 659	
οy	1151GCGTGAAGGTCATGAGGT 1134	
Op	660 GlyProGlyProSerGlySerArgGlyAspArgGlyPheProGlyGluArgGlyGlyIle 679	
δò.	CCATCCAGCTGCACACCAAGAGCGGCGCAGGGTGCGGGGCATGCGCAAG	
<u> </u>	bbu Glyseraladiyeroaladiyeroarqdiyalaasndiysereroolyasnaspolyala byy	•
δ d	1073ACAGCTGGTGCAGCCGGGAAGCAGGCGCCCAGGTTCCGGA 1032 1073ACAGCTGGTGCAGCCGGGAAGCAGGCCCCAGGTTCCGGA 1032 1070 ATGCTUGTUGTUGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAGTUATAATAATAGTUATAATAATAATAATAATAATAATAATAATAATAATAAT	
3 3		
<u> </u>	MetProGlyGluArqGlySerGlyGlyAsnSerGlyAlaLysGlyGluArqGlyAspGly	
ò		
7 A	GlyProLysGlyAlaAspGlyGlyPro	
οy	917 CTACGCAGGTGAGGAGATGAGGGTGAGCAGCCCAAAGAGGCACTCCTCGGTGCCCA 858	
QQ	749GlyLysAspGlyMetArgGlyMetThrGlyProlleGlyProPro 763	
οy	857 GGTAGGGGCCCAGGGCACTGGTGTCCCAGTCAATGGCAGGCA	
рþ	764 GlyProThrGlyAlaHisGlyGluLysGlyGluGlyGlyLeuGlyGlyProProGlyPro 783	
Οy	797 CCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCG 744	=
qq	784 ThrGlyGly	
٥y	743 GGTCCCGGAAGAGGTCAGAGGCCGTCCAGTGGAGTGAAGCACACCTGGCCACAGA 684	
qq	798 AlaProGlyProAlaGlyPheAlaGlyProProGlyAlaAspGlyGlnProGlyAsnLys 817	
Oy.	AGTCCAGCACCCCACGCCCAGGATGAGCA	
a a		
oy ea	653 GTGCCAGCTCCAGGGGCCTGGGATCCGGGCACAGCCGGCTGCTAGCCAGCCGGCCC 597	•
2		
λο λ	TTGGGATGAGAAAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGC	
2	Alakrosiyriokrosiyalasersiymetrio	
Oy Db	536 GGCGGCCATAGCGTCCACGCCAGTGGTCACGGCTGAGCCTGAGGAGCGGGACACAGACCA 477	
ΟÝ	476 GGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTT 417	
qq		
٥y	416 CCAGCAGCAGACGCGCCACATAGGTGATGCCTGCGGCCAAACACACCTCCAGGCCAAAGG 357	
qq	GlyLysGluGlyGlnL	
οy	356TTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCGGT 321	
QQ	902 GlyGluThrGlyIleAlaGlyArgProGlyGluAlaGlyAlaAlaGlyProProGlyPro 921	
οy	320GCCGCAGCAGC	
Db	922 SerGlyAlaSerGlyAlaLysGlyAsnAspGlyProMetGlyAlaProGlyThrProGly 941	
οy	287 CCATAGT	<u>.</u>
QQ	942 Pro-GlyGlyIleAlaGlyGlnArgGlyIleValGlyGlyProGlyGlyArgGlyProSe 961	_

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991 tGly-ProProGlyLeu-----SerGlyAlaProGlyGluAlaGlyArg---GluG 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514
                              ||| :::||| ||| ||| 961 rGlyThrAla6lyGluProGlyLysGl 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 CTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACC 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 TATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAAGTTCATGACCATGGTGCTG 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCGTGGACGCTATGGCCGCCGCCGCCTTCATCTGGGCACTGTCCTTGGGCATCCTG 574
257 GGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTC 198
                                                                                             197 TCCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTT 138
                                                                                                                                             976 nGlyProGlyGlyProValGlyGluArgGlySerProGly-------ProMe 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 LeuCysGlyProlleAlaGlyLeuIleValGlnProCysValGlyLeuTyrSerAspLys 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 LeuLeuThrProTyrIleGlnThrLeuGlyIleProHisAlaLeuThrSerValMetTrp 65
                                                                                                                                                                                             137 TGGTGCCGGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGCTGTGGGGCACCTCAGTG 78
                                                                                                                                                                                                                                                                                           ---- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     455 GGCATTGGTCCAGTGCTGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (indica cultivar-group).

Oryza sativa (indica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CV. IR 36;
Whitfeld P.R., Aoki N., Scofield G.N., Hirose T., Terao T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OSSUT3) from rice.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR19298; AAL14982.1; -.
InterPro: IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
TIGRFAMS; TIGR01301; GPH_sucrose; 1.
SEQUENCE 506 AA; 52774 MW; A4E73029D7022B64 CRC64;
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143
77
207
1129
21
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                             77 GGGACACGTCTCATCACTCAGATCCTGGCCGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                           45 ------GGCGCGCGCGCTGTCACCCGGAGCC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 AA.
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328.50
39.578
25.728
5.128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sucrose transporter.
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est Local Similarity:
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8:
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334 ProGlyPheProGlyGlyAlaGlyAlaLysGlyGluThrGlyProGlnGlyGlyArgGly 353 1981 GAGCCAGCCCT	SerGlyalaproclyathracggCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT	GluargGlyalaa GGCAGGAAGCTGG 31yGluProGlyM T OASPGlyLysVal TTCTCCCGGTGGT	AGAGGGAGGCAGAGAGAAGAGAAGAGAAGAGAGAGAGAG
4 6 6 6 6 6		9 60 60 60 60 60 60 60 60 60 60 60 60 60	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
SUL	ykiss (Rainbow trousaza; Chordata; Cre rygii; Salmoniforme 2; Neopterygii; Tele 2; Salmoniforme 2; N.A. N.A. N.A. N.A. N.A. N.A. N.A. N.A.	ignment Sco ed. No.: ore: rcent Simil st Local Si ery Match: : -09-759-143	Db 255 IleLysGlyHisArgGlyPheAsnGlyMetAspGlyAlalLysGlyAspGlyGlyProAla 274 Qy 2320 GCTCCCAAAACCCTTCTCTAGGTGTCTCAACTAGGAGGTAGCTGTAACCTGAGC 2261 Db 275 GlyProLysGlyGlu

286 CATAGGGGCCGGGCCGGGCGGGCGGGGGGGGGGGGGGGG	 b 149 nGlyProCysArg	2y 760 GGCCTACTCTGTC	b 169 rAlaAsnSerMet	180	יי מ	0 (0	209	2y 916 AGCAGCCACACTG	ob 229 elleAlaLeuCys	2y 976 GCTGTCGGCCCCC	ob 246GluAlaGly	1036 GAACCTGC	ob 262PheGlyAla	2y 1096 gegeegererre	ob 272 tTrpMetLeuLeu	2y 1156 TTACACGGATTTC	292 eAspT	2y 1216 CGAGGCCCGGAG	310 r	Dy 1276 GIGCGCCAICIC	ob 326 nservalvalLe	2y 1334	ob 346 yvalLysArgLe	2y 1363 AGCTTTC	Ob 366 lLeuIleThrLy	2y 1390 ATGCCTGTCC-	Ob 386 oThrLeuGlnPr	Dy 1438 CGGGTTCACCTT	Db 406 uGlylleProLe	2y 1498 GGAGAAGCAGGT	Db 425	2y 1558 CAGCCTG	Db 434 uSerLeuGlyVa	1582	Db 454 rGIyProTrpAs
SCCCAGGCGGCCCT 231 IPPTOPROGIAPTORITIEASPMELSEALAPPRAIAGLYLeuGlyGlanArg 122 TCCCAGAACTGCTTCCTCCCCCCAGAGCTGCC 203 I :::	qa 	δλ	qa **	, t	3 8	ζ, ·	aa .	δŏ	qa	Qy	qa	Qy	qa	δλ	qa	Qy	qa	δō	qa	δλ	qa	Qy	qa	ογ	qa	٥٧	q _Q	0y	ag De	QY	aa	0y	Ω	λο δ	<u> </u>
	CATAGTGGGCCAGGCGGTAGGGCTAGGGGCCGT 251	ro-ProGlyProProGlyProGlylleAspMetSerAlaPheAlaGlyLeuGlyGlnArg 122 TCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCG 203	:::	38	PRELIMINARY; PRT; 502	000 (TrEMBLrel. 13,)02 (TrEMBLrel. 20,)02 (TrEMBLrel. 21,	icrose transporter 1.	meridionalis.	Maryota; Vilatpiantas; Streptophyta; Embigophyta; itacheophyta; permatophyta; Magnollophyta; endicotyledons; core endicots; ttoridas; custorida I I Tamialae: Cynchhilatiandae	Sections; educaterius 1; bammares, scropmannareae, misma.	L) EQUENCE FROM N.A		the scropnurariaceae	Lanta 213:80-91(2001) MBL; AF191025; AF04295.2;	000000000000000000000000000000000000000	UZ AA; 3232/ MW; E/34CDU3U33Q3ZZD	· 2.51e-13 Length:	40.00% Conservative:	: 25.61% Mismatches: 5.17% Indels:	. caps:	-IIV (I-34IV) X VSOKI4 (I-302) -IIV (I-34IV) X OSOKI4 (I-302)	CCGCCTGCTGCGCACCGGAAAGCCCAGCTCTTGCTGGTCAACCTGCTAGCTTGG 3	ProproAlaGlinalaAlaProvalLys-AsnilelleValValAlaAlaLalleAlaAlaGli 3	CCTGGAAGGTGTTTGGCCGCAGGCATCACCTATGTGCCCGCCTCTGCTGCTGCGAAGGTGGG	yvaleinkneelyiiphlaledeelineeselledeelin. Fiolyivaleineelede	GGFAGGAGAAAGIICAIGACCAIGGIGGIGGGGCAIIGGGICCAGGGCCIGGGCCIGG					CFIGEOTRACION AND THE STANDARD CONTRACTOR TO THE STANDARD CONTRACTOR CONTRACT		GGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGCTGCTGCTTCTGTGGCCAGGTGTGCTT	::: ::: ::::::::::::::::::::::::::::

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---CTCCCACCTCCACCGCGCTCTG 1665
                                                                                                                                                                                                                                                                                                                                                                                                    SCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTT 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGTGGGCGAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCAC 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACACTATGATGAAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCA 1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGC-- 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ACTCGAGCAGTCTATTTGGCCAGTGTGGC 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ....-.-CTGTGGCTGCCGTGCCAC 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----CACAGTGTGGCCGTG---GTGACAGCTTCAGCCGCCCTCAC 1437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGA 1557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCCTGCTTCCCCGGCTGCACCTGTGCTGCCGCATGCCCCGCACCCT 1095
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euGlyValAlaSerLeuGlyValGlnValThrAlaArgGlyLeuGlyGl 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ysMetAlaGlnHisHisArgGluTyrAlaSerValGlyGlyAlaAlaPr 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euAlaAlaThrPheSerIleProPheAlaLeuAlaSerIleTyr---- 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SerSerAsnSerGlyAlaGlyGlnGlyLe 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alLeuAsnLeuAlaIleValIleProGlnMetPheValSerValAlaSe 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spAlaLeuPheGlyGlyGlyAsnLeuProAlaPheValValGlyAlaVa 474
AGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGT 915
                                                                                                                                                                                                                                                                                                                      recreerecreaceagecagecreececeaceagecageage 975
                                                                                                                                                                                                                                                                                                                                                            ysilevalargGluThrProTyrThrAlaProProGlu----- 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
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euLysSerCysPhePheIleSerValAlaLeuLeuThrValThrIl 229
                                                           PCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTAC----- 811
                                                                                                                                              -- CTCCTGCCTGCCATTGACTGGGAC---ACCAGTGCCCTGGCCCCTA 855
                                                                                                                                                                        111
lyThrValLysLysHisThrValProValPheGlyGluLeu------
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ą	531	YGluArgGlyProSerGlyLeuAlaGlyProLysGlyAlaAsnGl 546	9
٨̈	1883		1837
ą	546		53
λį	1836		1786
ą	563	rdlyargProGlyAspAlaGlyProGlnGlyLysValGlyProSerGlyAlaProGlyGl 583	33
 .	1785	AGCAGGAAGG	174
ą.	583	uAspGlyArgProGlyProProGlyProGlnGlyAlaArgGlyGlnProGlyValMetGl 603)3
Бi	1773	CTATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGC	735
ą	603	yPheProGlyProLysGlyAlaAsnGlyGluProGlyLysAlaGlyGluLysGlyLeuPr 623	23
Δi	1734 (GGAACCACCCTGGCTGGGTGGGCTCACCCACCACCACGTACGGAGACATCACAGGCA 167)	575
q	623	o-GlyAlaProGlyLeuArgGlyLeu-ProGlyLysAspGlyGluThrGlyAlaAla 641	11
<u>γ</u>	1674 (GAGGCCCGCAGAGCGCGGGTGGAGGTGGAGG	539
ą	642 (GlyProproGlyProAlaGlyProAlaGlyGluArgGlyGluGlnGlyAlaProGlyPro 661	51
Ā	1638	CCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAG 160	503
ą	662	SerGlyPheGlnGlyLeuProGlyProProGlyProProGlyGluGlyGlyLysProGly 681	31
ž	1602	GGAGCTCCAGGCTTAGGGCCTGGCAGGAAGC 1572	572
ą	682		1
λ	1571	15	522
ą	701		1
γ	1521	TTGGGCAGGAACACCTGCTTCTCCCCGTGGTAGAGGGAGG	77
a	721	uProGlyThrProGlyThrAspGlyProLysGlyAlaṢerGlyProAlaGlyProPr 740	0
¥	1476 (3TGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTG 141	19
Q	740	oGlyAlaGlnGlyProProGlyLeu-GlnGlyMetProGlyGluArgGlyAlaAlaGlyI 760	01
λ	1418	-	364
Ω	760	::: leAlaGlyProLysGlyAspArgGlyAspValGlyGluLysGlyProGluGlyAlaP 779	6
Y	1363 1	GCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGTC 1310	10
Д	179 1	rodlyLysAspGlyGlyArgGlyLeuThrGlyProlleGlyProProGlyProAlaGlyA 799	6
٨	1309 (CATGACCAGAGAGAAGACCAGGAGATGGCGCACTGCAGGAACAGCC 126	162
Д	799]	laAsnGlyGluLysGlyGluValGlyProProGlyProAlaGlyThrAlaGlyAlaA 818	80
λ.	1261	AGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGC 1202	:02
д	818	rgGlyAlaProGlyGluArgGlyGluThrGlyProProGlyProAlaGlyP 835	ıΩ
>	1201	CTGGGCACGCCCTGGTACA 1182	82
۵	835 1		ñ
۸.	1181 -	GCCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGT 1142	42
۵	855]	lyGlnLysGlyAspAlaGlyAlaProGlyProGlnGlyProSerGlyAlaProGlyP 874	4
۸.	1141 0	AGCTGCACAGCTCAG	82
۵	874 I	roGlnGlyProThrGlyValThrGlyProLysGlyAlaArgGlyAlaGlnGlyProP 893	m

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0y	1081	GCGCCAGCACCAGCTGGTGCAGCCGGGAAGCAGGGCGCCCCAGGTTCCGGAA 1031
qq	893	roGlyAlaThrGlyPheProGlyAlaAlaGlyArgValGlyProProGlySerAsnGlyA 913
Qy	1030	AGCCAAGCGGGCCCGGCATG 1011
QQ	913	31yProProG1yProProG1yProSerG1yLysAspG1yProLysG1
οy	1010	GACAGCAGTGGGGCGACAAGGGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCC 953
qq	933	lyaspserGlyProProGlyArgAlaGlyAspProGlyLeuGlnGlyP 949
٥y	952	CAGCGCTGCCTCTC 938
q	949	roAlaGlyProProGlyGluLysGlyGluProGlyAspAspGlyProSerGlyProAspG 969
δy	937	GTGGCTGCTACGCAGGTGA
qa	696	lyproPro
λχ	877	GCACTCCT
QQ	981	IleValGlyLeuProGlyGlnArgGlyGluAr
Σλ	854	849
qo	1001	 erGlyGluProGlyLysGlnGlyAlaProGlyAlaSerGlyAspArgGlyProProGlyP 1021
27	848	CCAGGCACTGTGTCCCAGTCAATGGCAGGAGGTAGCCCAGGCA 800
q	1021	roValGlyProProGlyLeuThrGlyProSerGlyGluProGly- 1035
λý	799	GCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTC 740
qc	1036	
λλ	739	CCGGAAGAGGTCAGAGGCAGGG
q;	1046	
27	703	GAAGCACACTGGCCACAGAAGTCCAGCAGCCCCA CGCCCAGGATGAGCAGTGCCAG 647
qc	1065	GlyAlaProGlyAlaProGlySerProGlySerProGlyProAlaGlyProT 1082
λλ	646	CTCCAGGGCCTGGGATCCGGGCACCAGCCTGCTAGCCAGCC
qc	1082	hrGlyLysGlnGlyAspArgGlyGluAlaGlyAlaGlnGlyProMetGlyP 1099
27	586	AAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCG 536
q	1099	roAlaGlyProAlaGlyAlaArgGlyIleProGlyProGlnGlyProArgGlyAspL 1118
λy	535	CCACGCCAGTGGTCACTGGCTGAGCCTAGGAGC
ą	1118	ysGlyGluAlaGlyGluAlaGlyGluArgGlyLeuLysGlyHisArgGlyP 1135
λ	479	
q	1135	heThrGlyLeuGlnGlyLeuProGlyProFroSerGlyAspGlnGlyAlaSerG 1155
λλ	457	GCCCAGCACCATGGTCATGAACTTCTCGTCTAGCCCCACTTCCAGCAGCAGAGG 404
q	1155	
λλ	403	CGGCACATAGGTGATGCCTGCGGCCAAACACACTCCAGGCCAAAGGTTAGCAGGTTGAC 344
q	1175	spGlyAlaAsnGlyIleProGlyProlleGlyProProGlyProArg 1190
λY	343	CAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCGGGCTCACCCACAGCCTCTGGAC 287
q	1191	GlyArgSerGlyGluThrGlyProAlaGlyProProGlyAsnProGlyProProGlyP 1210

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2177 CTTGGAAGGCCTC------CAGTCAGGCAGCCCTAGAGACTGGGGAGAGA 2133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2084 ACAGGGTGGCAGCAGAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCG 2025
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                                                                           2792 AAGGTCCTGGGTTAGGCATTTTGGGGGGCCCAGACCCCCAGGAGAAGATTCTGGCAATG 2733
                                                                                                                                                                                        2732 ATCAGCCCAATGACCAGCTATCTCAGGGACCTGATTGTTGGGGATCCCCCACCCTACCC 2673
                                                                                                                                                                                                                                                                                                       2672 AAATATTAGACACCAACACAGAAAGCTAGCAATGGATTCCCTTCTACTTTGTTAAATAA 2613
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                                                                                                                                   -----GlyAspAspGlyGluAlaGlyLys-----
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                                                                                       454 SerValGlyGlyGlyProPheAspGluLeuPheHisGlyGlyAsnIleProAla----- 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98340920; PubMed-9676231;
Du F., Acland G.M., Ray J.;
"Differential splicing of type II procollagen mRNA in canine retina.";
Anim. Biotechnol. 9:15-20(1998).
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A Du F., Acland G.M., Ray J.;
A Du F., Acland G.M., Ray J.;
Du F., Acland G.M., Ray J.;
T "Cloning and expression of type II collagen mRNA: evaluation as a candidate for canine oculo-skeletal dysplasia.";
C Gene 255:307-316(2000).
R EMB; AF023169; AAG62178.2; -
R InterPro; IPR0000887; Collagen..
R InterPro; IPR001007; VWF_C.
R Pfam; PF01410; CoLFT; 1.
R Pfam; PF01391; Collagen; 18.
R Pfam; PF000093; VWc; 1.
R Probom; PD000007; Collagen; 4.
R Probom; PD000007; Collagen; 4.
R Probom; PD000007; Collagen; 4.
R SMART; SW00014; VWC; 1.
R SMART; SW00014; VWC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canis familiaris (Dog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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Matches:
Conservative:
Mismatches:
Indels:
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332.50
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                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SEQUENCE FROM N.A.
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qa	QY	V 4	Λ _O	qa	Qy Db	Qy Dp	QY	δŏ	an .	y da	QY Db	Qy	qα	ÇQ GG	οy	qa	Qy Dp	Qy	qa	Qy Dp	δδ	qa (AZ QZ	oy.
Db 1519 GlylleThrGlyProSerGlyProlleGlyProProGly 1534	Qy 178 CTGCCTAGGAATCAGCCAGGCCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCT 119	Qy 118 CAGCCCATGCTCAACACCTGCTGGGGCACCTCAGTGGGGACACGTCTCATCACTC 59	49	1561 yPro	N.Y	DT 01-MAR-2002 (TrEMBLrel. 20, Created) DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DF 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	GN SUC2. OS Brassica oleracea (Cauliflower). OC Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	<pre>Spermarcopnyta; Magnoilopnyta; eudicotyledons; core er eurosids II; Brassicales; Brassicaceae; Brassica. NCBL_TaxID=3712;</pre>	SEQUENCE FROM N.A. COUDS S.A. Sinchair B K Buckmell T T Course S.A.		Senescence."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databas EMBL; AY065840; ALL58072.1;	DR Pfam; PF00083; Sugar_tr; 1. SQ SEQUENCE 508 AA; 54016 MW; FIAZADIDIC8EDD86 CRC64;	Alignment Scores:	Score: 2.34e-13 Length: 508 Score: 332.50 Matches: 125 Percent Similarity: 41.57% Conservative: 87 Best Local Similarity: 24.51% Mismarches: 193	5,18% Indels: 10 Gaps:	US-09-759-143-110 (1-3410) x Q8VYX3 (1-508)		392		Qy 452 CTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGAC 511	512 CACTGGCGTGGACGCTATGCCCGCCGCCCTTCATCTGGGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	Db 86 ArgCysThrSerArgPheGlyArgArgArgProPheIleValAlaGlyAlaGlyLeuVal 105	† † † †	620

,		Qy	1230
Οy	CAGTCAGGCACCCTAGAGACTGGGGAGAGAGGA 	qa	1243
οp	971 ysAspGlyLeuProGlyHisProGlyGlnArgGlyGluThrGlyPheGlnGlyLysT 990	Ó	1170
Οy	2130 GAGGGACGCCCCAGCCCCCAGCTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCA 2071	අු	1256
QQ	990 hrdlyProproGlyProProGlyValValGlyProGlnGlyProThrG 1006	λŎ	1110
ر مر	2070 GAGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCC 2017	. අ	1270
QQ	1006 lyGluThrGlyProMetGlyGluArgGlyHis-ProGlyProProGlyProProGlyGlu 1025	Ó	1059
oy.	2016 ATGGGGCTAACAGGAGGGGGGGGCCTGGGACCCAGTGAGGCCCTCCACCCCAATGTG 1957	· අු	1290
qq	1026 GlnGlyLeuProGlyLeu-AlaGlyLysGluGlyThr 1037	, ò	666
ΟŊ	1956 CTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTA 1897	, <u>4</u>	1310
QO	1037 1037	20	939
ov	1896 GCAAAGTAAATGGCGACCAGGCCTGCGGCAGACACCATATAGGCAGTGACAGAC 1837	7 원	1326
QQ	1038LysGlyAspProGlyProAlaGlyLeuProGlyLysAsp 1050	òò	879
δŏ	1836 TGGCTGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAAG 1777	qq	1335
đ	1051	ò	834
Qy	CCAGGCAGATGCCCCGGC	QQ	1354
ф	PheProGlyAspArgGlyLeuProGlyProValGlyAlaLeuGlyLe	δλ	774
Ολ		qq	1366
අු	1073 uLysGlyAsnGluGlyProProFroProGlyProAlaGlySerPro 1089	OY	717
δλ	1695 CGTACGGAGACATCACAGGCAGAGGCCCCGGAGAGCGGGGGGGG	qq	1381
qq	1090GlyGluArgGlyProAlaGlyAlaAlaGlyProIleGlyIleProGlyArgPro 1107	٥٥	657
Qy	1635 CTGCCTCCAGCACCACGTGTCCATTAGGGAAGGGAGCTCCAGGC 1591	1 සි	1395
οg	1108 GlyProGlnGlyProProGlyProAlaGlyGluLySGlyAlaProGlyGluLySGlyPro 1127	NO O	593
Qy	1590 TTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACCTCCAGTGTCC 1531	. d	1406
QQ	1128 GlnGlypro-AlaGlyArgAspGlyLeuGlnGlyPr 1139	2 :	, h
'n	1530 CCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGG	ζŏ	0.03
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ολ	GCCACACTIGTGGGACAGGCATGTGGGCA	q	145
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δλ	CCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGC :: :::	qa	146
qq	1194 erGlyAlaAspGlyGluProGlyProArgGlyGln 1205	Qy	30
٥y	TGCACCAGCCGGTCCATGACCAGAGAAGAACCAGGGAGATGGC	qa	147
qq		QY	28
δy	GCACTGCAGGAACACCCCCAGGCTGCCCATCCGAACGCCTTCATCATAG	qa	149
qq	1224 roGlyProvalGlyLeuGlnGlyLeuProGlyProProGlyGluLysGlyGluThrGl 1243	Qy	23

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54 yProAla-----LysGl 1366
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                                                                                                                                                                              0 ACGAAGACCGGCGCAGGG---TGCGGGGCATGCGGCAGCACCACCT-----GGTGCAGC 1060
                                                                                                                                                                                                            9 CGGGGAAGCAGGCGCCCCAGGTTCCGGAAAGCCAAGCGGGCCCGGCATGGACAGCAGTGG 1000
                                                                                                                                                                                                                                                                                                      .0 uLysGlyGluSerGlyProSerGlyAlaAla------GlyProProGlyProLy 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 yGluProGlyProSerGlyProProGlyLysArgGlyPro------ 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O ACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACCACCTCAGCC 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 CGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTG-----AGCCTAGGAGCGGGAC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ACAGACCAGGCCCA---GCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 TACCCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGCGGGCCAAACACACCTC 368
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0 TGTCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCC 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 TCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGCAGGCCAAAG 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 AGGCACTCCT-------CCTGGGTGCCCAGGTAGGGGCCCAGGGCACTGGTG 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 TCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCA 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 TAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGTCCCGGAAGAGGTCAGAGAGAGGG 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGGCAGCCCCACGCCCAGGATG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 CTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAAGGACAGTGCCCAGATGAAGGGCCGG 538
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1166 uLys-------GlyGluThrGlyLeuLeuGlyAlaTyrProGlyProLysGl 1181
                                            1201 roGlyArgLysGlyValMetGlyAspValGlyProGlnGlyProProGlyThrAlaGlyL 1221
                                                                                                                                                            1221 euProGly------ProProGlyLeuProGlyAlallelleProGlyProL 1236
                                                                                                                                                                                                                  1236 ysGlyAspArgGlyLeuProGlyLeuArgGlyAsnProGlyGluProGlyProProGlyP 1256
                         306 CICACCCACAGCCICIGGACCATAGIGG------CCAGGCGGGTAGGGCICAG 259
                                                                              258 GGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTCCAGAAGCTGCGGCCT 199
                                                                                                                                  198 CTCCTCCTIGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCT 139
                                                                                                                                                                                              -----GCCGGTCCAGCTTCTC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92105142; PubMed=1722213; Greenspan D.S., Cheng W., Hoffman G.G.; The pro-alpha 1(V) collagen chain. Complete primary structure, "The pro-alpha 1(V) collagen chain. Complete primary structure, distribution of expression, and comparison with the pro-alpha 1(XI)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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311
59
381
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01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Matches:
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                                                                                                                                                                                         138 TTGGT------
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InterPro: IPR000087; Collagen.
InterPro: IPR000087; Collagen.
InterPro: IPR001291; Laminin_G.
InterPro: IPR001292; TSPN
Pfam; PF01410; ColleT; 1.
Pfam; PF02210; TSPN: 1.
ProDom; PD000007; Collagen; 1.
ProDom; PD002078; Fib_collagen; 1.
SMART; SM00282; LamG; 1.
SMART; SM00282; LamG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen chain.";
J. Biol. Chem. 266:24727-24733(1991).
EMBL; M76729; AAA59993.1; -.
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31.57%
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3169 GCAGGGGGTGCTCCTGAGTTTCTGTGAGATTCCCCAAGCACAGATATACTCTGGGGGC 3110
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                                                                                                                                                                                                                                                                      3062 GCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGGAAAGTTGGGGGGTAGGGGAAAGTTG 3003
                                                                                                                                                                                                                                                                                                                                                                            2943 -----GAGTGGGGGGAACCAG 2922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2523 ATCAGCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGTCCCTCAG 2464
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708 LysGlyAsnValGlyProGlnGlyGluProGlyProProGlyGlnGlnGlyAsnProGly 727
                                                                                                      728 AlaGlnGlyLeuProGly------ProGlnGlyAlaIleGlyProProGly 742
                                                                                                                                                                                                                                                                                                                                                                                                                             781 lyProGlnGlyProIleGly-----TyrProGlyProArgGlyValLySGlyA 797
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QY Db

3217 AAACGGCACTTAAAACCCCCCTGAGAGATAAGACCTCCCTTAGCTCAG------ 3170

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ProGlyAspPro-Gly- ProGlyAspPro-Gly- AGTGTGTAGGCAGG GlyArgCysIleProGl III III III SCHOOLOAGGCAGG GCACCACGCCAGG III III III ProGlyIleProGlyM ICAGAGACAGGGA ICAGAGACAGGGA III III IIII I

863	 yGluMetGlyProProGlyGlnLysGlyTyFProGlyAlaProGlyPheProGlyProPr 883	Э
1209	GGCTCAG	9 65
64		33
1104	<pre>3GGGGGGGGAGCAGCAGCTGGTGCAGCCGGGGAAGCAGGGCG 10 11</pre>	145
1044		900
1005	CAGTGGGGCGACAAGGGGGGCCGACAGCCCTT	2 9
971	-CTGCTGGCTCGGTGGGCCCAGCGCTGCCT	36
941	CTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAGATGAGGTGAGCAGG 88:	36
885 998	CAAAGAGGCACTCCTCGGGTGCCCAGGTAGGGGCCAGGGCACTGGTGTCCCAGTCA 82	26 014
825	ATGGCAGGCAGGCAGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGGCATAGACAGAG 76	56 025
765	TAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAGGC 72	21 045
720	AGGCCTCCAGTGGAGTGAGCACACTGGCCACAGAAGTCCACACACCCCACGCCCAGG 66	661 1064
660	CCCTGCTAGCCAGCCG 6 111 ::	01 077
600	CCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAG 5 [44
543	GCTGAGCCTAGGAGCGGGACA 4	84 111
483	CAGACCAGGCCCAGCACCAGCACCAGCAGCAGCAGCAGCA	45 131
444	CTACCCCACTTCCAGCAGCAGGGGGG 4	00 150
399	ACATAGGTGATGCCTGCGGCCAAACACA	61 166
360	AAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGCGG 3	07

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οy	GGGTAGGGCTCAGGGGGCCGT	qa	318 GlyPhePı
qq	 884 ProProGlyProValGlyProGlnGlyGluArgGlyAlaAsnGlyPhePro 900	δλ	2981 AGTGCCT
οy	229 CGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGGCCAACTGCCT 173	qa	338 ProGlyPl
qq		Qy	2939 GGAAGTGC
οy	172 AGGAATCAGCCAGGCGCCCATTTCTGCCAGGCCTTTGGTGCC 131	qa	354 GlyGluAr
qq		Qy	2879 CCTGAAGC
٥y	130 GGTCCAGCTTCTCAGCCCATGCTCAACACCTGCTGTGGGGGCACCTCAGTGGGGACAC 71	qq	373 ProserG
QΩ		οy	2819 TTATCATI
οy	70 GTCTCATCACTCAGATCCTGGCCGAGGCGCGGCTGTCACCCGGAGC 23	qq	384
q	 GlyArgSerGlyAl	δλ	2778GGCATT
٥y	22 CAGCGCGTGCAGG 10	qa	397 rodlyteu
QQ		δλ	2732 ATCAGCCC
RESULT	. 34	qq	417 roGlyPro
0902S0 ID	9Q2SO PRELIMINARY; PRT; 1669 AA.	δλ	2712 TCTCAGGG
	(TrEMBLrel. 13, Cr	qq	437 ysProGly
00	el. 13, el. 21,	Qy	2686 CCCCCA
	agen IV.	qq	457 lyProPro
	Mus musculus (Mouse). Eukaryota; Metazoa; Chordata: Craniata: Vertehrata: Ruteleostomi:	ΟŊ	2628 CTACTITG
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;	qa	475
	[1] SEQUENCE FROM N.A.	Qy	2568 AAGGACCA
	TISSUE=XIDNEY; MEDLINE=20006934 Dubmed=10634307.	QQ	482 roGlyPro
	Lu W., Phillips C.L., Killen P.D., Hlaing T., Harrison W.R., Elder F.F.B., Miner J.H., Overbeek D. A. Moislar M.H.	QY	2508 GIGCIGIG
	col4a4 in a	qa	499 leProGly
	enomics 61:113-124(1999). MBL: AF169387: AAD50449-1: -	QY	2448 AATAAGTC
	GD: MGI:104688; COI433, nterPro: IPR000087: Collage	. qa	504
	InterPro; IPR001442; Procollanc4. InterPro; IPR000504; RNA rec mot.	Qy	2388 AGCTACAT
	Pfam; PF01413; C4; 2. Pfam; PF01391; Collagen: 21	qa	505
	ProDom; PD000007; Collagen; 6. ProDom; PD003923; ProcollagnC4; 1.	Qy	2328 TTTATTCA
	SMART; SM0111; C4; 2. PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.	qa	514
	Collagen. SEQUENCE 1669 AA; 161769 MW; 30976E59739A47B2 CRC64;	QY	2268 CCCTGAGC
Alignme	:	qa	523
Score:	2.64e-13 Length: 333.00 Matches:		2208 GCCTCCCT
Best L	Percent Similarity: 29.65% Conservative: 53 Best Local Similarity: 25.19% Mismatches: 379	qa	540 ly
Query P DB:	5.35% Indels: 11 Gaps:	δλ	2148 GAGACTGG
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US-09-759-143-110 (1-3410) x Q9QZS0 (1-1669)

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3CCCCACCTCTACCTTCCTTCAACACCCTAACCTTGGGTAACAGCATTTGGAA 2820
STIGGGGGTAGGGGAAAGTIGGGGGTA-------GGGGAAATTITGGGC 2982
                                                                                                         ---CTAGAGAGAGTAGAGGGGAGT 2940
                                                                                                                                                                                                          3GGGGGAACCAGGCTGGGCCAAGAGAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
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| heProGlyProThrGluTyrTyrAspAlaTyrLeuGluLys------ 353
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553 lyAspProGlyLeuArgGlyLeuProGlyArgLySGlyPheAspGlyThrProGlyGlyP 573
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258		0y 0b	1261 CAGGCTGCC 571GlyArgE
273 2081 293	eGlyproproglyproproglypheProGlyserSerClyalalysGlyAspalaGlyGl GGGTGCAGCAGCAGAGCCACATTACTTTGCAGCAACAGAAACTGGCGGCCAGCCC	QV .	
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1969	SGIYGLUMELGIYFIGGIAGT - GIYGLYFIGGLFIGGIYFIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGGIGG	Qy	1021 GGCCCGGC/ 637 lyProSer(
352		δλ	971
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1854	ATATAGGCAGTGACAGACTGGCTGGACCTGGAGCCCATAAACAGGGATGGGGCC 1795	da qa	940 CICAGCCAC 677 rogin
1794	OCITYSELELINGLYCIUVALELINGLYCIUCATYALGAUTOLYALGAUTOLYGUNGLYCLANGLYGUNGLYCLANGLYGUNGLYCLANGLYGUNG	yo,	880 GAGGCACTC
395	 uproGiyLeuProGiyGlnGluGlyLysArgGlyProLeuGlyAlaGlyGlyPr 413	g è	820 AGGCAGGAG
1743	CCCCGGCCCGGAACCACCTG-GCCTCGGTGGGCTCACCCACCACC 1699	g qq	
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433	yArgProGlyAlaAlaGlyValAlaGlyLysAspGlyAlaArgGlyLeuGlnGlyGluAr 453	2 6	706 AGTGAAGC
1693	TACGGAGACATCACAGGCAGAGGCCCGCAGAGCGCGGGTGGAGGTGGGGG 1643	qa —	
453	gG1yG1uAlaG1yG1nG1nG1yVa1AlaG61yAlaF1OG1ySerAlaG1yG1nTnF61yAl cachoarmachagasanchagasangasaagaaagaagaaga	δŏ	655 CAGTGCCAG
473		qa	743
1585	GCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTAGCACGCAGTGTCCCC	QY	595 TGG
490	ypro-alaGlyAsnProGlyValAspGlyAsnProGlyGluGlnGlyProG	අ ධ .	
1528		λ <u>α</u>	308 GCCCAAGG ::: 76 AlaArgGl
507	'lnGlylleGlnGlyProProGlyLeuGlnGlyProSerGlyAsnLysGlyAspThrG 526	ì 0	508 ACTGGCTG
1501	CTCCCGGTGGTAGAGGCAGGCCAGTGTGTAGGCAGGATCTGCAGGGTGAGAGGTGAA	Z qq	791 Asn-G
526		Q	448 CATGGTCA
1441	CCCGGTGAGGGCGCTGTGAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCCACC	ପୁଘ	u 608
542	GlyGluA	٥٧	388 GCCTGCGG
1381	GGCAGCCACAGGAAAGCTGCCACACTGGCCAAATAGACTGGTGGAGTGCCGAATTCGCTG 1322	qa	 824 rProGlyA
1321	CACCAGCCGGTCCATGACCAGAGAAGAAGACCAGGGAGATGGC	Qy	350
LO.		qa —	844 lyGluArg

	1261	CAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGCCCGGCTCAGC	1202 587
	1201	TCTGGGCACGCCCTGGTACAGCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGT	1142
	1141	CATGAGTGCCATCCAGCTGCACGAGCCACGAAGAGCCGGCGCAGGGTGCGGGGCAT	1082 617
	1081	GCGGCAGCACCAGCTGGTGCAGCCGGGAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCG	1022 637
	1021	GGCCCGGCATGGACAGCAGTGGGGCGACAAGGAGGGGCCGACAGCCCTT	972 657
	971	CTGCTGGCTGGGGGCCCAGCGCTGCT 	941
	940	유 :	881 687
	880	GAGGCACTCCTCTGGGTGCCCAGGTAGGGGCCAGGGCACTGGTGTCCCAGTCAATGGC	821 698
	820	SGAGGTAGCCCAGGCAGCCCCCAAGA	761 708
	760	CTGGCGACAGTGGTCCGGGTCCCGGAAGAGGTCAGAAGCAGGGCCTCCAGTGG	707
	706	AGTGAAGCACACT:GGCCACAGAAGTCCAGCAGCCCCAGGATGAG	656
	655	CAGTGCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCAGCTGCTAGCCAGCC	596 755
	595	TGGGATGAGAAGAGGCTCAGCAGAT TGG	569
	568	GCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCAgGCCAGTGGTC	509
	508	ACTGGCTGAGCCTAGGAGGGGACACAGACCCAGCCCCAGCACTGGACCAATGCCCAGCACACACA	449
	448	CATGGTCATGAACTTCTCTCTACCCCACTTCCAGCAGAGGGGGCACATAGGTGAT	389
	388	GCCTGCGGGCCAACACACCTCCAGGCCAAAGGTTAGCA	351 844
_	350		318
_	844	lyGluArgGlyGluThrGlyProProGlyArgSerGlyGluProGlyAlaProGlyMetP	864

Db 330 rAspMetGlyValArgAlaGlyAlaLeuGlyLeuMetLeuAsnSerValValLeuGlyAl 350	<pre>Qy 1294 CTTCTCTGTGATGGACGGGTGGTGCAGTTGGGACTCGAGCAGTCTATTTGGC 1353</pre>	OY 1354 CAGTGEGCAGCTTTCCCTGTGCCTGCCGGTGCCATGCCTGTCCCACAGTGTGGCGGT 1413	1414 GGTG	Db 386 ThrLysLeuAlaGlnHisSerArgGlnTyrAlaProGlyThrGlyGlyLeuGlnAspPr 406	Oy 1418ACAGCTTCAGCGGCCTCACCGGGTTCACCTTCTCAGCCT 1458 ::	1459 GCAGATC	426 eProLeuAlaileThrTyrSer	1504 GCAGGIGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCT 1	4.43	454	y 1588 TAAGCCTGGA	b 474 oʻʻrpaspalaLeuPheGlyGlyGlyAsnLeuProAlaPheValValGlyAlaValAlaAl 494	Y 1627 TGGAGGCAGTGGCCTGCTCCCACCTCCACCC 1657 	7405 7405 097405 097405 097405 097405 01-MAY-1999 (TrEMBLrel. 10, LOIL-MAY-1999 (TrEMBLrel. 10, LOIL-MAY-1999 (TrEMBLrel. 10, LOIL-MAY-1999 (TrEMBLrel. 11, LOIL-MAY-1999 (TrEMBLrel. 12, LOIL-MAY-1999 (TrEMBLrel. 12, LOIL-MAY-1999 (TrEMBLrel. 12, LOIL-MAY-1999 (TrEMBLrel. 12, LOIL-MAY-1999 (TrEMBLrel. 12, LOIL-MAY-1999 (TrEMBLrel. 12, LOIL-MAY-1960) NCBL_TAXID=36034; 1 SEQUENCE FROM N.A. TISSUER-MUSCLE; MEDLINE-99234051; PubMed=1021 Yoneda C., Hirayama Y., Nakay-Watabe S.; "The occurrence of two types Hallotis discus muscle."; Take Secondary (Trembr.) FR000087; Collagen InterPro; IPR000885; Fib_collagen: ProDom; PD000007; COLET: 1. ProDom; PD000007; COLET: 1. SMART; SM00214; VWC; 1.	
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3077 TGTGCTTCTGGTCCTGCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGGAAAGTTGGG 3018
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101 ---GlnGlyAsnValLysAlaAlaProAlaTyrSerProGlnTyrTyrSerProGlyAla 119
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Tegeder M., Wang X.D., Frommer W.B., Offler C.E., Patrick J.W.;
Tegeder M., Wang X.D., Frommer W.B., Offler C.E., Patrick J.W.;
"Sucrose transport into developing seeds of Pisum sativum L.";
Plant J. 18:151-161(1999).
INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF109922; AAD41024.1;
InterPro; IPR003662; sub_transporter.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 21, Last annotation update)
sucrose transport protein SUT1.
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1004 TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 1063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1244 GTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTG 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1304 GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 GlyAsnIleLeuGlyTyrAlaAlaGlySerTyrSerHisLeuPheLysValPheProPhe 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                944 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCCCCAC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 CTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCACCTCTTC 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 LeuAspValAlaAsnAsnMetLeuGlnGlyProCysArgAlaLeuLeuAlaAspLeuSer 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 CGGGACCCGGAC---CACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTT 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 GlyGlyLysSerGlyArgMetArgThrAlaAsnAlaPhePheSerPhePheMetAlaVal 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 SerLysThrLysAlaCysAspMetTyrCysAlaAsnLeuLysSerCysPhePheIleAla 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 -----LysSerLysValProPhe-----PheGlyGluIlePheGlyAlaLeu 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278 CCCACTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGGCACCGGAAAGCCCAGCTC 337
                                                24 ProLeuAlaProSerLysLeuTrp------LysIle 33
                                                                                                       338 TIGCIGGICAACCIGCIAACCITIGGCCIGGAGGIGIGITIGGCCGCAGGCAICACCIAI 397
                                                                                                                                                                                                                 GIGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGC 457
                                                                                                                                                                                                                                                                                                                         158 ATTGGTCCAGTGCTGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGG 517
                                                                                                                                                                                                                                                                                                                                                                                                                                   518 CGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGCTG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 ---CTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTG 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           833 ---GACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT---GGC 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281 LysGluLeu-----ProArgProMetTrplleLeuLeuLeuValThrCysLeu 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 PheGlyGly------GlnValGlyAsp-----AlaArgLeuTyrAspLeuGly 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 IleValValAlaSerIleAlaAlaGlyValGlnPheGlyTrpAlaLeuGlnLeuSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 AGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 ProGluLysAspGluGlnGluIleAspGluLysLeuAlaGlyAlaGly--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
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Db 53 SerLeuLeuThrProTyrValGlnLeuLeuGlyIleProHisLysTrpAlaAlaTyrIle 72 Qy 452 CTGGGCATTGGTCCAGTGCTGGGCTTGGTCTGTGTCCGGTCCTAGGCTCAGCCAGTGAC 511	Qy 512 CACTGGGGTGGACGTATGGCCGCCGCGCGCCTTCATCTGGGCATC 571 :: :: ::	Qy 572 CTGCTGAGCCTCTTTCTCATCCAAGGCCGCTGGCTAGCAGGCTGCTG 622 :: ::	Qy 623 TGCCGGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGC 667 11	Oy 668 GTGGGGCTGCTGGACTTCTGTGGCCAGGTGCTTCACTCGAGGCCCTGCTCTT 727 ::: :: Db 149 PheTrpIleLeuAspValAlaAsnAsnMetLeuGlnGlyProCysArgAlaLeuLeuAla 168	Oy 728 GACCTCTTCCGGGACCCGGACCACTGTCGCCAGCCCTACTCTGTCTATG 784 1 1 1 1 1 1 1 1 1	Qy 785 ATCAGTCTTGGGGCTGCCTGGGCTACCTCCTG 817 ::::::::	Oy 818 CCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGC 877	Qy 878CTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGG 934 ::::	Qy 935 GCTGAGGAGGCGCCGGACCGAGCAGCAGCAGGAAAAGGCTGTCGGCCCCTCCTTG 994	Qy 995 TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1054	QY 1055 CCCCGGCTGCACCGCGCGCGCGCGCGCCCGCGCCGGCTCTTCGTGGCT 1114	Qy 1115 GAGCTGTGCAGCTGATGACACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGC 1174	Qy 1175 GAGGGCTGTACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTAT 1234	1235	Qy 1295 TTCTCTGGGGGGGGGGGGGGGGGATTGGGCG 1354	1355 AGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGGCGTG	GlyLeuValAsnPheLeuLeuAlaIleGlyLeuVal	Oy 1415 GTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCTTCT 14/4 :: ::
Db 1241 LysGlyGluThrGlyAspValGlyGlnMetGlyProProGlyProArgGly 1260 Qy 314 GCAGGGGGCTCACCCACAGCCTCTGGACCATAGTGGGCCA	274GCCGGGTAGGGGTCAGGGGCCGTTCAGGCACTCCAGAACTGCTT	224	Qy 206 TGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCC 162		OY 113 CATGCTCAACACTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATC 54	53 CTGGCC : 373 roGlyG		AC Q92TB9; DT 01-MAY-1999 (TrEMBLrel. 10, Created) DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) DT 01-JUAY-1999 (TrEMBLrel. 21, Last annotation update)		OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; OC Asteridae; euasterids II; Apiales; Apiaceae; Apium. OX NCBL_TaxID-4045; RN fl	SEQUENCE FROM N.A. TISSUE-LEAF: Noiraud N., Delrot S., Lemoine R.; Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.	-i- SUBCELLULAR LOCATION: INTEGRAI EMBL; AF064100; AAC99332.1; InterPro; IPR003662; sub_transport Pfam; PF00083; sugar_Lr; 1.	DR TIGRFAMS; TIGR01301; GPH_sucrose; 1. KW Transmembrane. SQ SEQUENCE 512 AA; 54520 MW; 4D76A7854A7DF903 CRC64;	2.17e-13 333.00 40.54%	Mismatches: Indels: Gaps:	-110 (1-3410) x Q92TB9 (1-512)	Qy 332 CAGCTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATC 391	Qy 392 ACCTATGTGCCGCCTCTGCTGGAAGTGGGGGTAGAGGAAGTTCATGACCATGGTG 451

oy da	2159 AGGCAGCCCTAGAGACTGGGGAGAGGAGAGGGAC 2124	QQ	939 GlyGlyAspGlyPro
oy (. KÖ	1217 CGGTGCCCGGCTCAGCTCTGGGC 953 AsnGlyProGlnGlyProThrGl
o vo	o/o urroclyglukroclyProArgGlyLeuLeuGlyProLysGlyProFroGlyProProGl 696 2069 AGAGCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCGGGAGCCCGATGGGGC 2010	Qy	1157 AAAACAGCGTGAAGGTCATGAGT
Dp		qa	973 LysAspGlyLe
οy	2009 TAACAGGAGCGGGGAGCTGGGACCCAGTGAGGCAGCCCTCCACCCAATGTGCTGG 1953	کی _ک و	1130 TCCAGCTGCACCAGCTCAGCCACGGGGGGGGGGGGGGGG
qq	712 snValGiyProGlnGlyGluProGlyProProGlyGlnGlyAsnProGly 729	2 2	989 GINGLYLYSINGLYPIOPIOGIA 1070COMCGREGARCE
oy D	1952 AAGTTTTCTAGGCTGAGTATTGGCCAAGTGGCTCTTGTCAAATACTACCTGTGTAGCAA 1893 730Alaging Vien-ProglyDroglaging von 1750	7 A	GlyGl
δy		Qy	1019
QQ		qa	1028 GlnGlyLeuProGlyValAlaGl
Οy		δ, t	
QQ	766 HisProGlyLysGluGlyProProGlyGluLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyG	a .	1044GIYPFOATAGI
ΟŸ	1775 CACTATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGCAA	S 8	1056
Q	780 GlyProProGlyProGlnGlyProIleGlyTyrProGlyProArgGlyValLysGlyAla 799	ìè	1
Ολ	1731	7 E	1072 AlaLenglyLentyeglySergl
qq	800 AspGly11eArgGlyLeuLysGlyThrLysGlyGluLysGlyGluAspGlyPheProGly 819	3 8	
δy	1730CGACCTGGG 1716	r d	845 GGGCACTGGTGTCCCCAGTCAATG
qa	820 PheLysGlyAspMetGlyIleLysGlyAspArgGlyGluIleGlyProProGlyProArg 839	}	785 TCATGAAGGCATAGACAGAGTAG
ολ	CACCACCACGTACGGAGAC	7 6	
qa	840GlyGluAspGlyProdluGlyProLySGlyArgG 851	3 8	725 ACACCACCACCACCACCACCACCACCACCACCACCACCA
o O	1655 GTGGAGGTGGGAGCACTGCACTCCACGACCCACTTAGGGAAGGGAG 1599	. qa	1115ProGlyProAlaGlyGluLy
ò	1598 CHTCAGGGHTBGGGCOGGGGAGGAACGAACGAACAACAAAAAAAAAA	Oy	665 CCAGGATGAGCAGTGCCAGCTCCA
g d	lyT	qq	::: 1133 aGlyArgAspGlyLeuG
Qy	1544 CACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGT 1491	QY	605 AGCCGGCCCTTGGGATGAG
qq	882 lyProLysGlySer-IleGlyPheProGlyPheProGlyAlaAsnGlyGluLysGlyGly 901	a è	569 mcccoaaecacaeaccoccacaeca
0y	agtgtgtaggg 	Z G	1170 vSerLvsGlvAspLvsGlvGluG
g .;		, KO	509 CACTGGCTGAGCCTAGGAGCC
5 A	14.0 COUCLEARDOLISTACCARCOCCARCAGGCATCGGCCACCGGCACCGACCACC	qq	::: :: 1189 rolleGlyGlnProGlyProSer(
δ	GGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCACCGGT	Qy	452 GCACCATGGTCATGAACTTCTCC
qo		Ωp	1207 lnGlnGlyLeuPheGlyC
δ	1310 CCATGACCAGAGAGAAGACCAGGGAGATGGCGCACT 1275	Qy	392 TGATGCCTGGGGCCAAACACACCC 1222PheProGly-ProProGlyPro
o vo	919 FIGAIGGLYGLUAFGGLYPFOAIGGLYILGFINGLYLYSPIGGLYPFOLYSGLYASNSGF 938 1274 GCAGGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCGGGGCCF 1218	Qy	335 GCTGGGCTTTCCGGT

qq	939		952
. Хо	1217	TEGTACAGCCCTCGCCCACGAAAT	1158
qq	953	ı oGlyProP	972
ογ	5	GAAGGTCATGAG :	1131
QQ	973	LysAspGlyLeuProGlyHisProGlyGlnArgGlyGluThrGlyPhe	988
ر م	1130	TGCACAGCTCAGCCACGAGGGCGGGGGGGGGGGGGGGGG	0
3 8	o r	iisty Lystiiisty ktoktootoo kyki Okiootyvai vaistyki Okiiisiykki Olii Comedmon koosa koosa ka ka ka ka ka ka ka ka ka ka ka ka ka	o ?
<u>B</u> 5	00		1020
Qy	1019	AGCAGTGGGGCGA	696
QQ	1028	::: GlnGlyLeuProGlyValAlaGlyLysGluGlyThrLysGlyAspPro	1043
Qy	896	3GTGGGGCCCAGCGCTGCCTCCTCA	918
Db	1044		1055
Qy	917	CTACGCAGGTGAGGAAGATGAGGGTGAGCCAAAAAAGAGGCACT	873
QQ	1056		101
Qy	872	AGGGGG	846
QQ	1072	AlaLeuGlyLeuLysGlySerGluGlyProProGlyProProAlaGlySerPro	1091
٥y	845	CTGGTGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAG	786
qq	1092	yGluArgGlyProAlaGlyAlaAlaGlyProIleGlyIle	1106
Qy	785	TCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCCGGGAGAGGTCAG	726
qq	1107	GlyArgProGlyProGlnGlyPro	1114
Qy.	725	GCCACAGAAGTCCAGCAGCCC	999
qa	1115		1133
Oy Pr	9 (TGAGCAGTGCCAGGTCCAGGGGCCTGGGATCCGGGCACAGCAGCCTG	90
gn	ν,	gAspGlyLeuGInGlyProValGlyLeuProGiyProAlaGlyP	-
Qy	0	GGCCCTTGGGATGAG	570
qa	Ñ	oValGlyProProGlyGluAspGlyAspLySGlyGluIleGlyGluProGlyGlnLysGl	1170
Οy	569	CCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGT	510
QQ	1170	ySerLysGlyAspLysGlyGluGlnGlyProProGly-ProThrGlyProGlnGlyP	1189
Qy	509	ACJ	453
QQ	1189	lyProSerGlyAlaAspGlyGluPro	1207
Qy	452	· •	393
Dp	1207	 euPheGlyGlnLysGlyAspGluGlySerAr	1221
Qy	392	GGCCAAACACCTCCAGGC	336
qq	1222	PheProGly-ProProGlyProValGlyLeuGlnGlyLeuProGlyProProGlyGlu	1240
٥y	335	GCTGGGCTTTCCGGTGCCGCA	315

ογ	338AGAGCTGGGCTTTCCGGTGCCGCAGCGGGCTCACCCACAGCCTCTGGACCATAG 282	Query Match: 5.378 DB: 11	d Indels: 464 Gaps: 68
qa .	1134 GlyArgAspGlyLeuGlnGlyProValGlyLeuProGlyProAlaGlyPro-Va 1151	US-09-759-143-110 (1-3410) x Q60467	060467 (1-1840)
δ d	281 TGGGCCAGGGGGTAGGGCTCAGGGGCGGTTCAGGCACTCCAGAACTGCTTCG 228	Qy 3068 GGTCCTGCAGTAGCT	GGTCCTGCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGG
a è	TOTAL TOTAL OCTION TO THE TOTAL TOTA	600k	CLYFLOCLYMCCLLCALGABLALLASKILLLLACLYLGCLY AAGTTGGGGGTAGGGGAAATTTTGGGGAAATTTTGAGAGGGGA
경	rLysGlyAspLysGlyGluGlnGlyProProGlyProThrGlyProGlnGlyProThrGl	453	
Qγ	167 TCAGCCAGGCGCCCATTTCTGCC145	Qy 2951 GTAGAGGGG	
qq		Db 469 IleGluGlyProPro	::: TleGluGlyProProGlyProGluGlyProAlaGlyLeuPro
οy	144	Qy 2939 GGAAGTGGGGGAAG	GGAAGTGGGGGAACCAGGCTGGGCCAAGAGAGAGGGGTGG
qq	1211 heGlyGlnLysGlyAspGluGlySerArgGlyPheProGlyProProGlyProValGlyL 1231	Db 489 GlyProThrGlyGlı	GlyProThrGlyGlnValGlyAspProGlyGluArgGlyPro
δ	122 TICTCAGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATC 63	Qy 2879 CCTGAAGCC)
QQ	1231 euGlnGlyLeuProGlyProProGlyGluLysGlyGluThrGlyAspValGlyGlnM 1250	Db 509 ProGlyAlaAspGly	ProGlyAlaAspGlyLeuProGlyProProGlyThrMetLeu
Qy	62 ACTCAGATCCTGGCCGAGGCGCGCGCGTGTCACCCGGAGCC 22	QY 2834 TAACAGCATTTGGA	TAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCC.
QQ	yProProGlyPr	Db 526	PheArgPheGly
RES	RESULT 29	QY 2774 TTTGGGGGCCAGA	ACCCCAGGAGAAG
Sa:	OCO467 PRELIMINARY; PRT; 1840 AA.	Db 533 AspAlaGlySerLys	AspAlaGlySerLysGlyProMetValSerAlaGluGluSer
DT	USU45/; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Tast sequence undate)	Qy 2729 AGCCCAATGACCAGCTATCTCAGGGA	CTATCTCAGGGA
100	(TrEMBLrel. 21,	Db 553 GlnGlnAlaArgLe	GlnGlnAlaArgLeuAlaLeuArgGlyProAlaGlyProMet
800	rio-alpha-1 Lype V collagen. Cricetulus longicadatus (Long-tailed hamster) (Chinese hamster). Entarmota: Motadata: Craniata: Wortchrets Entalegatum:	Qy 2699 GATTGTTGGGGATCC	GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCA.
388	bunalyota; metazou; choluduc; claninuc; verestata; butereosculu; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	Db 573 GlyProMetGly-P	GlyProMetGly-ProProGlySerGlyGlyLeuLysGlyGly
388	CIICECLIUS.	Qy 2639 TGGATTCCCTTCTAC	TGGATTCCCTTCTACTTTGTTAAATAAATAAGTTAAATATTT
A A S	SEQUENCE FROM N.A.	Db 592 oGlnGlyProArg	
RA R	MEDLINE-9210142; PubMed-172213; Greenspan D.S., Cheng W., Hoffman G.G.;	QY 2579 GATGGCAACAGAAG	SACCAACAGGCCACATCCTGATAAAAGG
RT	"The pro-alpha-1(V) collagen chain: Complete primary structure, distribution of expression, and comparison with the pro-alpha-1(XI)	 Db 598 lGlnGlyProProG.	
RI.	collagen chain."; J. Biol. Chem. 266:24727-24733(1991).	Qy 2519 GCAAAAAGACAGTG	GCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGT
R Q (EMBL; M/b/30; AAA3/002.1; InterPro; IPR000087; Collagen.	Db 617	
DR.	InterPro; IPR000885; F1b_collagen_C. InterPro; IPR001791; Laminin_G.	QY 2459 CTTCCCCTACAAT	CTTCCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGA
DR DR	InterPro; IPR001230; Prenyl_site. InterPro; IPR003129; TSPN.	Db 617	
DR DR	Pfam; PF01410; COLFI; 1. Pfam; PF01391; Collagen; 18.	Qy 2399 TCCCATGCAAGAGC	TCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGTTAAGGG
# C	Pfam; PF02210; TSPN; 1. Probom: PD000007: Collagen: 2.	Db 618	
D D	Probom; PD00208; Fib_collagen_C; 1.	2339	AGGTGACTTTATTCAGCTCCCAAAAACCCTTCTAGG
OR DR	SM00282; La SM00210; TS	623	
DR	PROSITE; PS00294; PRENYLATION; UNKNOWN_1. Collagen	Ov 2279 CTAGCTGTTAACCC	CTAGGTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTC
Sos	SEQUENCE 1840 AA; 184174 MW; 32C56821EF64CE75 CRC64;	639	 EuProGlyGluLy
Alig Pred	nment Scores: 2.15e-13 Length:	QY 2219 GAGCCCTTCTGGCC	TCCCTGTATAAGTCCAGACTGAAACCCC
SCC	Score: 334.50 Matches: 302 Percent Similarity: 29.66% Conservative: 59		
не	24.82% Mismatches:		

Query DB:	Match:	5.37%	Indels: Gaps:	464 68	
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qq	433	GlyProGlyMetProAlaAsnGl	aAsnGlnAspThrIleTyrGlu	GlylleGlyGlyProArgGly	452
ΟY	3008	AGTTG	TTTTGGGCAGTGCCTTC	GGGGTAGGGGAAATTTTGGGCAGTGCCTTCATCAGCCAGTCCTAGAGAGA	2952
QQ	453	GluLysGlyGlnLysGlyGlu	ProAlaIle	ileGluProGlyMetLeu	468
Qy	2951	3G		T94	2940
qa	469	 IleGluGlyProProGlyProGluGlyProAlaGlyLeuProGlyProProG	luGlyProAlaGlyLeu	ProGlyProProGlyThrThr	488
Qy	2939	GGAAGTGGGGGAACCAGGCCAAGAGAAAGAGGGGTGGTTAGGGAAGCCGTTGAG	3GCCAAGAGAAGAGGGC	TGGTTAGGGAAGCCGTTGAGA	2880
qa	489	GlyproThrGlyGlnValGlyAspProGlyGluArgGlyProProGlyArgProGlyLeu	spProGlyGluArgGly	ProProGlyArgProGlyLeu	208
δλ	2879	CCTGAAGCC	CCACCCTCTACCTTC	CCACCCTCTACCTTCAACACCCTAACCTTGGG	2835
qa	503	ProGlyAlaAspGlyLeuProGlyProProGlyThrMetLeuMetLeuPro-	lyProProGlyThrMet	LeuMetLeuPro	525
Qy	2834	TAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGC	FTGGGATGAGTAGAATT	TCCAAGGTCCTGGGTTAGGCA	2775
qa	526	 		GlyGlyGly	532
Qy	2774	TTTTGGGGGCCCAGA		AAGAAGATTCTGGCAATGATC	2730
q	533	:::::: AspAlaGlySerLysGlyProMetVal	S	erAlaGlnGluSerGlnAlaG\$nAlaIleLeu	552
Qy	2729	AGCCCAATGACCAGCTATCTCAGGGGA	3GGGA	TOO	2700
qa	553	GlnGlnAlaArgLeuAlaLeuAr	rgGlyProAlaGlyPro		572
Qy	2699	GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAACACAGAAAAGCTAGCAA	racccaaatatagac <i>i</i>	CCAACACAGAAAAGCTAGCAA	2640
qa	573	GlyProMetGly-ProProGlyS	serGlyGlyLeuLysG	ProMetGly-ProProGlySerGlyGlyLeuLysGlyGluProGlyAspMetGlyPr	592
QY	2639	TGGATTCCCTTCTACTTTGTTAAATAAGTTAAATAATAATATTTAAATGCCTGTGTCTCTGT	aataaataagttaaat <i>i</i>	ATTTAAATGCCTGTGTCTCTGT	2580
qq	592	oGlnGlyProArg			298
Qy	2579	GATGGCAACAGAAGGACCAACAGCCACATCCTGATAAAAGGTAAGAGGGGGTGGATCA	SGCCACATCCTGATAA	AGGTAAGAGGGGGGTGGATCA	2520
qq	598	GlnGlyProProGlyProThr	SlyLysProGlyArgA	gGlyArgAlaGlySerAsp	617
Oy	2519	GCAAAAAAGACAGTGTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCCCTCAGGACT	rgagggacctggttci	TGTGTGTTGCCCCTCAGGACT	2460
qq	617				617
Oy	2459	CTTCCCCTACAAATAAGTCATA	TGTTCAAATCCCATGG1	ATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAAC	2400
QΩ	617		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		617
οy	2399	TCCCATGCAAGAGCTACATTAAA	acgaagctgcaggtta <i>i</i>	CCCATGCAAGACTACATTAAACGAAGCTGCAGGTTAAGGGGCTTAGAGATGGGAAACC	2340
qq	618			GlyAlaArgGlyMetPr	623
Qy	2339		CCCAAAACCCTTCTC	GAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGG	2280
Db	623	oGlyGlnThrGlyF	 ThrGlyProLysGlyAspAı	-AspArgGlyPheAspGlyLeuAlaGl	639
Qy	2279	CTAGCTGTTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCAT	SGTAATCCACCTGCAG	AGTCCCCCCATTCCAGTGCATG	2220
QQ	639	у	LeuProGlyG	-LeuProGlyGluLysGlyHisArgGlyAspPr	059
Qy	2219	GAGCCCTTCTGGCCTCCCTGTATAAGTCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTC	TAAGTCCAGACTGAAA (CCCCTTGGAAGGCCTCCAGTC	2160
qa	650				959

1123Valp	qa 		٠.
398 CATAGGIGAIGCCIGCGGCCAAACACACCIC	Qy	1346 AGACTGCTCGAGTGCCGAATCGTTGCACTGGTTCTATGACTATGACTAGAGAAAAAAAA	g ò
	· 6	TGTGGCACCGCCAGCCACAGGGAAAGCTGCCACACTGGCCAAAT	Oy 1
J#55#47	<u>a</u> è	852 GlyProAsnGly	qq
518 GCCAGTGGTCACTGGCTGAGCCTAGGAGGGG	δħ.	1466 GGATCTGCAGGGCTGAAGGTGAACCCGGTGAGGGCGGCTGAAGCTGTCACCACGGCCA 1407	Qy
	ପ୍ଧ		qq
578 TCAGCAGATGCCCAAGGACAGTGCCCAGAT	δλ		δ
	Dp	1303 TCAGGCTGCTGCTGCTGCTGCTCCCTCGGTATTTGGGAGGA 1512	А
638 GCCTGGGATCCGGGCACAGCAGCCTTGCTAG	Å0	/95 IYValLysGlyAlaAspGlyIleArgGlyLeuLysGlyThrLysGlyGluLys-GlyGlu 814	g ,
1071 GlyAlaLeuGlyLeuLysGlySerGluGlyP	ි සි —	1605AAGGGAGCTCCAGGCTTA	λο d
	a :	779 lnGlyProProGlyProGlnGlyProIleGlyTyrProGlyProArgG 795	qa
725 AGAGCAGGCCTCCAGTGGAGTGAAGCACAC	δ	1649 GTGGGAGCACTGCCTCCAGCACCACGTGTCCATTAGGG 1606	δ
1031 ProGlyAlaAlaGlyLysGluGlyThrLysG	qa		qa
761 CCTGGCGACAGTGGT	δδ	1709 CACCCACCACCACGTACGGAGACATCACAGGCAGAGGCCCCGCAGAGCGCGGGGGGG 1650	Qy
1019ProGlyProProGlyProProGlyG	qa		qa
821 CAGGCAGGAGGTAGCCCAGGCAGCCCCCAAG	Qy	AGGCAGATGCCCGGGCCCGGAACCACCTGGCCTTGGGTGGG	ò
 1005 GlyProThrGlyGluThrGlyProMetGlyG	qa	743 ProdlyGluLysGlyProLeuGlyLysProGlyLeuProGlyCuProGlyGluLysGlyPro	G qa
851 GGGCCA	Oy		3 8
 10 11 11 12 13 14 15 15 15 15 15 15 15	qa	1889 AAATUGUGAUCAGAUCKAGGCTIGUGGAAACKAATATAGGCAGTGACTGA 1830 723 G14G14G14G14AAAATUCAGGCTIGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	<u></u>
875 ACT	3 0	722 722	QQ
STGGCTGCT	03	1949 ITTICTACGCTGAGTATTIGGCCAAGTCGCTCTTGTCAAATACTACCTGTGTAGGAAAGT 1890	Qγ
956GlnGlyProThrGlyPhePro	qa	712 snValG1y 722	qq
995 ACAAGGAGGGGCCGACAGCCCTTCTGCTGG	03	GGAGCTGGGACCCAGTGAGGCCCCTCCACCCCAATGTGCTGGAGG	δλ
943 ProAlaGlyProProGlyGluArgGlyProP	qa	2069 AGACCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGGGGC 2010	ර් යි
931 LysProGlyProLysGly	a :	676 uProGlyGluProGlyProArgGlyLeuLeuGlyProLysGlyProProGlyProProGl 696	QQ
1115 CAGCCACGAAGAGCCGGCGCAGGGTGCGGG	δ	2123 GCCCCAGCCCCAGCTGTGCAGCTACGCACCTCAGCAGCACAGGTGGCAGCAG 2070	δλ
920 ArgGlyGluArgGly	qa —	 1yAspAspGlyGluValGlyProArgGlyLe	qa
1175 CGCCACGAAATCCGTGTAAAACAGCGTGAA	ΟŊ	2159 AGGCAGCCTAGAGACTGGGGAGAGGGAGAGGGAC 2124	δλ
900 GlyGlyArgGlyThrProGlyLysProGlyE	qa		QQ
1232 AGTGTCTCCGGGCCTCGGTGCCCGGCTC	Qy		
 	qa	639 y	73 PG
0/UGIYVALPIO 1286 AGATGGGAGTAGTAGAAGAAGAGGG	6 6	623 oGlyGlnThrGlyProLysGlyAspArgdlyPheAspGlyLeuAlaGl 639	ଫୁପ '
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	870	GlyTyrProGlyLeuProGlyTyrProGly 879
	1286	SCGCACTGO
_	880	GlnGlyProLysGlySerll
	m (CTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCT 11
	006	Į.
	1175 920	CGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACAGCT 1116
	1115	TGCGGCAGCAGGTGGTGCAGCGGG
	931	:: AsnSerGlyGlyAspGly 942
	1055	GAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGCGGCCCGGCATGGACAGCAGTGGGGCG 996
	943	ProAlaGlyProProGlyGluArgGlyProAsnGlyPro955
	995 956	ACAAGGAGGGGCCGACAGCCCTTCTGCTGGCTCGGTGGGGCCCAGCGCTGCCTCCTCAG 936 :::
	935	GTGGCTGCTACG
	970	Proprogly
	875	ACTAGG 852
	985	GluThrGlyPheGlnGlyLysThrGlyProProGlyProProGlyValValValGlyProGln 1004
	851	ORDER TO THE TOTAL ORDER TOTAL ORDER TO THE TOTAL ORDER TO THE TOTAL ORDER TO THE TOTAL O
	1005	GlyProThrGlyGluThrGlyProMetGlyGluArgGlyHis1018
		GGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATGAAGGCATAGA
	1019	FroGlyProProGlyProProGlyGluGlnGlyLeu 1030
	761	
	31	ProGlyAlaAlaGlyLysGluGlyThrLysGlyAspProGlyProAlaGlyLeuProGly 1050
	72	
	r)	LysAspGlyProProGlyLeuArgGlyPheProGlyAspArgGlyLeuProGlyProVal 1070
	99	CGCCCAGGATGAGCAG
	1071	yProProGly
	638 1088	GCCTGGGATCCGGGCACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGACAAAGAGGC 579
	578	TCAGCAGGATGCCCAAGGACAGTGCCCCAGATGAAGGGCCGGCGGCGGCGATAGCGTCCAC 519
	1096	ProAlaGly 1098
	518 1099	GCCAGTGGTCACTGGCTAGGGCGGGACACACAGACCAGCCCAGCACTGGACCAA 459
	458	TGCCCAGCACCATGGTCATGAACTTCTCCTCTACCCCCACTTCCAGCAGCAGGCGGCA 399
	1112	_
	39	33
	1123	

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SMART; SM00210; TSPN; 1

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1281 lGlyGluLysGlyGluProGlyGluAlaGlyAspProGlyLeuProGlyGluGlyGlyPr 1301
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                                                                 1262 AlaProGlyAlaAspGlyPro-GlnGlyProProGlyGlyIleGlyAsnProGlyAlaVa 1281
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SEQUENCE FROM N.A.

STRAINS=20428740; PubMed=10852920;

MEDLINE=20428740; PubMed=10852920;

A Chernousov M.A.; Rothblum K., Tyler W.A., Stahl R.C., Carey D.J.;

Chwann cells synthesize type V collagen that contains a novel alpha of schwann cells synthesize type V collagen that contains a novel alpha of fifthicty heperin binding of alpha4(v) collagen.";

A Chain. molecular cloning, biochemical characterization, and high a fifthirty heperin binding of alpha4(v) collagen.";

EMBL; AF272662; AAF76433.1; --

RICEPTO; IPR0000885; Fib_collagen.

RICEPTO; IPR001791; Laminin_G.

RICEPTO; IPR001791; Laminin_G.

RICEPTO; IPR001230; Prenyl_aite.

RICEPTO; IPR001230; FSPN.

P Ffam; PF01410; Collegen; 17.

PR Pfam; PF01391; Collagen; 17.
                                                                                                                                                             1242 ThrGlyAspValGlyGlnMetGlyProProGlyProProGlyProArgGlyProSerGly 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 TTTCTGCCAGCCCTTTGGT-----GCCGGTCCAGCTTCTCAGCCCATGCTCAA 105
                                                                                                                                                                                                                                                                                                                                                                    -----TCTGCTCCAGAAGCTGCGGCCTC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 TCCTCCTTGCTGCCGC------CAACTGCCTAGGAATCAGCCAGGGCCCCA 153
                                        383 CGGCCAAACACCACCTCCAGGC---CAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTT 327
                                                                                                                                                                                                                                                                                    274 -GGCGGGTAGGGCTCAGGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGC---- 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 CACCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCACTCAGATCCTGGCCGAG 45
                                                                                                                      326 TCCGGT-----GCCGCAGCAGCGGC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Alpha I type V collagen.
  1208 eu-----PheGlyGlnLysGlyAspGluGlySerArgGly-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2699 GATTGTTGGGGGATCCCCCACCCTACCCAAATATTAGACACCAACAACAGAAAAGCTAGCAA 2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2579 GATGGCAACAGAAGGACCAACAGGCCACATCCTGATAAAAGGTAAGAGGGGGGGTGGATCA 2520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2459 CTTCCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAAC 2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2399 TCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGTTAAGGGGCTTAGAGAGTGGGAAACC 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 533 AspAlaGlySerLysGlyProMetValSerAlaGlnGluSerGlnAlaGlnAlaIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           598 1GlnGlyProProGlyProThrGlyLysProGlyArgArgGlyArgAlaGlySerAsp--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 GlyProThrGlyGlnMetGlyAspProGlyGluArgGlyProProGlyArgProGlyLeu
                                                      AD38F5FF886B923C CRC64;
                                                                                                                             Matches:
Conservative:
Mismatches:
                                                                                                          Length:
                                                                                                                                                                                     Indels:
PROSITE; PS00294; PRENYLATION; UNKNOWN_1.
PROSITE; PS00761; SPASE_I_3; UNKNOWN_1.
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                                                      1840 AA; 183986 MW;
                                                                                                      1,99e-13
335.00
28.98%
24.94%
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                                      Collagen.
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900 alMetValGlyProProGlyAlaLysGlyGluLysGlyAlaProGlyAspLeuAlaGlyA 920	308GGCTCACCCACACACTCTGGACCATAGTGGG	CCAGGGGGGGTAGGGCTCAGGGCGTTCAGGC 24	940 LysGlyGluAlaGlyArgAlaGlyGluProGlyAspProGlyGluAspGlyGlnLysGly 959	244 ACTCCAGAACTGCTTCGTCTCGGC	GAAGCTGCGGCCTCTCCTTGCTTGCTGCCTCCTTGCTTGC	ProGlyProThrGlyProProGlyMetLysGlyAspValGlySerProGlyAlaProGly	200	998 ValValGlyPheProGlyGlnThrGlyProArgGlyGluThrGlyGlnProGly-ProVa 1017	151 TTCTGCCAGCCCTTTGGTG	1017 iGlyGluArgGlyLeuAlaGlyProProGlyArgGluGlyAlaProGlyPro 1034	1 TCTCAGCCCATGCTCAACACCTGCTGTGGGGCACCTCAGTGGGGACACGTC	1035 -LeuGlyProProGlyProProGlySerValGlyAlaProGlyAlaSerGlyLeuLysGl 1054	67 TCATCACTACATCCTGGC	1054 yAspLysGlyAspProGlyThrGlyLeuProGlyProArgGlyGluArgGlyGluProGl 1074	25 A 25	1074 y 1074	207 PRELIMINARY; PRT; 1838 AA. 207; NOV-1998 (TrEMBLrel. 08, Created) NOV-1998 (TrEMBLrel. 08, Last sequence update) JUN-2002 (TrEMBLrel. 21, Last annotation update) lagen al(V). AAl. Musculus (Mouse). Craniata: Vertebrata: Euteleostc	aryota; Metazoa; Chordata; Craniata; Verteorata; malia; Eutheria; Rodentia; Sciurognathi; Muridae; I_TaxID-10090;	4	Y.L., Sumiforni H., Khaleduzzaman M., Ninomiya Y., Toshloka H.; DNA sequence and expression of the mouse alphal(V) collagen gene."; oblin. Blophys. Acta 1397:275-284 (1998).	BL; ABU09993; BAA28'86.1; MGI:88457; COISA1.	InterPro; IPROUDO8/; Collagen.C. InterPro; IPROUDO85; Fib_Collagen_C. InterPro; IPROUDO91; Laminin_G. InterPro; IPROUDO910; Laminin_G.	terpro; IPR003129; TSPN. terpro; IPR003129; TSPN. am. PF01410; COLFT: 1.	Pfam; PF02210; TSPN; 1. ProDom; PD000007; Collagen; 2. ProDom; PD002078; Fib_collagen_C; 1.	SMART; SMUOUS8; COLF1: 1. SMART; SMOO228; LamG; 1. SMART; SMOO220; TSPN; 1. PROSITE; PSO0294; PRENYLATION; UNKNOWN_1.
qq	Oy G	λò	q	Qy Dp	ò	r qa	٥y	Db	Qy	ор	Qy	qq	οy	qq	ΟY	qq	088207 1D 0882 AC 0882 DT 01-1 DT 01-1 DT 01-1 COL 082 COL 062 COL 062 COL 062 COL 062 COL 062 COL 062 COL 063 COL		RP SE	RT "C	DR EN	DR DR	DR In	DR Pf	

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2699 GATTGTTGGGGATCCCCCACCTACCCAAATATTAGACACCAACACAGAAAAGCTAGCAA 2640
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                                                                                                                                                                                                                                           3008 AAGTTGGGG---GTAGGGGAAATTTTGGGCAGTGCCTTCATCAGCCCAGTCCTAGAGAGA 2952
                                                                                                                                                                                                                                                                                                                                                             2939 GGAAGTGGGGGGAACCAGGCTGGGCCAAGAAGAAGAGGGGTGGTTAGGGAAGCCGTTGAGA 2880
                                                                                                                                                                                                                                                                                                                                                                                                                     2879 CCTGAAGCC-----CCACCCTCTACCTTCCTTCAACACCCTAACCTTGGG 2835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2519 GCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGTCCCCCTCAGGACT 2460
                                                                                                                                                                                                                                                                                                      2951 GTAGAGGGG-----AGT 2940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2834 TAACAGCATTTGGAATTATCATTTGGGATGAGTAGAATTTCCAAGGTCCTGGGTTAGGCA 2775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2774 TITIGGGGGGCCAGA-------CCCCAGGAGAAGAAGATTCTGGCAATGATC 2730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2459 CTTCCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAAC 2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2399 TCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGTTAAGGGGGCTTAGAGATGGGAAACC 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2339 AGGIGACTGAGTTTATTCAGCTCCCAAAAACCCTTCTCTAGGTGTGTCTCAACTAGGAGG 2280
                                                                                                                                                                                     3068 GGTCCTGCAGTAGCTCCAAACAGGGTTGTGGAGCTGGTGGGGAAAGTTGGGGGGTAGGGGA 3009
                                                                                                                                                                                                                                                                                                                                                                                                                                                   523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296
                                                                                                                                                                                                                                                                                                                                                                                 524 ....-----BheArgPheGly------GlyGlyGly 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        571 GlyProMetGly-ProProGlySerGlyGlyLeuLysGlyGluProGlyAspMetGlyPr 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467 IleGluGlyProProGlyProGluGlyProAlaGlyLeuProGlyProProGlyThrThr 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         616 -----GlyAlaArg---GlyMetPr 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615
                                                                                                                                                                                                                                                                                                                                                                                                                                       590 oGlnGlyProArg-----GlyVa
             7A520B23D1851783 CRC64;
                                                      1838
301
60
395
458
68
                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                               Gaps:
                                                                                                                                                           US-09-759-143-110 (1-3410) x 088207 (1-1838)
             1838 AA; 183691 MW;
                                                      1.85e-13
335.50
29.74%
24.79%
5.39%
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                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                          Alignment Scores:
             SEQUENCE
Collagen
                                                       Pred. No.:
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119	SCAGACAGC 2065 Db 587 lvGluargGlvProProGlv	283 Qy 1234	2005		318 Db 624	1885 Qy 1			344 . Db 655	1832 QY 994	364 0 0.1	SAAGGCACT 1772 Dh 601 roftwelvalalatleaen610	383 00 892	1712 2 711 Db 711	OV 865 GGTGCCCAGGTAGGGGGCCA	1652 - 731 Db 731		1607		452 Db 771	1541 Qy 700	472 Db	1481 CY 665	491 Db 808	1433 Qy 635	510 bb 828	1395 QY 5//	530	1343	547 00 802	1320	567 0v 418	1271 Db 886	QY 358 GGTTAGCAGGTTGACCAGA QY 358 GGTTAGCAGGTTGACCAGCA
	J	lyvala	CACATT	2004 GGAGCGGGGAGCTGGGACCCAGTGAGGCCCTCCACCCCAATGTGCTGG	302GlyGluProGlyProProGlyProProGlyArgLeuValG		1egly	GCGACCA	::: lyGluP	;	erGlyG	GAGCTG	alArgG	ATCCAG 	Ð	CTCACC	GlyProHisGlyAl	AGGTGGGAGCAGG	GAAG			452 oGlyGluAspGlyArgLySGlyGluLys-GlyAspSerGlyAlaProGlyA:	1540 TCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTA	472 roAspGlyProLysGlyGluArgGlyAlaProGlyAspProGlyLeuA.	1480 CAGTGTGTAAGGGCAGGATCTGCAGGGCTGAGAAGGTGAA	491 roGlyLeuProGlyGln-ValGlyProProGlyGlnGlyPheProGlyVal	1432 GGGGGTGAAGCTGTCACCACGGCCACACTGTGGGACA	511 ThrGlyProLysGlyAspArgGlyGluThrGlySerLysGlyGluGlnG.	1394GGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACAGTGGC	530 lyGluArgGlyLeuArgGlyGluProGlySerLeuProAsnA.	1342 IGCTCGAGTGCCGAATCGCTGCA	547 euLeuGluThrAlaGlyIleLysValSerAlaLeuArgAspIleValGluT.	1319CCAGCCGGTCCATGACCAGAGAGAGACCAGGGAGATGGC	erGiyserPheLeuProValP

Query Match: 5.39% Indels: 444 DB: 11 Gaps: 73 IIS-08-750-143-110 (1-3410) y OKOMAA (1-1540)	3039 GGAGCTGGTGGGAAAGTTGGGGGTAGGGGAAAGTTGGGGGT	36 GlySerProGlyProGlnGlyProAlaGlyArgAlaGlyGluLySGlyGluLySGlyAsp	QY 29.19 TGCCTTCAT	QY 2964AGTCCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Db 76 ArgGlyThrProGlyIleThrGlyProLysGlyAspArgGlyGlnThrGlyThr 93	2925 CCAGGCTGGGCCAAGAAGAAGAGGGTGGTTAGGGAAGCCGTTGAAGCCTGAAGCCCCACC	Db 94 ProGly-GluProGlyGluLysGlyGluArgGlyProPro-GlyProValGlyProGlnG 113 Qy 2865 CTCTACCTTCCAACCTAACCTTGGGTAACAGCATTTGGAATTATCATTTGGGAT 2806		Qy 2805 GAGTAGAATTTCCAAGGTCCTGGGTTAGGCATTTTGGGGGGCCCAGACCCCAGGAGAAGAA 2746	Db 123ValGluGlyProGluGlyProProGlyProAlaGlyArgA 136 Qy 2745 GATTCTGGCAATGATCAGCCCAATGACCAGCTATCTCAGGGACCTGATTGTGGGGATC 2686	::	QY 2685 CCCCACCCTACCCAAATATTAGACACCAACAGAAAAGCTAGCAATGGATTCCCTT 2629	Db 148 roAlaValGlyProGlyGlyAlaGlyAlaLysGlyGluLysGlyAspAlaGlyLeuPro- 167	OY 2628 CTACTTTGTTAAATAAGTTAAATATTTAAATGCCTGTGTCTCTGTGATGGCAACAG 2569	Db 167 167	Qy 2568 AAGGACCAACAGGCCACATCCTGATAAAAGGTAAGAGGGGGGTGGATCAGCAAAAGACA 2509	2508 GIGCIGIGGCIGAGGGACCIGGITCITGIGIGITGCCCTCAGGACTCITCCCCIACA	Db 181 184	Qy 2448 AATAAGTCCATAGTTCAAATCCCATGGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAG 2389 ::: :::	QY 2388 AGCTACATTAAACGAAGCTGCAGGTTAAGGGGGCTTAGAGATGGGAAACCAGGTGACTGAG 2329	Db 194198	2328 TTTATTCAGCTCCC	199ArgGlyProIleGlyLeuThrGlyArgAlaGlyP	2268 CCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAGTGCATGGAGCCCTTCTG	210 roThrGlyAspSerGlyProProGlyGluLysGlyAspProGlyArgProGlyProProG	Oy 2208 GCCTCCTGTATAAGTCGG	QY 2166 TCCAGTCAGGCAGCAGAGACTGGGGAGAGAGGAGAGGGACGCC- 2120	Db 249 snProGlyAspProGlyLeuProGlyLysAlaGlyGluArgGlyLeuArgGlyAlaProG 269
	381 LeuThrValLeuValThrLysLeuAlaGlnHisSerArgGlnTyrAlaProGlyThrGly	GGTTC	1445	Db 421 SerValLeuGlyValProLeuAlaIleThrTyrSerIleProPheAlaLeuAlaSerIle 440	1490	441 PheSerSerThrSerGlyAlaGly	Qy 1550 AGTGAGGACAGCCTG	QY 1574 TTCCTGCCAGGCCTAAGCCTGGA	Db 469 ValLeuSerGlyProTrpAspAlaLeuPheGlyGlyGlyAsnLeuProAlaPheValVal 488	Qy 1613 GGACACGTGGGTGGAGGCAGTGGC 11 111 11 111 10 111111 11 1111111 11 11 111111	RESULT 26	Q00444 ID Q60444 PRELIMINARY; PRT; 1549 AA.	01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.		OS Cricetulus griseus (Chinese hamster). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	<pre>Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus. NCBI_TaxID=10029;</pre>	RP SEQUENCE FROM N.A. RC TISSUE-LUNG;			KL Hum. MOL. Genet. 2:2/3-2/8(1993). DR EMBL: LOG683: AAA36968.1; DR HESD: DAG081: 1,000				DR ProDom; PD000222; Kunitz_BPTI; 1. DR PROSTUE: POS00280; BPTI KUNITz_1; 1.			Alignment Scores: 1.8e-13 Length: 1549 Score: 33 Score: 3.4	t Similarity: 30.87% Conservative: ocal Similarity: 25.98% Mismatches:

1223 CGGAG 325 GLUG1 1280 GCCAT 345 ValVa	oy oy ob	Pred. No.: 1.12e-13 Length: 523 Score: 337.50 Matches: 134 Percent Similarity: 40.38% Conservative: 76 Best Local Similarity: 25.77% Mismatches: 185 Query Match: 5.26% Indels: 125 BB: US-09-759-143-110 (1-3410) x 004077 (1-523)
1103 CTCTT	Qy Db	DR EMBL; 293774; CAB07811.1; DR InterPro; IPR003662; sub_transporter. DR Pfam; PF00083; sugar_tr; 1. DR TIGRFAMS; TIGR01301; GPH_sucrose; 1. KW Transmembrane. SQ SEQUENCE 523 AA; 55229 WW; F8EBF170212D191A CRC64;
989 TCCTT :: 271 GlyMe 1043 GGCGC	oy Oy Oy	ROUGHOUS FROM N.A. RC TISSUE-COTYLEDON; RA Weber H., Borisjuk L., Heim U., Sauer N., Wobus U.; RT "A role for sugar transporters during seed development: Molecular RT characterization of a hexose and a sucrose carrier in faba bean RT seeds.; RL Plant Cell 0:0-0(0).
233 941 GAGGC 251 GluTh	d Qy	
213 ProPP 884 GGCCT	7 a 7	DT 01-JUL-1997 (TrEMBLrel. 04, Created) DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update) DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) DE Sucrose transport protein.
788 AGTCT ::::: 193 Alave		RESULT 25 004077 ID 004077 PRELIMINARY; PRT; 523 AA.
731 CTCT7 173 LeuCy	λο da	Qy 1859TCTGCCGCAGCCTGGGTCTGGTCGCCATT 1888
671 GGGC1 153 TrpI	oy D	OY 1805 CTGTTTATGGGCTCCATGTCCAGGTCAGCCAGTCTGTCACTGCCTATATGGTG 1858 :::
620 133 GlyAs	Oy Dp	Qy 1745 ATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCC 1804
572 CTGCT 116 AlaI	oy Dp	Qy 1721 GCCAGGGGGGTYCCG
	ÅÖ qa	Oy 1661 CTCTGCGGGCCTCTGCCTGGATGTCTCCGTACGTGGGTGG
	λσ qq	Oy 1601 CCCTTCCCTAATGGACACGTGGGTGCAGGCAGTGGCCTGCTCCCACCTCGCGG 1660
	Oy Op	
332 CAGC	- Oy	Qy 1481 GCCTCCTCTACCACCGGGAGAAGAAGAGGTGTTCCTGAAATACTGAGGGAAAAAAA 1540

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TGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTG-----GCTTTCCGGAACCTG 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1340 GCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCC 1399
                                                                                                                                                                                                                                                                                                      CTCTTGCTGGTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATC 391
                                                                                                    TATGTGCCGCCTCTGCTGCAAGTGGGGGGTAGAGGAGAAGTTCATGACCATGGTG 451
                                                                                                                                                                                                     3GCATTGGTCCAGTGCTGGCCTGGTCTGTGCCGGCTCCTAGGCTCAGCCAGTGAC 511
                                                                                                                                                                                                                                                                                                                                                                                                                CTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTG------- 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----CTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTG 670
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| SpSerLeuAspGlnLysValArgProArgAlaIleGlyIlePheValValGlyPhe 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGAC 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :::|||||||
| IleLeuAspValAlaAsnAsnMetLeuGlnGlyProCysArgAlaLeuLeuGlyAsp 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fTCCGG---GACCCGGACCACTGTCGCCTACTCTGTCTATGCCTTCATGATC 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysAlaGlyAsnGlnArgLysThrArgAsnAlaAsnAlaPhePhePhePheMet 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG----GCTGAG 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCAGCGCTGGGCCCCACCGAGCCAGCA------GAAGGGCTGTCGGCCCCC 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....-LysArgProMetTrplle 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpMetGlyLysGluValTyr------GlyGlyThrValGly 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SlyHisAlaTyrAspMetGlyValArgGluGlyAlaLeuGlyLeuMétLeuAsnSer 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /alLeuGlyAlaThrSerLeuGlyValAspIleLeuAlaArgGlyValGly---Gly 363
                                                                                                                                                                                                                                   IleMetValValAlaSerIleAlaAlaGlyValGlnPheGlyTrpAlaLeuGlnLeu 55
                                                                                                                                 ::: |||| ::: ::: LeuLeuThrProTyrValGlnLeuLeuGlyIleHisHisThrTrpAlaAlaTyrIle 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTGGGGGCTGCCTGGCTACCTCCTGCCTTGCCATTGAC------
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Page 33

53 SerLeuLeuThrProTyrValGlnLeuLeuGlyIleProHisLysTrpAlaAlaTyrlle 72 452 CTGGGCATTGGTCCAGGCCTGGTCTGTCCGGTCCTAGGCTCAGCCAGGAC 51	dy 620 CTGTGCCCGGATCCCAGGCCCTGGAGCTGCTGCTGCTGGGCTGGTG 679 :::::	927 GACTGGGACACCAGTGCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTT	Db 279
AGTGAGGACAGCCTGATGACCAGCCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCT	425 ThrArgIleGluSerLeuGlyLeuGlyGlnGlyLeuSerMetGlyValLeuAsnL 1778 TTCCTGCTGCCAGGGGCCCCATCCTGTTTATGGGCTCCATGTCCAGGTC 445 IlevallieProGlnValIleValSerTeuGlySerGlyProTrpAspGlnLeuP 1832AGCCAGTCTGTCACAGCCTATATGGTGTCTGCCGCAGGCCTGGGTC 1832AGCCAGTCTGTCACACAGCTATATGGTGTCTGCCGCAGGCCTGGGTC 1883 GCCATTACTTACTACACAGGTAGTATTGAAAAAAAAAAA	RESULT 24 095725 1D 095725	

153 ATTCTGCCAGCCCTTGGTGCCGGTCCAGCCCATGCTCAACACCTGCTGCT 94	9SP63 PRELIMINARY; PRT; 501 AA. 9SP63; PRELIMINARY; PRT; 501 AA. 1-MAY-2000 (TrEMBLrel. 13, Created) 1-MAY-2000 (TrEMBLrel. 13, Last sequence update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation update) 1-UN-2002 (TrEMBLrel. 21, Last annotation) 1-UN-2002 (TREMBLRel. 21, Last BERRY; 1-UN-2002	CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY). DR EMBL, APIS2445, AAD55269.1; DR InterPro; IPRO083; Sugar_tr; 1. DR TIGRRAMS; TIGRO1301; GPH_sucrose; 1. RW Transmembrane. SO SEQUENCE 501 AA; 54075 MW; 4FD19DFAFE539077 CRC64; Alignment Scores: 9.57e-14 Length: 501 Score: 338.50 Matches: 163 Pred. No: 300.29 Conservative: 84 Best Local Similarity: 26.59 Mismatches: 159 Query Match: 10 Gaps: 25	-143-110 (1-3410) x Q9SP63 (1-501) 191 AGGAGGAGGCCGAGCTTCTGGAGCAGACCGAGCGAGCGAG
60 00 00 00 00 00 00 00 00 00 00 00 00 0	ins safe	CC -1-SUBLE PRICE PROPERTY PRO	us-09-759 Qy Db Qy Db Qy Qy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy

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989 TCCTIGICGCCCCACTGCTGT------CCATGCCGGGCCCGGTTGGCTTTC 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1034 CGGAACCTGGGCGCCCTGCTTCCCCGGCTGCAGCTGTGCTGCCGCATGCCCCGCACC 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1190 GGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGG 1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1370 CCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCCGTGGTGACAGCTTCAGCC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1310 GACCGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTC 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1490 TACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGC 1549
                                                                                                                                                                                                                                                                                                                                    ||| ||| ||| ||| 249 SerArgSerThrHisIleSerGluGluMetAlaGluSerThrHisAlaGluGluAlaPhe 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 ------GlyThr 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||||||||| :::||| 276 LeuArgTyrLeuSerGlySerIleTrpIleIleLeuPheValThrAlaLeu---ThrTrp 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGGGGTGCCTC 880
                                                                                                                                                                                                                                                                                                                                                                              881 -----TITIGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACATG 928
                                                                                                                                                                                                                                                                                                                                                                                                  217 AsnLeuLysSerAlaPheLeuLeuAspIleIlePhe-----IleAlaIleThrThr 233
                                                                                                                                                                                                                                                                                                                                                                                                                                          929 CTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCAGAAGGGCTGTCGGCCCCC 988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234 TyrIleSerIleThrAlaAla-------GlnGluLeuProLeuSerSerSer 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 GluLysLeuCysArgLysTrpGlyAlaGlyPheValTrp------ 361
511 GCAGGCTGCTG-----TGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTG 664
                                                                                                                          665 GGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTC 724
                                                                                                                                                        142 GlyPheTrpLeuLeuAspValAlaAsnAsnValThrGlnGlyProCysArgAlaLeuLeu 161
                                                                                                                                                                                      725 TCTGACCTCTTCCGGGACCCGGACCAC----TGTCGCCAGGCCTACTCTGTCTATGCC 778
                                                                                                                                                                                                                                                                                  181 LeuPhelleAlaValGlyAsnValLeuGlyPheAlaThrGlySerTyrSerGlyTrpPhe 200
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804 oProGlyProAlaGlyPheAlaGly-------ProProGl 815
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                                                                                                                                                                                                                                                                                                                                                                                                     780 AAGGCATAGACAGAGTAGGCCTGGCGACAGTGGT---CCGGGTCCC-----GGAAGAGG 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 yAla-----proGlySerGlnGlyAlaProGlyLeuGlnGlyMetProGlyGluArgGl 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 CTCAGCAGGATGCCCAAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCGCCATAGCGTCCA 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423 CCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGCGGCCAAACACACCTCCAGG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 AGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCT----C 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          868 roGlyAlaThrGlyPheProGlyAlaAlaGlyArgValGlyProFroGlyProSerGlyA 888
                     614 yAlaGlnGlyProProGlyProAlaGlyProAlaGlyGluArgGlyGluGlnGlyProAl 634
                                                                                                                                                                                                                                                                                                                        816 AGGA-------GGTAGCCCAGGCAGCCCCAAGACTGATCATG 781
                                                                                                                                                                                                                                                                                                                                                      213 CAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCC 154
                                                                                                               580 oGlyProLysGlyAlaAla------GlyGluProGlyLysAlaGlyGl 594
                                                                                                                                                                                                                                         854 ------AGGGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGGC 817
                                                                          929 -------GCAGTGTGGCTGCTACGCAGGTGAGGAAGATGAGGGTGAGGCCAGGCCA 883
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GCTCCAGG
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947 -----CTGCCTCCTCAGCCACCA--
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; AF017178; AAB94054.2; -.
InterPro; IPR000087; Collagen.
InterPro; IPR000885; Fib_collagen_C.
InterPro; IPR001007; VWF_C.
                                                                                                                      Last sequence update)
Last annotation update)
                                                                      PRT; 1461 AA
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MEDLINE-89025644; PubMed-3178743;
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                                                                                                01-NOV-1998 (TrEMBLrel. 08, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01410; COLFI; 1.
Pfam; PF01391; Collagen; 18.
                                                                    PRELIMINARY;
                                                                                                                                                       Pro alpha 1(I) collagen.
3571 nProGly 3573
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                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                 076045;
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----- AGGACCAAC 2559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2318 TCCCAAAAACCCT-----TCTCTAGGTGTGTCTCAACTAGGAGGCTAGCTGTTA---AC 2268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2207 CCTCCCTGTATAAGTCCCAGACTGAAACCCCCTTGGAAGGCCTCCAGTCAGGCAGCCTAG 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2147 AGACTGGGGAGAGGAGGACGCCCCAGCCCCCAGCTGTGCAGCTACGCACCTCAGC 2088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 ------ThraspGlnGluThrThrGlyValGluGlyAspThrGlyProArgGlyPr 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 nLeuSerTyrGlyTyrAspGluLysSerThrGlyGlyIleSerValProGlyProMetGl 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 yProProGlyProProGlyProProGlyProProGlyLeuGlyGlyAsnPheAlaProGl 159
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                                                                                                                                                                                                                                                                                                                                                                      60 IleCysValCysAspAsnGlyLysValLeuCysAspAspVallleCysAspGluThr--- 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 gProGlyGluArgGlyProProGlyProGlnGlyAlaArgGlyLeuProGlyThrAlaGl 257
                                                                                                                                                                                                                                                                                                                                                                                                                                             79 -----LysAsnCysProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 AlaGluValProGluGlyGluCys-CysProValCysProAspGly------
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                                                                                                                           9ACF6DE30EA78E21 CRC64;
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                                                                                                                                                                                                Matches:
                                                                                                                                                                                 Length:
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                                                                                                                                                                                                                                                                                                                                    2591 CTGTGTCTCTGTGATGGCAACAGA-----
                                                                                                                                                                                                                                                                                                 US-09-759-143-110 (1-3410) x 076045 (1-1461)
Pfam; PF00093; vwc; 1.
Probom; PD000007; Collagen; 2.
Probom; PD002078; Fib_collagen_C; SMART; SM00038; COLFI; 1.
SMART; SM00214; VWC; 1.
                                                                                                                         1461 AA; 138630 MW;
                                                                                                                                                                           6.3e-14
342.50
31.26%
26.65%
5.50%
                                                                                     PROSITE; PS01208; VWFC; 1.
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Db Qy

λ.	1604 TTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTCCTCCCACCTCCACCCGCGTC 1663
q	3024
λλ	1664 IGCGGGCCTCTGCCTGTGATGTCTCCGTAGTGGTGGTGGTGAGCCCACCGAGGCC 1723
qc	
λζ	AGGGTGGTTCGTGCCGGGCGGGCATCTG
qC	306
λζ	GACCTCGCCATCCTGGATAGTGCCTTCCT178
q	lyproAlaProGlyValCysProProGlyLysArgTrpLeuAspCysAlaGlnGlyP 3
YG Op	1783GGGC 1816 110
λχ	
qq	::: ::: 3103 ysTyrCysProSerGlyMetLeuLeuLeuAsnAsnAlaCysValProThrGlnAspCysP 3123
۵y	1844 ACTGCCTATATGGTGTCTGCCGCACGCCTGGGTCTGGGTCGCC 1885
QD	3123 roCysThrHisGlyGlyArgLeuHisProProGlySerAlaValLeuArgProCysGluA 3143
۵y	1886 ATTTACTTTGCTACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 1942
qq	:: ::
ργ	1943 TAGAAAACTTCCAGCACATTGG1964
q	::: 3162 yGlnProThrTrpSerProTrpThrProTrpSerGluCysSerAlaSerCysGlyProAl 3182
οy	1965GGTGGAGGGCCTGCTCACTGG 1987
qa	3182 aArgArgHisLysHisArgPheCysThrArgProProGlyGlyAlaProSerSerMetal 3202
οy	1988 TCCCAGCTCCCGCTCCTGTTAGCCCCCATGGGGCTGCCGGGCTGGCCGCCAGTTfCTGTT 2047
qq	3202 aproProLeuLeuSerSer
Οy	2048 GCTGCCAAAGTAATGTGGCTCT
Db	3210 -ValproproLeuCysproGlyProGluAlaGluGluGluProCysLeuLeuProGluCy 3229
Οy	2084 IGCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCCTCTCTCCCCA 2143
QQ	3229 sAsp 3236
٥y	2144 GTCTCTAGGGCTGCCTGCACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGG 2203
qq	3237ProTrpGlyProTrpSerSerCysSe 3245
٥y	2204 GAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGACTCTGCAGGTGGATTACCCAG 2260
Db	3245 rArgSerCysGlyGlyGlyLeuArgSerAr 3255
Qy	2261 GCTCAGGGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGA
qq	3255 gSerArgAlaCysAspGlnProProProGlnGlyLeuGlyAspTyrCy 3271
Oy	2304 -GAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTT 2362
ρp	3271 sGluGly
٥y	2363 AACCIGCAGCITCGTITAAIGIAGCICTIGCAIGGGAGITICIAGGAIGAAACA 2416
QQ	3279 aAlaCysGlnAlaLeuProCysProValThrAsnCysThrAlaileGluGlyAlaGluTy 3299
Qy	2417 CTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGAAGAGTCCTGAGGGCCAACA 2476

qq	3299	: ::: rSerAlaCysGly3	303
Qy	2477	CTCAGCCCACAG	517
QQ	3304	o-CysproArgSerCysAspAspLeuValHisCysValTrpH 3	319
Qy	2518	CACCCCCCTTACCTTTATCAGGATGTGGCTGTTGG 2.	9
Db	3319	ProGlyGlnValLeuSerAlaAspGlyThrValH 3	339
Qy	2564	TT	6
QQ	3339	uArgHisArgProG 3	359
Qy	2593	TAACTTATTTATTAACAAGTAGA 2	
Db	3359	TyrCysThrCysSerG 3	375
QY	2630	GGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGTGG 2	683
Db	3375	LeuThrCysThrAspLeuProCysPro-ValProGlyAlaTrpCysProTrp 3	394
Qy	2683	2	683
qq	3395	SerGluTrpThrAlaCysSerGlnProCysGlnGlyGlnThrArgThrArgSerArgAla 3	414
Οy	2684	ATCAGGTCCCCTGAGATAGC 2	716
qq	3415	HisGlyGlyAlaProCysProGlyGluAla 3	431
Qy	2717	TGATCATIGCAGAATCTTCTTCT 2	752
Dp	3432	 AlaGlyAlaGlnHisGlnArgGluThrCysAlaSerThrProGluCysProVal 3	451
Qy	2753	STCTGGCCCCCCAAAATGCCTAA	812
qq	3452	AlaTrpSerProTrpGlyProT	462
Qy	2813	ATTCCAAATGCTGTTACCCAAGGTTAGGGTGT	872
qa	3463	roCysGluValCysLeuGly	471
Qy	2873	AACCACCCTCTTCTTGGCCCAGCCTGGTT	932
qq	3471	srArgGluCysProp	481
Oy	2933	CCTCTACTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAA	992
Db	3481		486
Qy	2993	CCTACCCCAACTTTCCCCTACCCCAACTTTCCCCACCAGCTCCACAAACTT	1052
Dp	3487	roCysProGlyGlyHisArgGlnSerArg	1498
QY	3053	AGCTACTGCAG	083
Db	3499	CysGlnGlyAsnSerThrGlnCysThrAspCysAlaGlyGlyGlnAspLeuLe 3	516
ζŎ,	3084	GGTTTCCCAAGCCTTTGTCCATCTCAGC	1128
Db	3516	roCysGlyGlnProCysProArgSerCysGluAspLeuSerProGlyValGl	536
Qy	3129	GCTTGGGGAATCTCACACAGAAACTCAGGAGCACCCCCTGCCTG	1181
Db	3536	erMetGlyCysGlnGlnProArgC	551
oy 4	3182	AGGTCTTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT	1241
a :	, ,	Your Board Annual Post 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
Š	3242	Access 3248	

Qy 774 ATGCCTTCATGATCAGTCTTGGGGGCTGG	Db 2776LeuargSerArgSerArgLeuCysP. Qy 960 CCGAGCCAGCAGAAGGGCTGTCGCCCCCCCCCCCCCCCC	Oy 1080 GCATGCCCGCACCCTGCGCCGGC 11111	Qy 1224 GGAGACACTATGATGAAGGCGTTCGGATC 11111 :::::: Db 2867 G148PMetValPheATGSETA1GG1uG1 Qy 1284 TCTCCCTGGTCTTCTCTCTGGTCATGGAC Db 2884 - CysProG1yLeuCysLeuAlaArgG1y1 Qy 1317 TGGTGCAGCGATTG Db 2903 aG1yCysAlaCysProThrG1yLeuPhel Qy 1356 GTGTGGCAGCTTTCCCTGTATTG Qy 1356 GTGTGGCAGCTTTCCCTGT	1375 2940 gLeuAspserCy 1394 CTGTCCCACAGT 2960 oCysProValAl 1454 GCCTGCAG 1484 TCCCTCTACCAC 2994 oProAlaAlaPh 1544 GCTAGCAGTGAG 1544 GCTAGCAGTGAG 3012 eCysSerLeuAr
RP SEQUENCE FROM N.A. RA Meiniel A.; RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. RN [2] RN SUBMITTED (OCT-2001) to the EMBL/GenBank/DDBJ databases. RN [2] RN FEDENCE-SUBCOMMISSURAL ORGAN; RX MEDLINE-20465125; PubMed-11008217; RA GODTON S.; RA GODTON S.; RY SUBCOMMISSURAL ORGAN; RY SCO-spondin, a glycoprotein with potent activity on neurite outgrowth."; RI Glia 32:177-191(2000). RE EMBL; A416457; CAC94914.1; SO SEQUENCE 5146 AA; 543576 MW; 724C5FB8727E13DA CRC64;	Alignment Scores: 5.76e-14 Length: 5146 Pred. No.: 5.76e-14 Length: 5146 Score: 308 Score: 29.12\$ Conservative: 79 Best Local Similarity: 23.18\$ Mismatches: 379 Query Match: 6.37\$ Indels: 564 DB: 6.759-143-110 (1-3410) x Q8SPM4 (1-5146)	Qy 120 GAAGCTGGACCGACCAAAGGGCTGCAGAAATGGGCGCCTGGCTGATTCCTAGGCAGT 179 Db ::	279 CCACTATGGTCCAGAGGC 2577 ProGlnGluArgalaPro 324 GGAAAGCCCAGCTCTTGC 411::: 2597 GlyArgvalHisValSer. 369 AGGTGGTTTGGCCGCAG 369 AGGTGGTTGGCCCCAG 429 AGGAGAAGTTCATGACCA 429 AGGAGAAGTTCATGACCA	0y GCTCCTAGGCTCACCACTGGCGTGACCCTATGGCGCGCGC

oy S	774	ATGCCTTCATGATCAGTCTTGGGGGTGCCTGGGCTACCTCC 815
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op Op	2743	Unconcoccarioaciaeacacacasiaece
Qy	873	AGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTAGCGTAGCAGCCACACTGCTGG 932
QQ	2762	AlacysSerGinSerCysLeuValProGlyGlyGlyProAla 2775
QY	933	TGGCTGAGGAGGCAGCGCTGGGCCCCA
qq	2776	SerArgSer
Qy	096	
Db	2795	AlaThrGluGluGluProCysSerProProValCysLeuGlyLeuGlyVal 2811
Qy	1020	
Db	2812	TrpGlyGlnTrpAla
Qy	1080	GCATGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCT 1127
Db	2820	AlaCysSeralaProCysAsnGlyGlyValGlnThrArgGlyArgArgCysSerAlaSer 2839
Qy	1128	GGATGGCACTCATGACCTTCACGTGTTTACACGG 1163
Db	2840	AlaProGlyAspProGlyCysGlnGlyProHisSerGlnThrArgAspCysAsnThr 2858
Oy	1164	ATTTCGTGGCCGAGGGCTGTACCAGGGCGTCCCCAGAGCTGAGCCGGGCACCGAGGCCC 1223
QQ	2859	
Qy	1224	AGCCT
QQ .	2867	GlydspWetValPheArgSerAlaGluGlnCysArgTrpGluGlyGlyPro 2883
Oy	1284	1 - 46 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -
QQ	2884	3lyValGluCysThrGlyValCysThrA
QY	1317	TGGTGCAGCGGGCCA 1355
. qa	2903	ysProThrGl
Qy.	1356	GTGTGGCAGCTTTCCCCTGT1374
qq	2923	nCysProCysGlnLeuArgGlyGlnLeuTyrAlaProGlyAlaValAlaAr 2940
Qy	1375	
qq	2940	gLeuAspSerCysSerAsnCysThrCysIleSerGlyGluMetValCysAlaSerGluPr 2960
Oy	1394	CTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACGGGTTCACCTTCTCA 1453
Dp ·	2960	ocysprovalAlaCysGlyTrpSerproTrpThrProTrpSe 2974
Qy	1454	CACTG
Db	2974	Ś
Qy	1484	
QQ	2994	OProklaklaPheGlyGlyklaklaClySGlnGlyProksnMetGluklaGluph 3012
Qy	1544	GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
QQ	3012	eCysSerLeuArgProCysGlyGlyProAlaGly3023

4		Db 1216	ProGlyLeuProGlySerLys
3 ,	Lear 1 Lyadi	Qy 2343 TTCCCATCTAAGCCC	TTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGG
ογ	GCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCTACA	Db 1227 PheGlnGlyPheProGlyMet-Pro-	::: yMet-Pro
qq	944 yGlu 945	Qy 2403 TCTAGGATGAAACACTC	TCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGACTTA
ΟŊ	1476 CACTGGCCTCCCTCACCACG1497	1235	
οp	946 -ProGlyLeuProGlyProProGlyProMetHisProAspPheLeuGlySerLysGlyGl 965	2463	COACACCAACAACAACAACAACAACAACAACAACAACAAC
Qy	1498GGAGAGGTGTTCCTGCC	1246	
QΩ	965 uLysGlyGluProGlyLeuProGlyIleProGlyLeuSerGlyProLysGlyTyrGlnGl 985	2523	TO CACCCCTTTTA ACCTTTTA ACCATTTC COLOR
Qy	1521 AATACCGAGGGACACTGGAGTGCTAGCAGTGAGGACAGCCTGATGACCAGCT 1574	1260	
qq .	985 yLeuPro-GlyAspProGlyGlnProGlyLeuSerGlyGln998	2583	САСАСАСАСАРИТТААНТИТААСТТАТТАТТАТТААСТС
ογ	1575 TCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGTGCTGGAGGCA 1634	0 0	
Db	999ProGlySerProGlyLeuProGlyProLysGlyAsnProGly 1012	1260	
οy	CCTCCACCGGCGCTCTGCGGGGCCTCTGCCTGTGATGTCT	2043	CIAGCITITCIGIGITGICIAAIATTTGGGGTAGGGTGGGGGG
QQ	1013LeuProGlyProProGlyLeuThrGlyProProGlyProLysGlyAsnIleG 1030	1921	GLYArgProciyE
ò	1695 GTGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGG 1754	2703	TCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTT
qq	1030 lvAspMetGlyPheProGlyProGlnGlyValAspGlyProProGlyProProGl 1048	Db 1270 yPro	
		Qy 2763 GGCCCCCCAAAATGCCT	GGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCA
i á		Db 1272ProGlyThrGluGlyProArgGly	lyProArgGly
3 8		QY 2823 CAAATGCTGTTACCCAA	CAAATGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGG
ò 6		Db 1284	9
a	yotukiootiyvaisetoiyleenkiootiyleenkio	QY 2883 CAACGGCTTCCCTAACC	CAACGGCTTCCCTAACCACCCCTCTTCTCTTGGCCCAGCCTGGT
Š í	TGTCTGCCGCAGGCCTGGGTCGCCCATTTACTTTGCTACACAGGTAGTTTGACA 191	Db 1289 uArgGlyAsnPro	GlyProProGlyG
QQ O	yProLysGlyGluProGlyLeuProGlyTyrProGlyAsn	Qy 2941	
δλ	AGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGGCCT :::	1303	yLeuLysGlyAspGlnGlyProProGlyLeuProGlyAsnProG
Q	1094ProGlyIleLysGlySerValGlyGluThrGlyLe 1105	Qy 2971ATGAAGGCACTGC	ATGAAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTC
ΟŊ	1977 GCCTCACTGGGTCCCAGCTCCCGCTCTGTTAGCCCCATGGGGGCTGCCGGGCTGGCCGC 2036	1323 nG	
QQ	1105 uProGlyLeu-ProGlyAsnProGlyAlaLysGlyGlnProGlyLeuProGlyPheProG 1125	2013	
ογ	AAGTAATGTGGCTCTCTGCTG		
qq	1125 lyThrProGly-LeuProGlyProLysGlyMetAsnGlyProProGlyAsnProGlyPhe 1144	7 L	d trongporteriors to the control of
Qy	2085 GCTGCTGAGGTGCGTAGCTGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCT	3055	GCIACTGCAGGACCACAAAGIGCGGII 308
qq		1363	lyProSerGlyGlnSerlleVal 137
δλ	2145 TCTCTAGGGCTGCCTGAC 2162	21	
r qa	vGlnAspGlvIleProGlyProAlaGlyGlnLysGlyGluPro	SPM4 PRELIMINARY; SPM4;	PRT; 5146 AA.
δ	TGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCAT	DT 01-JUN-2002 (TrEMBLrel. 21, DT 01-JUN-2002 (TrEMBLrel. 21,	, Created) , Last sequence update)
qa		DT 01-JUN-2002 (TrEMBLrel. 21 DE SCO-spondin.	, Last annotation update)
٥y	2223 GCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCT 2282	O-SPOND s tauru	
qa		Eukaryota Mammalia; Bovidae:	; Metazoa; Chordata; Cranlata; Vertebrata; E Butheria; Cetartiodactyla; Ruminantia; Peco Bovinae, Ros
Qy	2283 CCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCAG	OC BOVIDAE; BOS. OX NCBI_TaxID=9913; RN [1]	

AGAAGGGAATCCATTG 2642 1260 ATCCCCAACAATCAGG 2702 TCCCCCACTTCCA-- 2940 ||| ||||||||| |nProGlyLeuProGl 1303 CTAGGACTGGGCTG-- 2970 ||| |||||||| |1yArgProGlyLeuAs 1323 TGTTTGGA----- 3054 || || ||| |euThrGlyProProGl 1363 ---GlyGluProGly 1226 STCTTGCATGGGAGTT 2402 FTTGTAGGGGAAGAGT 2462 |||::: |----ProGlyGlnAl 1246 ||| | roProGlyPheGlnGl 1270 PCTTCTCCTGGGGTCT 2762 1271 STGGGGCTTCAGGTCT 2882 |||||| |yGlyIleLysGlyGl 1289 CC----- 3012 ACTGTCTTTTGCTGA 2522 TTCTGTTGCCATCACA 2582 1234 uteleostomi; ra; Bovoidea;

qa	489 SerGlyValLeuAlaIleValLeuLeuProLysProSerLysAspAlaAlaSerLysLeu 508	Qy	447 TGGTG
ογ	1682 GATGTCTCC 1690	qq	
qq	::: 509 SerLeuSer 511	δλ	495 TAGGCTCAGCCAGTGAC
RESULT	7 20	QQ	651 oLys
ID	PRECIMINARY; PRT; 1691 AA.	δy	555 CACTGTCCTTGGGCATC
	JESQ2; 11-WAR-2001 (TrEMBLrel. 16, Created)	qa	653GlyAspP
	OI-WAK-2001 (TrEMBLE). 15, Last sequence update) 01-JON-2002 (TrEMBLE). 21, Last annotation update)	Qy	615 GGCTGCTGTGCCGGAT
	Type IV collagen alpha o chain. COL4AS.	qu	664 sProGlyLeuProGlyS
	Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Jammalia: Enthoria: Endontia: Edinomathi: Muridae, Muridae, Musica	Qy	667CGTGGGGCTGCTG
	neria; rodentia; 090;	qq	684 yLeuProGlyGlnProG
	SEQUENCE FROM N.A. SEDITARE-20536494 DIMMON-1065041.	Qy	723 TCTCTGACCTCTTCCGG
	January Natio I., Seki T., Obbashi T., Kimura E., Momota R.,	qa	702 yileProGlyileGlyP
	Atshiro I., Sado I., Toshioka H., Niholliya I.; Vifferential Expression of Mouse a5(IV) and a6(IV) Collagen Genes in	Qy	771 TCTATGCCTTCATGATC
	Spiriteliai basement Membranes.;; T. Blochem. 128:427.434(2000).	qa	722
	SMBL; AB041350; BAB13673.1; 4GD; MGI:86455; Col4a5	QY	831 GGGACACCAGTGCCCTG
	InterPro; IPR00087; Collagen. InterPro; IPR001442; ProcollagnC4.	අු	: 733 tGlyProAspGlyProP
	Pfam; PF01413; C4; 2. Pfam; PF01391; Collagen; 24.	QY	871 -GGAGTGCCTCTTTGGC
DR.	ProDom; PD000007; Collagen; 3. ProDom; PD03923; ProcollagnC4; 1.	qa	::: 753 eGlyLeuProGlyProP
	SMAKT; SMUUIII; C4; Z. COOllagen 1601 AA. 161922 MW. 9124AART7022ABRA CREA.	δλ	930 TGGTGGCTGAGGAGGCA
700	1031 AA; 101023 MW;	qa	773 oLysGlyAspArgGlyP
Pred.	ent Scores: 4.14e-14 Length:	Qy	990 CCTTGTCGCCCCACTGC
. Perce	t Similarity: 28.91% Conservative:	qa	786 oGlyArgThrGlyLeuA
Best Ouery	BEST LOCAL SIMILATITY: 24.08 MISHATCHES: 309 QUETY MATCh: 5.388 Indels: 440	Qy	1050 TGCTTCCCCGGCTGCAC
. ga	. daps.	qa	806 nProGlyProValGlyP
20 ((QY	1098 GCCGCCTCTTCGTGGCT
δ	CCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGTTCCTAGGCAGTTGGCGGCAG 18	අ _ධ	 826 oProGlyThrProGlyP
g (FrogryFroProGryAlaProGryPheFroGrySeFrySGryAsp	Qy	1156
à à		qa	842 oGlyGluLysGlyAspP
a :	54/ FIGGLYASDVALLEUTHILDGLYMGTLYSGLYASDLYSGLYGLUDEUGLYFHEFIG 300	Qy	1170 TGGCGAGGGGCTGTAC
3 6	GlvalabroglvLenbroglvLenbroglvLenbroglvLe	qa	SerProGly
5 8	-CCacacacacacacacacacacacacacacacacacaca	δλ	1230 ACTATGATGAAGGCGTT
Z QO	uproGlyProLysGlyGlyGlyGlyIleThrPheLysGlyGlyBroProGl	QO	878GLYS
ò	PACECORPUTED TO TREADED TO A STATE TO A STATE OF THE STAT	QY	1275 AGTGCGCCATCTCCCTG
g qq		qa	yvalLysGlyGluMe
δλ	387 GCATCACCTATGTGCCGCCTCTGCTGGAAGTGGGGGTAGAGGAGGAAGTTCATGACCA 446	Oy	
. a	::: ::: :::	qa	
		l oy	1365 CTTTCCCTGTGGCTGCC

λ	447		494
3 8	ר ס	TECOLIDATE VALIDACION CONTROL) LC
7 A	n n		
λλ	555	STCCTTGGGCATCCTGCTGAGCCTCTTTCTCATC	614
qo	653	GlyAspProGlyGlnThrIleThrGlnProGlyLy	664
ρy	615	CTCATCCTGGG	9
qq	664	Д	684
ογ	299	CGTGGGGCTGCTGCGACTCTGTGGCCAGTGCTTCACTCCACTGGAGGCCCTGC	722
qq	684	- 124	702
Qy	723	TCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCCTACTCTG	170
qq	702	ylleProGlyIleGlyProProGlyProProGlyProLysGlyPheProGlyIlePro	721
٥y	771	TCTATGCCTTCATGATCAGGTCTTGGGGGGCTGCCTGCCT	830
qq	722		733
Οy	831	GGGACACCAGTGCCCCTACCTGGGCACCCAGGA	870
qq	733	tellyProAspGlyProProGlyProGlyProGlyPheProGlyProLysGlyGluProGlyPh	753
Qy	871	-GGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGC	929
qq	753	eGlyLeuProGlyProProGlyPheProGlyPheProGlyPhreProGlyPr	773
٥y	930	TGGTGGCTGAGGGAGGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTCGGCCCCCT	686
QQ	773	oLysGlyAspArgGlyPheProGlyProSerGlyProPr	786
Qy	066	CCTTGTCGCCCCACTGCTGTCCATGCCGGCCCGCTTGGCTTTCCGGAACCTGGCCGCCC	1049
Dp	786	oGlyArgThrGlyLeuAspGlyLeuProGlyProLysGlyAspValGlyProAsnGlyGl	908
QY	1050	TGCTTCCCGGCTGCACCTGTGCTGCCGCATGCCCGCACCCTGC	1097
Db	806	nProGlyProValGlyProProGlyLeuProGlyLleGlyLeuGlnGlyProProGlyPr	826
ΟŽ	6	GCCGGCTCTTCGTGGCTGAGCTGTGCAGCAGCACGCATGACCTTCAGGCCTGTTC	1155
QQ	Ō	ProGlyThrProGlyProIleGl	N .
Qy	1156	TTACACGGATTCG	-
QQ O	842	$\tt oGlyGluLysGlyAspProGlyProProGlyPheAspValProGlyLeuProGlyGluArights and the proglyGluArights and the programmer of the$	162
οy	7	o .	1229
qq	862	gGlySerProGlyLeuProGlyAlaProGlyLeuIleGlyProPro-	877
QY	1230	TGATGAAGGCGTTCGGATGGGCAGCCTGGC	1274
. qq	878	GlySerProGlyValProGlyLysAlaGlyValProGlyP	893
ΟY	1275	GTCTTCTCTGGTCATGGACCGGCTGGT	1320
QQ	893	alLysGlyGluMetGlyMetMetG	913
QY	1321		1364
Dp	913	oGlyArgSerGlyAlaProGlyLeuLysGlyAspAspGlyMetGlnGlyGlnProGly	932
ΛO	1365	CTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGG	1415

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264
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                                                                                             808 rSerArgThrGlyGlnArgThrArgGlnArgProGlyHisProProProGluArgGlySe 828
  ---HisProProProGluArgGlySerGlyProArgGlyThrArgProPro-AlaProSe 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     392 ACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAAGTTCATGACCATGGTG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGGCCAGTGAC 511
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                                              100 TGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCATCATCATCATCGTGGCCGAGGGGC 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sucrose transporter protein.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
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Budous carota (Carrot).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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Pfam; PF00083; sugar_tr; 1.
TIGRFAMs; TIGR01301; GPH_sucrose; 1.
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174 GlyAspThrArgArgMetArgSerAlaAsnAlaPheTyrSerPhePheMetAlaValGly 193
                                                                                                                                                                                                                                           AsnIleLeuGlyTyrAlaAlaGlySerTyrAsnAsnLeuTyrLysLeuPheProPheSer 213
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                                                                                                       ---GACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGG
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1864 GGCAGACCATA 165 rgGlnArgPro- 1804 GGATGGGGCCAC 176 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	-G1y-ThrArgProProAlaProSerSerArgThrGlyGlnArg-ThrA 165 -G1y-ThrArgProProAlaProSerSerArgThrGlyGlnArg-ThrA 165 -G1y-ThrArgGCAGCAGAGCTGGAGCTGGAGCCCATAAACAG 1805	### STATEMENT OF THE PROPERTY	AACACCTGCTTCTCCGGTGGTA 1490 AAGACTGCTTCTCCCGGTGGTA 1490 B	aradacrecred erargthrelyg gaagareccaca y TCTCCGGCCTC Threlyglna Gaagreccrera gaagreccecc Threlyglna Gaagreccecc
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Db 46	2 gProbroAlaProSerSerArgThrGlyGlnArgThrArgGlnArgP 8 GGGGCCGACGCCTTCTGCTGGGTGGGTGGGCCCAGCGCTGCCTCCTCAGCCACC
47	
92	8 CAGTGTGGCTGCTACGCAGGTGAGGAGATG
88 51	9 CAGGCCAAAGAGGCACTCCTGGGTGCCCAGGT
85 53	3 GGGGCCAGGGCACTGGTGTCCCAGTCAATGGCAGCAGGAGGTAGCCCAGGCA 800 ::
79	9 GCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGGGACAGTGGTCCGGGTC 740
73	9 CCGGAAGAG 8 rgGlyserG
68	2 GTCCAGCAGCCCCAGGCCCAGGATGAGCAGGTGCCAGCTCCAGGGGCCTGGGATCCGGGCA 623 ::
622	CAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCCAA 563
Oy 562 Db 624	2 GGACAGTGCCCAGATGAAGGGCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGC 503
502	2 TGAGCCTAGGAGCGGGACACAGGCCCAGCACTGGACCAATGCCCAGCACCATGGT 443
44	42 CATGAACT
434	TCTCCTCTACCCCCACTTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGC
382	82 GGCCAAACACCTCCAGGCCAAAGGTTAGCAGGTTGACCA
Oy 341 Db 713	.1GCAAGAGCTGGGCTTTCCGGTGCCGCAGGCGGCTCACCCACAGCCTCTG 290 :::
Qy 28 Db 73	9 GACCATAGTGGGCCAGGGGGTAGGGCTCAGGGGGCCGTTCAGGC 245
24. Db 75.	4
Qy 208 Db 770	08 GCTGCGGCCTCTCCTCCTTGCTGCGCCAACTGCCTAGGAATCAGCCAGGC 158
. 15	7 GCCCATTCTGCCAGCCCTTTGGTGCCGGTCCAGCTTCTCAGCCCAT

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1627
1529 GGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCT 1588
                                                                                                                                     -----CCTCCACCCGCGCTCTGCGGGGCCTCT 1675
                       487 AlaIleSerGlyValLeuAlaIleValLeuLeuProLysProSerLysAspAlaAlaSer 506
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rivailler P., Jiang H., Cho Y.-G., Quink C., Wang F., "Complete Nucleotide Sequence of the Rhesus Lymphocryptovirus: Genetic Validation for an Epstein-Barr Virus Animal Model."; J. Virol. 76:421-426(2002).
                                                                   ----GCTCCCTTCCCTAATGGACACGTGGGTGCT
                                                                                                   467 PheAspSerLeuPheGlyGlyGlyAsnLeuProAlaPheValValGlyAlaIleSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rao P., Jiang H., Wang F., "Control of the rhesus lymphocryptovirus viral capsid antigen and Epstein-Barr virus-encoded small RNA homologues and use in diagnosis of acute and persistent infections."; J. Clin. Microbiol. 38:3219-3225(2000).
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MEDLINE=99412410; PubMed=10482645;

Rivailler P., Quink C., Wang F.;

"Strong selective pressure for evolution of an Epstein-Barr virus

LMP2B homologue in the rhesus lymphocryptovirus.";

J. Virol. 73:8867-8872(1999).
                                                                                                                                                                                                                                                                                                                                                                                                               cercopithicine herpesvirus 15.
Yıruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammahherpesvirinae; Lymphocryptovirus.
NCBI_TaxID=104228;
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                                                                                                                                                                                                                                                                                                           890 AA.
                                                                                                                                     1628 GGAGGCAGTGGCCTGCTCCCA----
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MEDLINE=20440633; PubMed=10970361;
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MEDLINE-20304984; PubMed-10846073;
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                                                                  1589 AAGCCTGGA-----
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Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               Rivailler P., Jiang H., Cho Y.-G., Quink C., Wang F.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY037858; AAK054470.1; - 149077C89D3B5574 CRC64; SEQUENCE 890 AA, 95097 WW.
                                                                                           Wang F.;
the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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                392 ACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTG 451
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                                                              467 PheAspSerLeuPheGlyGlyGlyAsnLeuProAlaPheValValGlyAlaIleSerAla
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34 LysLeuValLeuValAlaAlaIleAlaAlaGlyValGlnPheGlyTrpAlaLeuGlnLeu
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                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
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TIGREAMS; TIGR01301; GPH_sucrose; 1
SEOUENCE 515 AA; 54425 MW; 9580978C726523DC CRC64;
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131
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EMBL; AJ303199; CAC19689.1; -...
InterPro; IPR003662; sub_transporter.
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294 CysLeuAsnTrpIleAlaTrpPheProPheIleLeuPheAspThrAspTrpMetGlyArg 313
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131 GlyAspAspWetSerLysThrLeuLysProArgAlaValThrValPheValIleGlyPhe 150
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151 TrplieLeuAspValAlaAsnAsnMetLeuGlnGlyProCysArqAlaLeuLeuAlaAsp 170
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1118 CTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAG 1177
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94 HisCysGlnSerSerPheGlyArgArgArgProPheIleAlaSerGlyAlaGlyCysVal 113
                                                                                                                                             131 GlyAspAspMetSerLysThrLeuLysProArgAlaValThrValPheValIleGlyPhe 150
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     425 ThrArgIleGluSerLeuGlyLeuGlyGlnGlyLeuSerMetGlyValLeuAsnLeuAla 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 -----ProArgAlaLeuIleGlyGluProValArg---ProArgValProLeuArgArg 29
                                                                                                                               vitis Vinifera (Grape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisAlaTrpSerSerIleIleTrpLeuCysGlyProLeuSerGlyLeuLeuValGlnPro
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|LeuValGlyHisLeuSerAspArgCysAsnSerArgPheGlyArgArgArgProPheIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 GAGAAGTICATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 ACGGCCCCCTGAGCCCTACCCGCCTGCCCCACTATGGTCCAGAGGCTGTGGGTGAGCCGC
                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=SHIRAZ; TISSUE=FRUIT;
Davies C., Wolf T., Robinson S.P.;
"Three putative sucrose transporters are differentially expressed in
                                                                                                                                                                                                                                                         grapevine tissues.";
Plant Sci. 147:93-100(1999).
--- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
EMBL; AF021808; ARF08329.1;
InterPro; IPR003662; Sub_transporter.
Pfam; PF00083; Sugar_tr; 1.
TIGRFAMS; TIGR01301; GPH_SUCrose; 1.
                                                                                                                                                                                                                                                                                                                                                         501 AA; 53938 MW; 4D0D4DE2EF2F4BA8 CRC64;
                                                         09-SOK6;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
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Indels:
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                                                 PRT;
                                                                                                            Putative sucrose transporter.
                                                                                                                                                                                                                                                                                                                                                                                             2.17e-14
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40.628
26.758
5.438
                                                PRELIMINARY;
alArg 748
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                                                                                                                                                                                   NCBI_TaxID=29760;
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Best Local Similari
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DB:
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1190 GGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGG 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GlyPheTrpLeuLeuAspValAlaAsnAsnValThrGlnGlyProCysArgAlaLeuLeu 161
                                                                                                                                                       |||:::::::|||
| 181 LeuPheIleAlaValGlyAsnValLeuGlyPheAlaThrGlySerTyrSerGlyTrpPhe 200
                                                                                                                                                                                                                                                                                                                                                 ---ATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTC 880
                                                                                                                                                                                                                                                                                                                                                                                                       -----TITGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTG 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               929 CTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCC 988
GGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTC 724
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                                                                                                                                                                                                                                383 LysHisMetAsp-----
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CTGCGGCAGACACCATATAGGCAGTGACAGCTGGACTGGACAATGGAGCCCATAA 1809 :::			### CCGAAGGCCTTCAGGCCTCGGCCTCGGCTCAGGCAGCC 1191 GlyalaArgGlyalaProGlyProGln
1868 CTGCGGCAGACACATATAGGCAGTGACAGACTGGCTG :::	1730CCACCCTGGCCTCGC 240 LeuProGlyThr-AlaGlyLeuPr 1690GGAGACATCACAGG 259 pGlyAlaLySGlyAspThrGlyPr 1647	1625 CACCCACGTGTCCATTAGGG 299 1yProSerG1yProAlaG1yAlaA 1577 GGAAGCTGGTCATCAGGCTGTCCT 317	1250 TCCGAACGCCTTCATCATAGTCTCCCGGGCCTCGGTGCC 1398 GlyAlaArgGlyAlaProClyProGln 1190 CCTGGTACAGCCCTCCCCCACGAATCCGTGTAAACAG 1111
99 99 99 99	64 64 65 65 65	60 60 60 60 60 60 60 60 60 60 60 60 60 6	

qa	461(
Οy	899 TGA	CAGGCCAAAGAGGCACTCCTCCTGGGTGCCCAG
QQ	469	::: AlaGlyGluArgGlyAlaProGlySerArgGlyPheProGlyAlaAspGly 485
yo da	854 AGGG	GGG
	6	CAGCCCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGCGACAGT 75
	04	:: SerGlyArgProGlyGluPro 51
	749 GGT	11111
Dp	1 y	roGlyProAspG
,	731 GGT	CAGTGGAGTGAAGCACACCTG
	538 Thr	
	71 CCA	
qq	558 Ala <i>l</i>	rgGlyGlnSerGlyValMetGlyPheProGlyProLysGlyAlaAl
	35 TGG	GGGACAGCAGCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAGAGGCTCA 57
an	5/5 GIY	LuProG1yLysProG1yGLuArgG1
	575 GCA(TGCCCAGATGAAGGGCCGGCGGCGGCCATAGC
qa	- a	lyProF
Qy	₽	ACTGGCTGAGCCTAGGAGCGGGACACAGACCAGGCCCACTGGACC
qa	293	yAla
Qy ,		CACCATGGTCATGAACTTCTCCTCTACCCCCCACTTCCAGCAGCAGAG
qa	909	
οy	395 AGG:	CAAACACACCTCCAGGCCAAAGGTTAGCAGGTTGAC
qa	616 Arg	
Qy		TTGGGCTTTTCCGGTGCCGCAGCAGGGGGTT
qq	636 Ala	 YLysProGlyGluGlnGlyAlaProGlyAspVal
 Vo	281 TGGG	CAGGCGGGTAGGGCTCAGGGGCCGTTCAGGCACTCCAGAACTGCTTCGTC
qq	655 rGly	rid ProAlaGlySerArgGlyGluArgGlyPheProGlyC
Qy .	224 CGG	GCTCCAGAAGCTGCGGCCTCTCCTTGCTGCCGCCAACTGCCTAGGA
QQ	673 eGl	 ProGlnGlyProArgGlyAlaAsnGlyAlaProGlyAsn
	164 G	CCAGGCGCCCATTTCTGCCAGCCCTTTGTGC
Op qu	691 pGly	GluAlaGlyAlaProGlyAlaProGlyGlyGlnG
ογ	128 TCC	AGCTTCT CAGCCCATGCTCAACACCTGCTGTGGGGGCACCTCAGTGGGGACA 72
qq	- C	SerGlyLeuGlnGlyMet-ProGlyGluArgGlyAlaGlyGlyLeuProG
Qy	71 CGT(CTCATCACTCAGATCCTGGCCGAGGCGCGGCGGCTGTCACCCGGAGCCAGCGGT 15
qa	727 ysG]	GlyAlaA
Qy	14 GCAC	GG 10

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812
670 eProGlyGluArgGlyValGlnGlyProProGlyProAlaGlyProArgGlyAsnAsnGl 690
                                                                                                                                                        708 ySerGlnGlyAlaProGlyLeuGlnGlyMetProGlyGluArgGlyAlaAlaGlyLeuPr 728
                                                                                                                                                                                                                                                                     504 GCTGAGCCTAGGAGCGGGACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCATG 445
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                                                                                                                                                                                          564 AAGGACAGTGCCCAGATGAAGGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTG
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                                        ----GCTCCAGGGCCTGGGATCCGGG
                                                                           590 yAlaProGlyAsnAspGlyAlaLysGlyAspThrGlyAlaProGlyAla-----ProGl
                                                                                                                 624 CACAGCAGCCCTGCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGGCTCAGCAGGATGCCC
                                                                                                                                                                                                                                 oGly-----ProLysGlyAspArgGlyAspAlaGlyProLysGlyAlaAspGly----
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                                                                                                                                                                                                                                                                                                            ----SerProGlyLysAspGlyValArgGlyLeu--
                                                                                                                                                                                                                                                                                                                                                                                                                                -----CCAGGCCAAAGG--
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1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 21, Last annotation update)
Alpha 1 type I collagen.
Alpha 1 type I collagen.
Bukaryota; Metazoa (Bull frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annra; Neobatrachia; Ranoidea; Ranidae; Rana.
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2528 GGTGGATCAGCAAAAAGACAGTGCTGTGGGCTGAGGGGACCTGGTTCTTGTGTGTTGCCC 2469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2108 TGTGCAGCTACGCACCTCAGCAGCACAGGGTGGCAGCAGAGAGCCACATTACTTTGGCAG 2049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2168 CCTCCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGAGGGACGCCCCAGCCCCCAGC 2109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 ----GlnProGlyIlePro-------GlyProProGlyProProGl 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 y-------ProalaGlyLeuGlyGlyAsn-------PheAlaPr 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 oGlnMetSerTyrGlyTyrAspGluLysSerAlaGlyIleSerMetProGlyProMetGl 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ProGly--ProGln---Gly 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 pGluGlyThrIleLeuCysAspGluValIleCysGluAsp---IleGlyAspCysProAs 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 nProGluIleProMetGlyGluCys------CysProValCysGlyGluGlyGl 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 ---AspValTrpLysProGluAlaCysGlnIle------CysVal-CysAs 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 nTyrGlnThrGlySer---valvalGluGlyProLySGlyGluThr----
                                                                                                                                                                                                                                                        F59BB550C9873F04 CRC64;
                                                                                                                                                                                                                                                                                                              1445
256
51
307
353
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Mismatches:
Indels:
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Matches:
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Matrix Biol. 18:89-103(1999).

EMBL; AB015440; BAA29028.1; -
InterPro; IPR000087; Collagen.
InterPro; IPR001007; VWF_C.
Pfam; PF01410; CoLFI; 1.
Pfam; PF01419; CoLFI; 1.
ProDom; PD000007; Collagen; 3.
ProDom; PD000078; Fib_collagen; 3.
ProDom; PD000078; Fib_collagen_C; 1.
SMATT; SM00314; VWC; 1.
                                                                                                                                                                                                                                      Collagen.
SEQUENCE 1445 AA; 137252 MW;
                                                                                                                                                                                                                                                                                                                            354.50
31.75%
26.47%
5.69%
                                                                                                                                                                                                                   PROSITE; PS01208; VWFC; 1.
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                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                              Alignment Scores:
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alGluG
TCTIGIGIGITGCCCCTCAGGACTCTTCCCCTACAAATAAGTCATATGTTCAAATCCCAT 2424
GGAGGAGTGTTTCATCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT 2364
TAAGGGGCTTAGAGATGGGAAACCAGCTGACTGAGTTTATTCAGCTCCCAAAAACCCT 2306
CCAGTCAGGCAGCCCTAGAGACTGGGGAGAGAGAGAGAGCGCCCCAGCCCCAGCTGT 2106
GCAGCTACGCACCTCAGCAGCACAGCGCAGCAGAGACCACATTACTTTGGCAGCAA 2046
CAGAAACTGGGGGCGGGCGGGGGGGGGGGGGGGGGGGGG
CCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCTTGTCAA 1911
ATACTACCTGTGTAGCAAAGTAAAYGGGGGAGACCAGGCCTGGGGGAGACACCATAT 1851 :::
AGGCAGTGACAGACTGGCTGAGGTGGACCATAAACAGGGATG 1800
GGGCCACCTCGGACAGCAGGACGCACTATCCAGGATGGCGAGG 1756
TCCAGGCAGATGCCCCGGCCCGGAACCACCCTGGCCTCGGTGGCCTCACCACCACCACA 1696
CGTACGGAGACATCACAGGCAGAGGCCCCGCAGAGCGCGGGGGGGGGT 1648 :::::
GGGAGCAGGCCACTGCCTCCAGCACCCACGTGTCCATTAGGGAAGGGA 1600
GCTCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCAGGCTGTCCTCACTGCTA 1546
2501 2483 104 104 107 119 2305 2305 1190 2222 2225 203 188 1987 2105 2045 2045 2045 2045 2045 2045 2045 20

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1485 GAGGCCAGTGTAGGGCAGGATCTGCAGGGCTGAGAAGGTGAACCCCGGTGAGGGCGCCT 1426
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                                                                                                                                                                                                                                                                                    1425 GAAGCTGTCACCACGCCACACTGTGGGACAGGCATGTGGCACCGGCAGCCACAGGGAAA 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1179 CCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCAC 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1059 CGGGGAAGCAGGCGCCCCAGGT-----TCCGGAAAGCCAAGCGGGGCCCGGCAT 1012
                                                                             1545 GCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCTTCTCCCGGTGGTAGAGG 1486
                                                                                                                                                                                                                                                                                                                                                                                         1365 GCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCTGCACCAGCCGGT---- 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1119 AGCTCAGCCACGAGGAGCCGGCGCGCAGGGTGCGGGCATGCGGCAGCAGCTGGTGCAGC 1060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 aGlyProLysGlySerPro----- 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 ------Glyrle---AlaGlyAlaProGlyPheProGlyAlaArgGl 405
                                                                                                                                                                                                                            405 y-------ProSerGlyPro-GlnGlyProSerGlyAlaProGlyProLysGlyT 421
                                                                                                                                                                                                                                                                                                              466 oSerGlyLeuProGlyProProGlyGluArgGlyGlyProGlySerArgGlyPheProGl 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 -----GlyGluAlaGlyArgPr 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      556 oAlaGlyProProClyAlaArgGlyGlnAlaGlyValMetGlyPheProGlyProLysGl 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591 yProProGlyAlaValGlyProAlaGlyLySAspGlyGluAlaGlyAlaGlnGlyAlaPr 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      765 TAGGCCTGCCGACAGTGGT---CCGGGTCCC-----GGAAGAGGTCAGAGAGCAGGCC 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         951 AGCGCTGCCT------CCTCAGCCACCAGC 928
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Qy	qa	oy G	a a	cy Cy	۸٥	qq	RESULT 1								RT FOI		RC STE				DR Pfe		DR SM			Alignmer Pred No	Score:	Best Loc	DB:	12-60-SD	Qy	qa	Qy	QO
1149 GTGAAGGTCATGAGTGCCATCCAGCTGCACAGCTCAGCCACGAAG 1105		1104 AGCCGGCGCAGGGTGCGGGGCATGCGGCAGCACACACGGTGGTGCAGG 1056	311 rGluGiyAlaGiyCysProAlaArgGlyAlaGiyProProAlaTrpGlyAlaGiyProPr 331	GAAGCAGGGGCGCCAGGTTCCGGAAAGCCAAGC	oArgArgAspGlyGlyAsnArgGlyAspGlyAlaProGluArgGlySerGlyLeuProGl	1020 GCCCGGCATGGACAGCAGTGGGGCGACAAGGAGGGGCCGACAGCC	TOTAL TOTAL	oGlyGlyArgGlyProGlyAlaArgGluArgAlaAlaArgProGlyValArgValProAr	941CCTCAGCCACCAGCAGTGTGGCTACGCAGGTGAGGAAGATGAGGGTG 892	Vall	891 AGCAGGCCAAAGAGGCACTCCTGGGTGCCCAGGTAGGGGGCC 847	401 tGlyGlyThrGlyThrGlyProArgSerGluGlyAlaGlyCysProAlaArgGlyAl 421	AGGCACTGGTGTCCCAGTCAATGGCAGGCAGGA	421 aGlyProProAlaTrpGlyAlaGlyProProArgArgAspGlyGlyAsnAr 438	TAGCCCAGGCAGCCCCAAGACTGATGAAGGCATAGACAGAGTAGGCTGGCGACAG	438 gGlyAspGlyAlaProGluArgGlySerGlyLeuPr 450	750 TGGTCCGGGTCCCGGGAGGAGGTCAGAGCAGGCCTCCAGTGGAGGTGAAG 700	450 oGlyProGlyCysGlySerProGlyLeuGlySerArgSerProProAlaGlyTrpGl 469	699 CACACCTGGCCACACAGCA	GlyArgGlyProGlyAlaArgGluArgAlaAla.	651 GCCAGCTCCAGGGCCTGGGATCCGGGCACAGCAGCCCTGCTAGC 607	GluProValProProGlyGlyMetGly(606 CAGCCGGCCCTTGGGATGAGAAGAGGCTCAGGAGGAGCCCAAGGACAGTGCCCAGATG 547	507ThrdlyProArgSerGluGlyAlaGlyCySProAlaArgGlyAlaGlyPr 523	546 AAGGCCCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGG 487	523 oProAlaTrpGlyAlaGlyProProArgArgAspGlyGlyAsnArgGlyAspGlyAlaPr 543	486 ACACAGACCAGGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATG 439	Gly(438 AACTICICCICIACCCCCACTICCAGCAGAGGCGGCACATAGGTGATGCCTGCGGCC 379	559 uGlySerArgSerProProAlaGlyTrpGlyGlyDroGlyGlyArg 574	378 AAACACATCCAGGCCAAAGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGC 319	AlaArgGluArgAlaAlaArgPro	318 CGCAGCAGCGCCTCACCCACACACCATAGTGGCCCAGCGGGTAGGGCTCAG 259	590 roArgProGlyGluProValProProGlyGlyMetG 602
δ	q	Qy	qq	ογ	Q C	S S	ò	g q	οy	qq	οy	qq	ολ	g	ò i	8	δλ	ф	Qy	o O	ογ	QQ	Óλ	qq	Qy	q	δ	QQ	δλ	qq	Qy	qq	οy	QQ

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2594 TGCCTGTGT-------CTCTGTGATGGC-----AACAGAAGGACCAAC 2559
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                                                                                                                       258 GGGGCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCT 199
                             ||||||
| 602 lyGlyThrGlyGlyThrGlyProArgSerGluGlyAlaGlyCysProAlaArgGlyAlaG 622
                                                                                             198 CICCTCCTTGCTGCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCT 139
                                                                                                                                                                                       ------GGTCCAGCTTCTCAGCCCATGCTCAACA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 CysProAsnProGlnLysArg---GluGly-------GluCysCysPro 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUENCE OF 1-1092 FROM N.A.
RAIN=SPRAGUE-DAWLEY; TISSUB-TOOTH;
andsten C., Lundmark C., Christersson C., Hammarstrom L., Wurtz T.;
xpression of Collagen alphal(I) mRNA variants during Tooth and Bone
rmation in the Rat.";
Dent. Res. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             llagen alphal (Fragment).
ttus norvegicus (Rat).
karyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Bl_FaxiD=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wurtz T.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 278279; CAB01633.1; -
InterPro: IPR000087; Collagen.
InterPro: IPR000885; Fib_collagen_C.
InterPro: IPR000885; Fib_collagen_C.
Ffam; PF001301; CoLFI; 1.
Pfam; PF001301; CoLFI; 1.
ProDom; PD002007; Collagen; 18.
ProDom; PD002007; Collagen; 2.
ProDom; PD002078; Fib_collagen_C; 1.
SMART; SM0038; CoLFI; 1.
PROSITE; PR00214; VWC; 1.
                                                                                                                                                                                                                     |||||||
| 640 spGlyAlaProGluArgGlySerGlyLeuProGlyProGly-----
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283
50
362
352
59
                                                                                                                                                                                                                                                                                                             NOV-1996 (TrEMBLrel. 01, Created)
JUN-1998 (TrEMBLrel. 06, Last sequence update)
JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                  102 CCTGCTGCTGTGGGGCACCTCAGTGGGGACACGTCTCA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUENCE FROM N.A.
RAIN=SPRAGUE-DAWLEY; TISSUE=TOOTH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_TER 1 1
QUENCE 1453 AA; 137887 MW;
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357.00
31.84%
27.06%
5.73%
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cal Similarity:
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us-09-759-143-110.rspt

:::	OY 1382 CGGCAGCCACGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGAATCGCT 1323 1::::: Db 153 GlnArgProSerGlyProThrGlyGlyHisProAla 164	Qy 1322 GCACCAGCCGGTCCATGACCAGAGAAGACCAGGAGATGGCGCACTGCAGGAACAGCC 1263 	Qy 1262 CCAGGCTGCCCATCCGAACGCCTTCATCATGTGTCTCCGGGCCTCGGTGCCCGGCTCAG 1203	Qy 1202 CTCTGGGCACGCCCTGGTACAGCCCCTCGCCACGAAATCCGTGT 1158	Db 197 rGlyProThrGlyGlyHisProAlaAlaProGlyAlaProGlyProArgSerProArgTh 217	Qy 1157 AAAACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACACGCTCAGCCACGAAGAGCGGGC 1098 :::::::	1097 GCAGGGTGCGGGGCATGCGGCAGCACTGCTGCTGCTGCAGCC	232 yAlaGlyGlnArgProSerGlyProThrGlyGlyHisProAlaAla	Db 248 oGlyAlaProGly-ProArgSerProArgThrGluArgArgArgGlySerAlaGlnArgG 268 Qy 998 GCGACAAGGAGGGGCCGACAGCCCTTCTGCTGGTGGGGGCCCAGGGTGGCTGCT 942	Db 268 lyHisProProProGlyAlaGlyGlnArgProSerGlyProThrGlyGlyHisProAlaA 288	Qy 941 CCTCAGCCACCAGCAGTGGGCTGCCAGGTGAGGAGGAGGTGAGGTGAGGCCAA 882 :: ::	Qy 881 AGAGGCACTCCTGGGTGCCCAGGTAGGGGGCCAGGGCACTGG 837	836 TGTCCCAGTCAATGGCAGGCAGGAGGTAGCCCAGGCAGCCCCCAAGACTGATCATGAAGG	Db 327ProAlaAlaProGlyAlaProGlyProArgSerProArgThrGlu 341	Qy 776 CATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGAAGAGGTCAGAGA 723 	Qy 722GCAGGGCCTCCAGTGGAGTGAAGCACACAGGCCACAGAAGTCCAGCAGC 672	Qy 671 CCACGCCCAGGATGAGCAGTGCCAGCTCCAGGGGCCTGGGATCCGGGC 624	Oy 623 ACAGCAGCCTAGCCAGCCGGCCCTTGGGATGAGAAAGAGCTCAGCAGGATGC 567	556CCAAGGACAGTGCCCAGAAGAAGGCCGGCGGCGCCAT	413 GlyAlaProGlyProArgSerProArgThrGluArgArgGlySerAlaGln	Qy 52/ AGCGTCCACGCCAGTGGTCACTGGCTAGGACGGGACACACAACCAGGCCCA 4/1 	Qy 470 GCACTGGACCAATGCCCAGGACCATGAACTTCTCCTCTACCCCCACTTCCAGCA 411
166 CAGCCAGCCCATTCTGCCAGCCTTTGGTGCCGGTCCAGCTTCTCAGCCCATGCTC	OY 106 AACACCTGCTGTGGGGCACCTCAGTGGGGACACGTCATCATCATCACTCAGATCCTGGC 49	-0 -	Db 991 oGlnGlySerArgGlyGluLysGlyAspThrGlyAlaSerGlyAlaAsnGlySerPro 1010 RESULT 11	QYQXX) ID QYQSK9 PRELIMINARY; PRT; 608 AA.	01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,			RN {1] RP SEQUENCE FROM N.A. RC STRAIN-BABOON LYMPHOCRYPTOVIRUS BA65; RA Zong JC., Ryan J., Ling P.D., Loeb D.D., Pagano J.S., Hayward S.D.,	Hayward G.S.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databas EMBL; AF200364; AAF23950.1; - AFF823-CDAA20627 CDCAA	5	Pred No. 3.51e-15 Length: 608 Score: 0. 361.00 Matches: 203 Percent Similarity: 35.05% Conservative: 28 Part foral chilbrity: 30.00% Ministriction of 200	5.80% Indels:	-09-759-143-110 (1-3410) × Q9Q5K9 (1-608)	OY 1805 GGGATGG T761 OY 1805 GGGATGG T761 Db 11 GlyProGlyArgProGlyThrPheProGlyArgGluAlaGlyArgGluAlaGlyArgGluAlaGlyArgThr 30		1700 CCACACGTACGGAGACATCACAGGCAGAGCCCCGCAGAGCGCGGGT	1652 GAGGTGGGAGCACTGCCTCCAGCACCCACGTTAGGGAAGGGAGCTCCAG	DD 68 LYALAGIYGINArgProSerGLYProThrG1yGLYHisFroAlaAlaProG1yAlaProG 88 Qy 1592 GCTTAGGGCCTGGCAGGAAGCTGGTCAFCAGGCTGTCCTCAC 1551	Db 88 lyProArgSerPro-ArgThrGluArgArgArgGlySerAlaGlnArgGlyHisProPro 107 Ov 1550 IGCTAGCACCICCAGGTGTCCCTCGGTATTTGGGCAGGAACACATGCTTCTCCGGTGGT 1491	108 ProGlyAlaGlyGlnArgProSerGlyProThrGlyGlyHisProAlaAlaProGlyAla	GGCTGAGAAGGTGA	DD 128 FIOGLYFIOALGSEFFIOALGINEGINALGARGALGSEFALA 142 Qy 1442 ACCCGGTGAGGCGGCTGAAGCTGTCACCGGCCACACTGTGGGACAGGCATGTGGCAC 1383

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656 hrGlyAlaGlnGlyArgArgGlyIleGlyGlyArgAlaGlyAsnTyrGlyAlaThrGlyP 1067GGTGCAGCGGGGAAGCAGGGCGCCCAGGTTCCG 111	Db 676 roProGlyGlnLysGlyGluMetGlyProProGlyAsnValGlyLeuGlnGlyProProG 696 Qy 1033 GAAAGCCAAGCGGGCCCGGCATGGACAGCAGCAGGGGGGGGGG	:::	Qy 979 CAGCCCTTCTGCTGGTGGGGCCCAGCGCTGCCTCCAGCCACCAGCAGTGTGGC 920	Qy 919 TGCTACGCAGGTGAGGATGAGGCTGAGCCCAAAGAGGCACT	QY 872CCTCCTGGGTGCCCAGGTAGGGGGCCAGGGCACT 839	Qy 838 GGTGTCCCAGTCAATGGCAGGAGGTAGCCCAGGCAGCCCCAAGACTGATCATGAA 779	Qy 778 GGCATAGACAGAGTAGGCCTGGCGACAGTGGTCCGGGTCCCGGAAGAGGGTCAGA 725	GAGCAGGGCCTCCAGTGGAGTGAAGCACCTGGCCACAGAAGTCCAGCAGGCCCACGC	Oy 665	Qy 628 CGGGCACAGCGCCTGCTAGCCGGCCCTTGGGATGAGAAGAGGCTCAGCAGGAT 569	QY 568 GCCCAAGACAGTGCCCAGATGAAGGCCGGCGGCGGCCATAGCGTCCACGCCAGTGGTC 509 Db 835	Qy 508 ACTGGCTGAGCCTAGGAGCGGACACAGGCCCAGCACCAGGACCAATGCCCAGCAC 449	OY 448 CATGGTCATGAACTTCTCTCTACCCCACTTCCAGCAGCAGGGGGCACATAGGTGAT 389	Oy 388 GCCTGCGGCCAAACACATCCAGGGCAAAGGTTAGCAGGTTGAC 344 Db 868SerProGlyGlnProGlyAlaArgGlyGlnProGlyGlnSerGlySerP 884	Qy 343 CAGCAAGACTGGGGCTTTCCGGTGCCCAGCA	Qy 304 CACCCACAGGCCTTGGACCATAGTGGGCCAGGCGGGTAGGGGCTCAGGGGGCCGTTCA 248 ::	Qy 247 GGCACTCCAGAACTGCTTCGTCTCGGCTCTCCAGAAGCTGCGGCCTCTCCT 194	Qy 193CTTGCTGCCGCCAACTGCCTAGGAAT 167
do Oy	qa .	ପ୍ର	δ 	QQ Dp	δδ	QQ Qa	Qy	δο Paga	QQ	da da	Qy	QQ .	da da	Qy	QQ Dp	QQ Dp	QQ Dp	QQ Oy
	419 hrGlyProAlaGlyProPro	1923 TCGCTCTTGTCAAATACTACCTGTGTGTGAAAGTAAATGGCGACCCAGGCCTGCG 1864		CAGGGATGGGGCCACCTGGGACAGCAGA	GCCACTATCCAGGATGCCGAGGT	GATGCCCGGCCCGGAACCACCTGGCTCGGTGGGCTCACCCACC	GACATCACAGGCCAGAGGCCCGCAGAGCGCGGGAGGTGGGAGGCCACTGCCT		aGlyAlaProGlyGluProGlyAsnSerGlyProAlaGlyAlaSerGlyGlnArgGlyLe TCCAGGCTTA	1579 CAGGAAGCTGGTCATCAGGCTGTCCTCACTAGCACCTCCAGTGTCCCCTCGGTATT 1520	gggcaggaacaccrgcrrcccggrggradggggggggggg	CAGGGCTGAGAGGTGAACCGGTGAGGGCGCTGAAGCTGTCACCACGGCCACACTGTG	GGACAGGCATGTGGCACCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGAC	TGCTCGAGTGCCGAATCGCTGCACCACGGTCCATGACCAGAGAAAACCAGGGAGAT GlnalaglySerMetGlyDroproflyDro	GGCGCACTGCAGCAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTG	TCTCCGGGCCTCGGTGCCCGGCTCAGCTCTGGGCACGCCCTGGTACA	-GCCCTCGCCCACGAAATCCGTGTAAAACAGCGTGAAGGTCATGAGTGCCATCCAGCT	GCACAGCGCGCGAGGGCCGCGCGCGGGGGGGGGGGG
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2897 TTAGGGAAGCCGTTGAGCCCCACCCTCTACCT	2699 GATTGTTGGGGATCCCCCACCCTACCCAAATATTAGACACCAACACAAAAAGCTAGCAA 2640 11111 111		2286 TAGGA	330
		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	60 60 60 60 60 60 60 60 60 60 60 60 60 6	oy oy oy
Db 644	SULT 10 698 Y 6634 Q26634 Q26634; Q1-NOV-1996 01-JUN-2002 O1-JUN-2002 A1-Jun-2002		DR Pfam; PF01391; Collagen; 18. DR ProDom; PD00007; Collagen; 2. DR SWART; SM00038; CoLFT; 1. KW Collagen. SO SEQUENCE 1414 AA; 133025 MW; 94D9CDA71A9FD73D CRC64; Alignment Scores: Pred. No.: 2.58e-15 Length: Pred. No.: 364.00 Matches: Percent Similarity: 26.23 Mismatches: 381 Best Local Similarity: 26.23 Mismatches: 381 Best Watch: 5.859 Indels: 467 Conservative: 57 Gaps: 78 Gaps: 78	GTAGGGGAAA Aspalaaspi Aspalaaspi ProglyPros

Οy	2121
QQ	129 lyProProArgArgAspGlyGlyAsnArgGlyAspGly-AlaProGluArgGlySer 147
Qy	2120CCAGCCCCCAGCTGTGCAGCTACGCACCTCAGCAGGGTGGCAGCAGAGA 2067
qq	161
οy	GCCACATTACTTTGGCAGCAACTGGCGGCCAGCCCGGCAGCCCCATGG 2013
qq	162
δλ	1977
Db	171 ProGlyGlyArgGlyProGlyAlaArgCluArgAlaAlaArgProGlyValArgValPro 190 Qy
oy	AGGCCCTCCACCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCT 1917
Д	191 ArgProGlyGluProVal
y o	1916 TGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACA 1857 1016 TGTCAAATACTACCTGTGTAAATAATAAATGGCGACCAGACCTGCGGCAGACA 1857 1017 1017 1017 1017 1017 1017 1017 10
n (1117 \$10 \$100 \$100 \$100 \$100 \$100 \$100 \$
g ç	1uGlyAlaGlyCysProAlaAri
٥٥	TGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCCACCTGGGACAGCAGGAAGGCAC
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07	1772 TATCCAGGATGCCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACC 1725
qa	DD ::: :: DD ::: DD ::: DD ::: ::: DD ::: DD ::: DD ::: ::: DD ::: ::: DD :::: DD :::: DD :::: DD :::: DD :::: DD :::: DD ::::: DD ::::::
Qy	1724 IGGCCTCGGTGGGCTCACCACCACCACGTACGGAGACATCACAGGCAGAGGCCCCGC 1665
Db	257 oGlyLeuGlySerArgSerProProAlaGlyTrpGlyGluProGlyGlyArgGlyProGl 277
Qy	1664 AGAGCGCGGGTGGAGGTGGGAGCAGCCACTGCCACCAC 1623
Dp	GlyGluProvalP 297
δδ	CCACGTGTCCATTAGGGAAGGTCCCAGGCTTAGGGCCTGGCAGGAAGCTGGTCATCA 1563
qq	
٥y	SCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCT 1503
Dp	315 GlycysProAlaArgGlyAlaGlyProProAlaTrpGlyAlaGlyProProArg 332
Οy	AAGG 1446
QΩ	333 ArgAspGlyGlyAsnArgGlyAspGlyAlaProGluArgGlySerGlyLeu 349 Ov
Oy	1389
qq	350 359 ProGlyProGlyCysGlySerProGlyLeu
Qy	1388 TGGCACCGGCACCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGA 1329
QQ	360 GlySerArgSerPro 364
٥y	1328 ATCGCTGCACCGGTCCATGACCAGAGAGACCAGGGAGATGGCGCACTGCA 1272
рр	372
οy	1271 GGAACAGCCCCAGGCTGCCCATCCAACACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGC 1212 11.1
Db	382

Qy	1211 C	CGGCTCAGCTCTGGGCACGCCCTGGTACAGCCCCTCGCCCACGAAA
Db	383 -	
Qy	1154 A	ACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCAGCTCAGCCA 1110
QQ	396 -	
Qy	6	SAGCCGGCGCAGGGTGCGGGGCATGCGGCAGCAGCAGCTGTGCAGCCGGG 10
qq	410 A	serGluGlyAlaGlyCysProAlaArgGlyAlaGlyProProAlaTrpGlyAlaGly 4
οy	1055 -	GAAGCAGGCGCCCAGGTTCCGGAAAGCCAAGC
QQ	430 P	roProArgArgAspGlyGlyAsnArgGlyAspGlyAlaProGluAr
Qy	1022 -	9
qq	450 P	roGlyProGlyCysGlySerProGlyLe
QY	974 -	
QQ	470 G	luProGlyGlyArgGlyProGlyAlaAr
Qy	944 C	TGCTACGCAGGTGAGGAAGAT
οgα	490 P	roGlyGl
οy	968 -	GGTGAGCAGGCCAAAGAGGCACTCCTCTTTTTTTTTTTT
qq	500 G	γAl
Qy	851 G	GGCCAGGGCACTGGTGCCCAGTCAATGGCAGGAGA
qq	520 G	
Qy	812 -	GGTAGCCCAGGCACCCCCAAGACTGATCATGAAGG
qa	. 537 A	AsnargGlyAspGlyAlaProGluArgGlySer
Qy	755 G	
qq	6	LeuproGlyProGlyGsGlySerProGlyLeuGlySerArgSerProProAlaGly 567
Qy	704 T	SAAGCACACCTGGCCA
qq	568 T	rpGlyGluProGlyGlyArgGlyProGlyAlaArgGl
Oy	656 G	CAG.
qq	ω.	ArgvalproArgproGlyGluProValProProGly599
Qy	599 C	CCTTGGGATGAGAAGAGGCTCAGCAGGATGCCCAAGGACAGTGCCCAGATG
qa	- 009	
δλ	539 G	GCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTGAGCCTAGGAGCGGGACACA
qq	611 -	J9S
QY	479 C	CAGGCCCAGCACTGGACCAATGCCCAGCACCAT
QQ	616 -	
QY	419 C	CTTCCAGCAGCAGAGGCGGCACATAGGTGATGCCTGCGGCCAAACACACTCCAGGCCAA 360
QO	619	
Qy	359 A	AGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGCGGCTCACC 300
QQ	627 G	ProArgArgAspGlyGlyAsnArgGlyAspGlyAlaP
Qy	Z99 A	ACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGGGGGCCGTTCAGGCACTCC 240

g	278 euTyrPheAlaGluGluValProLeuMetAlaTyrGlnProHisHisLeuSerAspSer- 297	RI "Complete sequence and genomic analys
οy	977 CTGTCGGCCCCCTCGTGTCGCCCACTGCTGCTCCATGCCGGGCCCGCTTGGCTTT 1032	RT 68."; RL J. Virol. 71:5894-5904(1997).
QQ		RN [2] RP SEQUENCE FROM N.A.
ŏ	1033CCGGAA- 1038	RC STRAIN-WUMS; RA Latreille P., Wamsley P., Waterston R
g G	311 snSerLysSerLysLeuAspMetSerAlaValAspAsnAlaThrGlyAsnAsnProGluS 331	<pre>RL Submitted (APR-1997) to the EMBL/GenB</pre>
οy	1038 1038	KW Hypothetical protein. SQ SEQUENCE 706 AA; 66413 MW; 9AD7A4
q	331 erSerTyrGluIleAsnLysAsnAlaLysHisLeuThrProIleValGlnGluGlnAsnG 351	nment Scores:
Óλ	1039CCTGGGGGCCCTGCTTCCCCGGCTGCACCAGCTGCGCG 1081	Pred. No.: 1.84e-15 Lengtl Score: 365.50 Match
qa ·	351 luSerPheSerAspGlyPro-GlyAlaValLeuValAsnLeuLeuThrSerLeuArgHis 370	ilarity: 29.39% Similarity: 25.54%
ý	1082 AIGCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATG 1141	5.87% 12
QQ	ProAlaMetHisSerValLeuL	US-09-759-143-110 (1-3410) x 041972 (1-706)
οy	ACCTTCACGCTGTTTTA	AAC
අ ර	391 ProPhePheLeuPheAspThrAspTrpMetGlyArgGluValTyrHisGlyAspProLys 410	ю
g 5	120z Gritanscususcanuckanskanantarianianskanskontroskanskontroskanskontroskanskontroskanskontroskanskanskanskanskanskanskanskanskanskan	OY 2879 CCTGAAGCCCCACCTCTACCTTCCAAC
Οÿ		2819
qq	429 GlyLeuLeuAsnSerValAspLeuGlyIleSerSerPheLeuIleGluProMetCys 448	Db 26
δλ	1322 CAGCGATTCGGCACTCGAGGAGTCTATTTGGCCAGTGTGGGCAGCTTTCCCTGTGGCT 1378	Qy 2759 CCCCAGGAGAAGAATTCTGGCAATGATC
qq	GinArgMetGiyAlaAr	Db 30 ProProArgArg
ογ	GCCGGTGCCACATGCCT	Qy 2699 GATTGTTGGGGGATCCCCCACCCTACCCAAA
අ	AlaGlyThrAlaIleIl	Db 33
ò	CACAGIGIGGCCGIGGIGACAGCTTCAGCCGCCCTCACC	26
2	HisAlalleGlyGluAs	33
ογ		Qy 2579 GATGGCAACAGAAGGACCAACAGGCCACATG
q	509 GlyPheProLeuSerIleThrTyrSerValProPheSerIleThrAla 524	31.yAsn
D Q	1499 GAGAAGCAGGTTCCTGCCCAAATACCGAGGGACACTGGAGGT 1543 :::	Qy 2519 GCAAAAGACAGTGTGTGGGCTGAGGGAA 111
RESULT	2 T. 9	CII
A CE	041972 PRELIMINARY; PRT; 706 AA.	::: 62 ArgSerProProAlaGly
255	1998 (TrEMBLrel. 05:1998 (TrEMBLrel. 05	Qy 2405 AGAAACTCCCAIGCAAGAGCTACAITAAACC
DT DE	(TrEMBLrel. 66.4 kDa pı	Db 74 ArgGlyProGlyAlaArg
S S S	GAMMAHV.MIOB. murid herpesvirus 4. Viruses; dsDNA viruses, no RNA staqe; Herpesviridae;	Qy 2345 GAAACCAGGTGACTGAGTTTATTCAGCTCCC Db 90 OATGPTG[10]
2 X S		2285
7 2 Z	SEQUENCE FROM N.A. STRAIN=WUMS:	Db 104 rGlyGly
RA RA	MEDLINE=97366649; PubMed=9223479; Virgin H.W. IV, Latreille P., Mamsley P., Hallsworth K., Weck K.E., Dal Canto A.J., Speck S.H.;	Qy 2225 TGCATGGAGCCCTTCTGGCCTCCCTGTATAL :::
		ATON 211

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ACACCCTAACCTTGGGTAACAGCATTTGGAA 2820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTCCTGGGTTAGGCATTTTGGGGGGCCAGA 2760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATATTAGACACCAACACAGAAAAGCTAGCAA 2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTTAAATATTTAAATGCCTGTGTCTCTGT 2580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAAGCTGCAGGTTAAGGGGCTTAGAGATGG 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCCAATGACCAGCTATCTCAGGGGACCT 2700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTAATCCACCTGCAGAGTCCCCGCATTCCAG 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTCCAGACTGAAACCCCCTTGGAAGGCCT 2166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :::
ArgGlyAlaGlyProProAlaTrpGlyAlaG 129
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|-yProGlyCysGlySerProGlyLeuGlySer 61
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-TrpGlyGluProGlyGly------73
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| UArgAlaAlaArg-ProGiyValArgValPr 90
is of murine gammaherpesvirus
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nnk/DDBJ databases.
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			ose transporters are dif
qq	577 LeuProGlyProGlyCysGlySerProGlyLeuGlySerArgSerProProAlaGly 595		0(1999).
Οy	704 TGAAGCACACCTGGCCACAGAAGTCCAGCAGCCCCACGCCCACGATGA 657	CC -!- SUBCELLULAR LOCATION: INTEGRAL DR EMBL; AF021809; AAF08330.1;	TION: INTEGRAL MEMBRANE 8330.1;
qa	596 TrpGlyGluProGlyGlyArgGlyProGlyAlaArgGluArgAlaAlaArgProGlyVal 615		GPH_sucrose; 1.
Qy	656 GCAGTGCCAGCTCCAGGGCTGGGATCCGGGCACAGCCAGCCTAGCCAGCCGG 600		65711 MW; 8FC3FBD6AB439
qa	616 ArgvalProArgProGlyGluProValProProGly		
Qy	599 CCCTTGGGATGAGAAAGAGGCTCAGGATGCCCCAAGGACAGTGCCCAGATGAAGGGCC 540		Matches:
qq	628 638	Percent Similarity: 40 Best Local Similarity: 26	40.50% Conservati 26.44% Mismatches
. Оу	539 GGCGGCGGCCATAGCGTCCACGCCAGTGGTCACTGGCTTGAGCCTAGGAGCGGGACACAGA 480		
qa	639 643	US-09-759-143-110 (1-3410)) x Q9SQK5 (1-612)
Qy	479 CCAGGCCCAGCACTGGACCAATGCCCAGCACCATGGTCATGAACTTCTCCTCTTACCCCA 420	QY 219 GAGCCGAGAGG	
qq	644	Db 29 GluProArgHis	
Qy	419 CITCCAGCAGCAGAGGGGGCACATAGGIGATGCCTGGGGCCAAACACACCTCCAGGCCAA 360	Qy 270 CCGCCTGGCCCA	CCGCCTGGCCCACTATGGTCCAGAGGCTGTGGGTC
qq	653 AlaTrpGlyAlaGlyPro	Db 48 rSer	SerProSerSerIlePro
ΟY	359 AGGTTAGCAGGTTGACCAGCAAGAGCTGGGCTTTCCGGTGCCGCAGCAGGC 309	Qy 330 CCCAGCTCTTGC	CCCAGCTCTTGCTGGTCAACCTGCTAACCTTTGGC
QO	666 ArgGlyAspGlyAlaProGluArgGlySerGlyLeuProGlyProGlyCysGlySerPro 685	Db 64 rgThrLeuIleI	rgThrLeuIleLeuSerCysMetIleAlaAlaGl)
οy	308 GGCTCACCCACAGCCTCTGGACCATAGTGGGCCAGGCGGGTAGGGCTCAGG 258	Qy 390 TCACCTATGTGC	TCACCTATGTGCCGCCTCTGCTGCTGGAAGTGGGG
qa	686 GlyLeuGlySerArgSerProPro-AlaGlyTrpGlyGluProGlyGlyArgGlyProGl 705	Db 84 euSerLeuLeuT	enSerLeuThrProTyrIleGlnThrLeuGl)
οy	257 GGGCCGTTCAGGCACTCCAGAACTGCTTCGTCTCGGCTCTGCTCCAGAAGCTGCGGCCTC 198	Qy 450 TGCTGGGCATTG	TGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGT
QΩ	705 yAlaArg12	Db 104 leTrpLeuCysG	GlyProlleThrGlyLeuValVa
δy	197 TCTCCTTGCTGCCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTT 138	Qy 510 ACCACTGGCGTG	ACCACTGGCGTGGACGCTATGGCCGCGCGCGGCCC
QQ	712 gProGlyValArgValProArgProGlyGluProVa 724	Db 124 spLysCysSerS	SerLysTyrGlyArgArgArgPro
Qy	137 T	Qy 570 TCTGCTGAGCC	TCTGCTGAGCCTCTTTCTCATCCCA
qq	724 lProProGlyGlyMetGlyGlyThrGlyGlyThrGlyProArgSerGluGl 741	Db 144 leSerValAlav	leSerValAlaValThrIleIleGlyPheSerAla
Qy	104 CACCTGCTGCCA 72	QY 621 TGTGCCCGGATC	TGTGCCCGGATCCCAGGCCCCTGGAG
qa	741 yalaGlyCysProAlaArgGlyAlaGlyProProAlaTrpGlyAlaLysAlaArgSerSe 761	Db 164 hrAsnMetAspC	hrasnMetaspCysArgLysPheLysGlyThrArg
Qy	71 CGTCTCATCACTCAGATCCTGGCCGAGGCGCGCT 35	Qy 663 TGGGCGTGGGGC	TGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTC
QΩ	761 rThraiaGluValargProValalaArgArgGlyAla 773	Db 184 euGlyPheTrpM	euglyPheTrpMetLeuAspLeuAlaAsnAsnTh
RES	RESULT 8	Qy 723 TCTCTGACCTCT	TCTCTGACCTCTTCCGGGACCCGGACCACTGTCGC
ID A	O9SOKS PRELIMINARY; PRT; 612 AA.	Db 204 euAlaAspLeu-	SerGlyProAspGlnArgAsı
בים בים	01-MAY-2000 (TrEMBLrel, 13, Created) 01-MAY-2000 (TrEMBLrel, 13, Last sequence undate)	Qy 783 TGATCAGTCTTG	TGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTC
DI	01-JUN-2000 (TIEMBLICE: 1) Last annotation update) Dutative sucrose transmorter	Db 223 rpMetAlaValC	GlyAsnIleLeuGlyPheSerAl
SSS	Vectors of the second of the s	Qy 831 GGGACACCAGTC	GGGACACCAGTGCCCTGGCCCCCTACCTGGGCACC
388	vicis vinitata (stape). Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;	Db 243 rp	PheProPheLeuLeuAsr
0 8 8	Vitis. NCBI TaxID=29760:	Qy . 878CTCI	-CTCTTTGGCCTGCTCACCCTCATCTTC
RP	[1] SEQUENCE PROM N.A.	Db 258 snLeuLysAlaA	snLeuLysAlaAlaPheLeuIleAlaValValPhe
RA RA	STRAIM-SHIRAZ; TISSUE-FRUIT; Davies C., Wolf T., Robinson S.P.;	Qy 927 TGCTGGTGGCTG	TGCTGGTGGCTGAGGAGGCAGCGCTGGG

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TCCTCACC --TGCGTAGCAGCCACAC 926
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||aaspIleGlyTyrLeuLeuGlyAspT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----CCCCACCGAGCCAGCAGAGGG 976
                                                                                                                                                                                                                                                                         GTGCCTGAACGGCCCCTGAGCCCTAC 269
                                                                                                                                                                                                                                                                                                                                                                                       GCCTGGAGGTGTGTTTGGCCGCAGGCA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTAGAGGAGAAGTTCATGACCATGG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGTCCCGCTCCTAGGCTCAGCCAGTG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rgThrTrpAlaAlaIleIlePheValL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGCTTCACTCCACTGGAGGCCCTGC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCAGGCCTACTGTCTATGCCTTCA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| ::::::::
|snSerAlaAsnAlaIlePheCysSerT 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCCTGCCATTGAC ----- 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              laGlyAlaSerGlyHisTrpHisArgT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       snLysAlaCysCysGluAlaCysGlyA 258
                                                                                                                                                                                                                                                                                                                                TGAGCCGCCTGCTGCGGCACCGGAAAG 329
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|alGlnProCysValGlyIleTrpSerA 124
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|lyvalGlnPheGlyTrpAlaLeuGlnL 84
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                                         IE PROTEIN (BY SIMILARITY).
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ογ	2639 IGGATICCCTICTACITIGTIAAATAAATAAGTIAAATATITAAAIGCCTGIGICTGI 2580	QY	1664 AGAGCGC
qq	61	Dp	305 yAlaArgGluArgAlaAlaArgE
ò	GATGGCAACAGAAGGACCAACAGGCCAACATGATAAAAAGGTAAGAGGTGGATCA	Qy	1622 CCACGIGICCATIAGGGAAGGG
7 Q		qq	325 roProGlyGlyMetGlyGly
2		Qy	1562 GGCTGTCCTCACTGCTAGCACCT
7 원	AlaProGluArgGlySerGlyLeuProGlyProGlyCysGlySerProGlySer	Dp	343 GlyCysProAlaArgG
ò	2465 AGGACTCTTCCCCTACAAATAAGTCATATGTTCAAATCCCATGGAGGAGTGTTTCATCCT 2406	δy	1502 TCTCCCGGTGGTAGAGGGAC
음		QQ	
, oy	AACTCCCATGCAAGAGCTACAT	Qy	1445 TGAACCCGGTGAGGGCGGCTGAA
qq	 102 ArgGlyProGlyAlaArgGluArgAlaAlaArg-ProGlyValArgValPr 118	qa	378
ΟŅ	ATTCA	ΟŸ	1388 TGGCACCGGCAGCCACAGGGAAA
QQ		qq	
οy	2285 AGGAGGCTAGCTGTAACCCTGAGCCTGGGTAATCCACCTGCAGAGTCCCCGCATTCCAG 2226	ΟŸ	ATCGCTGCACCAGCCGGT
QQ	132 rGlyGlyThrGlyBroArgSerGl 140	q	
δ	ā.	Qy	1271 GGAACAGCCCCAGGCTGCCCAT(
· qa		ΩP	401 GlyArgGlyProGlyAlaA
δ		Qy	1211 CCGGCTCAGCTCTGGGCACGCCC
୍ ପ୍ର	SluArgGlySer	qq	411AlaArgP
ογ		ΟY	1154 ACAGCGTGAAGGTCATGAGTGC
qq		qq	
Qy	2066 GCCACATTACTTTGGCAGCAACAGAAACTGGCGGCCAGCCCGGCAGCCCCATGG 2013	ΟŊ	1109 CGAAGAGCCGGCGCAGGGTGCG(
QQ	190	QQ .	
οy	2012GGCTAACAGGGGGGGGGGGTGGGACCCAGTGAGGC 1977	oy o	
eg G	199 ProGlyGlyArgGlyProGlyAjaArgGluArgAlaAlaArgProGlyValArgValPro 218	g ;	r.
δ	1976 AGGCCCTCCACCCCAATGTGCTGGAAGTTTTCTACGCTGAGTATTTGGCCAAGTCGCTCT 1917	δo	
qq	219 ArgProGlyGluProVal 224	g è	478 FIGGLYFIGGLYCYSGLYSELF
ογ	1916 TGTCAAATACTACCTGTGTAGCAAAGTAAATGGCGACCAGACCCAGGCCTGCGGCAGACA 1857	G E	A 98 Glubroclustical
q q	ProGly(3 8	
Qy	1856	Ş 2	
ą	233 GlyGlyThrGlyProArgSerGluGlyAlaGlyCysProAlaArg 247	G d	olo Floatyriosiystuklovale
ογ	1832 TGAGCTGGACAATGGAGCCCATAAACAGGGATGGGGCCACCTGGGACAGCAGGAGGCAC 1773	QY 40	896 GGGTGAGCAGGCCAAAGAGGCA
ą	248GlyalaGlyProProAlaTrpGlyAlaGlyProProArgArgAspGly-GlyAs 265	3 8	
Qy	1772 TATCCAGGATGGCGAGGTCCAGGCAGATGCCCCGGCCCGGAACCACCC 1725	<u> </u>	
qq	265 nArgGlyAspGlyAlaProGluArgGlySerGlyLeuProGlyProGlyCysGlySerPr 285	a a	י פ
ογ	1724 TGGCCTCGGTGGGCTCACCCACCACCACGTACGGAGACATCACACAGGCAGAGGCCCGC 1665	Š Š	
qq	285 oGlyLeuGlySerArgSerProProAlaGlyTrpGlyGluProGlyGlyArgGlyBroGl 305	g :	565 ASBArgGIYASPGIYALAProG
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QY	1664	AGAGCGCGGGTGGAGGTGGGAGCACTGCCTCCAGCAC 1623
Dp	305	yAlaArgGluArgAlaAlaArgProGlyValArg-ValProArgProGlyGluProValP 325
Qy	1622	CCACGTGTCCATTAGGGAGGAGCTCCAGCCTAGGGCCTGGCAGGAAGCTGGTCA 1563
Db	325	roProGlyGlyMetGlyGlyThrGlyGlyThrGlyProArg-SerGluGlyAla 342
Qy	1562	GGCTGTCCTCACTGCTAGCACCTCCAGTGTCCCCTCGGTATTTGGGCAGGAACACCTGCT 1503
qq	343	GlyCysProAlaArgGlyAlaGlyProProAlaTrpGlyAlaGlyProProArg 360
Qy	1502	TCTCCGGTGGTAGAGGAGGCCAGTGTGTAGGGCAGGATCTGCAGGGCTGAGAAGG 1446
Dp	361	ArgaspGlyGlyAsnArgGlyAspGlyAlaProĠluArgGlySerGlyLeu 377
Qy	1445	TGAACCCGGTGAGGCGGCTGAAGCTGTCACCGCCACGGCCACTGTGGGACAGGCATG 1389
Db	378	
Qy	1388	TGGCACCGGCAGCCACAGGGAAAGCTGCCACACTGGCCAAATAGACTGCTCGAGTGCCGA 1329
QQ	388	èr
Qy	1328	ATCGCTGCACCAGCCGGTCCATGACCAGAGAGACCAGGGGAGATGGCGCACTGCA 1272
qq	393	ProAlaGly
Qy	1271	GGAACAGCCCCAGGCTGCCCATCCGAACGCCTTCATCATAGTGTCTCCGGGCCTCGGTGC 1212
pp	401	GlyargGlyProGlyalaargGluargAla410
Qy	1211	CCGGCTCAGCTCTGGGCACGCCTGGTACAGCCCCTCGCCCACGAAATCCGTGTAAA 1155
qq	411	
Qy	1154	ACAGCGTGAAGGTCATGAGTGCCATCCAGCTGCACAGCTCAGCCA 1110
Db	424	
Qy	1109	AGAG
qq	438	ArgSerGluGlyAlaGlyCysProAlaArgGlyAlaGlyProProAlaTrpGlyAlaGly 457
Οy	1055	GAAGCAGGCGCCCCAGGTTCCGGAAAGCCAAGC 1023
Db	458	ProProArgArgAspGlyGlyAsnArgGlyAspGlyAlaProGluArgGlySerGlyLeu 477
Οy	1022	GGGCCCGGCATGGACAGCAGTGGGCCGACAGGAGGGGCCGACAGCC 975
Db	478	ProGlyProGlyCysGlySerProGlyLeuGlySerArgSerProAlaGlyTrpGly 497
Qy	974	GCT.
Db	498	GluProGlyGlyArgGlyProGlyAlaArgGluArgAlaAlaArgProGlyValArgVal 517
ΟŸ	944	CCTCCTCAGCCACCAGCAGTGTGGCTGCTACGCAGGTGAGGAAGATGA 897
Db	518	ProArgProGlyGluProValProProGly527
Qy	968	GGGTGAGCCAGGCCAAAGAGGCACTCCTCCTGGGTGCCCAGGTAGG 852
Dβ	528	uGlyA
٥y	851	GGGCCAGGCACTGGTGTCCCAGTCAATGGCAGGA
Db	548	GlyalaGlyProProAlaTrpGlyAlaGlyProProArgArgAspGlyGly 564
Οy	812	GGTAGCCCAGGCACCCCAAGACTGATCATGAAGGCATAGACAGAGTAGGCCTGGC 756
Db	265	
Qy	755	GACAGTGGTCCGGGT

TCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTC 1831

qq	219 AlaCysGlyTyrLeuValGlyAlaMetAspTrpGlyHisSerValLeuGlyArgLeuLeu 238	-
٥y	860 GGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTC 898	-
Ωp	239 GlySerGluTyrGlnVallleTyrPhePheSerAlaLeuThrTrpGlyValPheLeuile 258	540
Qy	899 ATCTTCCTCACCTGCGTA 916	1832
qa	::: 259 ValHisLeuPheSerIleProGluLysProLeuAlaLysValProSerGluSerSerAla 278	547 AlaG
Qy		Oy 1892 TTT 1894 Db 567 Phe 567
q _Q		7
Qy	956 CCCACCGAGCCAGCAGAGAGGGCTGTCGGCCCCCTTGTCGCCCCCACTGCTGTCCATGC 1015	6
qq	299 ProvalSerProvalIleProThrSerSerProGlulleArgProArgSerTyrSerAla 318	041971;
δy	1015 1015	01-JAN-1998 01-JAN-1998
qa	319 LeuGlyGluArgProArgSerPheSerAlaLeuGlyGluAlaAsnSerValThrSerSer 338	
οy	1016	
qq	Thr	OC VILGORY, USDING VILGORY, OC Gammaherpesvirinae. OY NCBI Tavile 33708.
٥y	1052 CTTCCCCGGCTGCACCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTG 1111	
qq	355LeuMetLysalaIlePheAsnMetProAsnHisTyrArgPheLeuCysIle 371	RC STRAIN=WUMS:
٥y	1112 GCTGAGCTGTGCAGCTGGATGGCCACTCATGACCTGTTTATACACGGATTTCGTG 1171	
qq	372 SerHisLeuLeuGlyTrpAlaAlaPheLeuCysAsnMetLeuPhePheThrAspPheMet 391	
δy	1172 GGCGAGGGCTGTACCAGGGCGTGCCCAGAGCCGGGCACCGAGGCCCGGAGACAC 1231	RL J. Virol. 71:5894-5904(1
qq		
Oy	FATGATGAAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCTG	RA Latreille P., Wamsley P. RL Submitted (APR-1997) to
g ,	<pre>iyrcıuArgciyValGluValGlyCySTrpGlyLeuCySILeASnAlaValSerSerAla</pre>	
Š f	1292 GTCTTCTCTCTGGTCATGGACCGGTGGAGGGATTCGGCACTCGAGGAGTCTTTG 1351	
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δy	GCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCCACATGCCTGTCCCACAGTGTGGGCC	Score: 382.5 Percent Similarity: 29.90
qa	452 MetGlyTyrPheValPheGlyMetGlyThrSerLeuIleGlyLeuPheProGluValIle 471	Best Local Similarity: 25.98
ογ	1412 GIGGIGACACCITCAGCCCCCTCACCGGGITCACCTICTCAGCCCTGCAGAICCTGCCC 1471	
QQ	472 AlaThrLeuIleLeuCysSerValPheGlyValMetSerSerThrLeuTyrThrIlePro 491	US-09-759-143-110 (1-3410) x
δλ	1472 TACACACTGGCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGG 1531	Qy 2939 GGAAGTGGGGGAAC
qq	492 PheAsnLeuIleAlaGluTyrGlnArgGluGluGluGluGluGlnValLysLeuGluGly 510	Db 31 GlyThrGlyGly
Qy	1532 GACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAG 1591	Qy 2879 CCTGAAGCCCCACCC
Db	510 510	Db 48 GlyAlaGlyProPro
δλ	1592 CCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGAGTGGCCTGCTCCCACCT 1651	Qy 2819 TTATCATTTGGGATG
QQ	511 520	Db 54
ΟŻ	1652 CCACCCGCGCTCTGCGGGGCCTCTGCCTGTACGTGTGGTGGTGGTGAG 1711	Qy 2759 CCCCAGGAGAAGA
qa	MetValGln	Db 58 ProProArgArg
Οy	CACCGA	Qy 2699 GATTGTTGGGGATCC
qa	532AlaGinIleIleValGlyAlaGly539	Db 61

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GCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTAC 1891
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ivalValValLeuSerAlaSerSerIleSerLeuIleGlyCysIle 566
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Ala-----53
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Le P., Wamsley P., Hallsworth K., Weck K.E.,
H.;
genomic analysis of murine gammaherpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Waterston R.H.;
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MW; DIB37F264C92C42C CRC64;
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285
43
291
478
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05, Last sequence update)
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      1700 GTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCG------GGCCGGGGCATCTGC 1750
                                              1751 CTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCCATCCCTGTTT 1810
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                          -------GluIleValProLeuLysGlnAlaArgGlyLeuGly 544
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                                                               545 ThrAspValAlaIleIleSerSerMetValPheIleAlaGlnLeuIleValSerLeuSer
                                                                                                         565 ValGlyProLeuValSerTrpMetAspThrThrCysAlaValLeuTyrAlaSerThrPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                             1871 CTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTT 1912
                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR.2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024519; AAH24519.1; -.
Hypothetical protein.
                                                                                                                                           |||| :::|||
|LeuSerPheLeuAlaAlaIleAlaAlaMetPheValLeuTyr 598
                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 11.4 kba protein (Fragment).
Mus musculus (Mouse).
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Matches:
Conservative:
Mismatches:
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512.00
95.50%.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 TTCATGACCATGGTGCTGGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA 496
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                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-21372467; PubMed-11479596; Fukamachi S., Shimada A., Shima A.; Fukamachi S., Shimada A., Shima A.; Fukamachi S., Shimada A., Shima A.; Mutations in the gene encoding B, a novel transporter protein, reduce melanin content in medaka... Nat. Genet. 28:381-385(2001).

EMBL: AF33210; AAK77024.1; -.
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                                                                                                                   Membrane-associated transporter protein B.
Oryzias latipes (Medaka fish).
Bukaryota: Metazoa: Chordata: Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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|154 ValSerGluLeuValSerAspArgSerSerArgSerThrTrp----
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144
95
198
164
                                          (TrEMBLrel. 19, Created)
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Matches:
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PRELIMINARY;
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                                                                                                                                                                                                                                                                            NCBI_TaxID=8090;
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225 Pr	815 CT	245 II	875 TG	265 Th	626	285 Ph	958	305 G1	626	325 Th	977 CI	345 Se	1001	365 TF 1049 CT	385	1109 GT	394 Le	1169 GJ	414 Va	1229 CA	434 As	1289 CI	454 Se	1349 TI						1520 AI		1580 55	150	
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CACTATGATGAGGCGTTCGGATGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCC 1288
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                                                TECCTECCATTGACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAG 874
                                                                                   GCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTG----- 928
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roLysAlaMetThrMetPheAlaLeuPheAlaGlyPheGlyGlyThrIleGlyTyrAla 244
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Li P.W., Hoskins R.A., Galle R.F.,
S.A., Ashburner M., Henderson S.N.,
Gell M.D., Zhang Q., Creen L.X.,
Slazej R.G., Champe M., Pfeiffer B.D.,
Helt G., Nelson C.R., Miklos G.L.G.,
Helt G., Nelson C.R., Miklos G.L.G.,
J., Andrews-Pfannkoch C., Baldwin D.,
J., Bayraktaroglu L., Beasley E.M.,
B.P., Bhandari D., Bolshakov S.,
G., Brokstein P., Brottler P.,
H., Cadleu E., Center A., Chandra I.,
C., Davenport L.B., Davies P.,
C., Davenport L.B., Davies P.,
Z., Mays A.D., Dew I., Dietz S.M.,
Z., Mays A.D., Dew I., Dietz S.M.,
Ferraz C., Ferriera S., Fleischmann W.,
GRIS., Gelbart W.M., Glasser K.,
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!racheata; Hexapoda; Insecta;
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QY 1244 GTTCGGATGGCAGCTGGTTCCTGCAGTGCGCCATCTCCTGTTCTTCTTG 1303 Db 321 ValargMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340 QY 1304 GTCATGGACCGGTGGTGCAGTGTGCGATTCGGCAGTGTTTGGCCAGTGTGGCA 1363 I IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 1424 TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCC 1483	1544 GCTAGCAGCACAGCCTAACCAGCTACCAGGCCCTAAGCCTGGAGCTCCC 1	Db 461 CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480 Qy 1724 AGGGTGGTTCCGGGCCGGGCATCTGCCTGGACCTCGCATAGTGCCTTCTG 1783	SUI	AC 095KC5; DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) DE Hypothetical 53.4 kDa protein. OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey). OC Edvaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Edvaryota; Macaca. OC Cercopithecinae; Macaca. OC NOBI_TAXID=9541; RN 1] RP SEQUENCE FROM N.A. RC TISSUE-MEDULLA OBLOGATA; RA SUZUKi Y., Sugano S., Hashimoto K.; RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K., RA Suzuki Y., Sugano S., Hashimoto K.; RT Tisolation of full-length cDNA clones from macaque brain cDNA RT Tibraries."; RI Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB062977; BAB60745.1; KW Hypothetical protein.
ignment Scores: ed. No.: 2.98e-172 Length: 553 ore: 2798.00	### CTARCTGGTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCATG ####################################	464 CCAGTGCTGGGCCTGGTGTGTGTGTGTGTGTGTGTGTGTG	Db	764 TACTGTCTATGCCTTCATGATCATCTTGGGGGTGCTGCTGGGCTACCTCTGCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	Db 201 GiyLeuLeuThrieuTheritain CysvalAlaAThrieuLeuValAlaGluGlu 220 Oy 944 GCAGCGCTGGGCCCACCAGAGGGCTGCGCCCCCTTGTCGCCCCAC 1003

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"Identification and characterization of prostein, a novel prostate-specific protein."
Cancer Res. 61:1563-1568(2001).
EMBL: AY033593; AAK54386.1; -.
SEQUENCE 553 AA; 59322 MW; OAFA23FBC742A667 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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11565.772 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                  protein search, using frame_plus_n2p model
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AL033941
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Homo sapiens
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Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Bordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 9 10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                 1 (bases 1 to 272)
Billing-Madel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 11 10-0CT-2000;
Location/Qualifiers
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                                                              PAT 16-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Score 270; DB 6; 99.6%; Pred. No. 2.8e-36;
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                                                                                         Sequence 11 from patent US 6130043.
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Matches 265; Conservative
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JOURNAL
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AR112288
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JOURNAL
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                RESULT 43
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1 (bases 1 to 342)
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 8 10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    2207 GCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAG 2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2327 AACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAG 2386
                                         PAT 16-MAY-2001
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Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Bolling-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Boldon, J., Grandos, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 12_10-ocT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GGTTAACAGCTAGCTCCTAGTTGAGACACACCTAGAGAGGGTTTTTGGGAGCTGAATA 120
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AR112291
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Sequence 8 from patent US 6130043.
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AR112287.1 GI:14092187
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RESULT 40
AR112287
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                                                                                                     3034 AGCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAA 3093
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Pred. No. 3.4e-39;
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 Score 291; DB 6; L. Pred. No. 7.1e-40; ); Mismatches 3;
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Query Match 8.5%;
Best Local Similarity 99.0%;
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* 79788 82504: contig of 2717 bp in length 82505 82604; gap of unknown length 82605 86873: contig of 4269 bp in length 86874 91613: contig of 4640 bp in length 91614 91613: contig of 4640 bp in length 91614 91613: contig of 4640 bp in length 91714 94992: contig of 3279 bp in length 94992: contig of 3279 bp in length 95092 97134: gap of unknown length 97135 97134: contig of 2042 bp in length 97135 100423: contig of 4159 bp in length 100524 100523: contig of 4159 bp in length 104681: contig of 3189 bp in length 104682: contig of 3189 bp in length 104683: contig of 3189 bp in length 104683: contig of 3531 bp in length 10813: gap of unknown length 108144 113868: contig of 3821 bp in length 113969 113968: gap of unknown length 113969 113968: gap of unknown length 117990: 117999: contig of 3821 bp in length 117990: 120979: contig of 3000 bp in length 117990: 121079: gap of unknown length 117990: 121079: gap of unknown length 117990: 121079: gap of unknown length 117990: 121079: gap of unknown length 123744 123843: gap of unknown length	Query Match 10.6%; Score 361.8; DB 2; Length 198037; Best Local Similarity 77.3%; Pred. No. 1e-51; Matches 486; Conservative 0; Mismatches 122; Indels 21; Gaps	OY 1505 CAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACGCTG	QY 1565 ATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGACACGTGGGT	QY 1625 GCTGGAGGCAGTGCCTCCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGAT	OY 1685 GTCTCCGTACGTGGGTGGGTGGGCCACGAGGCCAGGGTGCTTCCGGCCGG	OY 1745 ATCTGCCTGGACCTCGCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCATCC	Qy 1805 CTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTCTGCC	Oy 1865 GCAGGCCTGGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGAC [OY 1925 TIGGCCAAATACTCAGGGTAGAAAACTICCAGCACATIGGGGTGGAGGGCCTGCCTCACT	OY 1985 GGGTCCCAGCTCCCGCTCTTAGCCCCATGGGGCTGCCGGGCTGGCCGCAGTTTCT	Qy 2045 GTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGAGGTGCGTAGCTG	Qy 2105 CACAGCTGGGGGCTCCTCTCC 2133

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Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbarda, J., Benton, J., Binnge, K., Blankenburg, K., Bonnin, D.,
Buck, J., Bowle, S., Erieva, M., Brown, B., Brown, M., Bryant, N. Bryant, N. Bunde, S., Catrein, T.E., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carroin, T.F., Catter, M., Cavacos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escetto, P., Frantz, P.,
Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
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Hernandez, O., Hodgson, A., Holloway, C., Hollins, B.,
Homsl, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
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                                                          ------GATGTTCCTG 1145
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Mammalla, Eutheria, Rodentla, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                               1205 AGTTTGGTTCCCTGATTGCCCACTTCTCCCTA-------TGGGAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCCAAGCCTT
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                                                                                                                  2859 GGTAGAGGGTGGGGCTTCAGGTCTCAACGGCTTCCCTAACCACCCCTCTTCTTTGGCCC
                                                       1109 TCTCTTCATCCTAATTGAGAGCCATAA-----
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Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratoyic, J., Kucsehi, A., Landry, N., Lead, B., Lewis, L.,
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Walliams, G., Walliamson, A., Waleczyk, R., Wooden, S.,
Walliams, G., Walliamson, A., Waleczyk, R., Wooden, S.,
Weinstock, G. and Gibbs, R.,
Direct Submission

All Dubblished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (06-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One aylor Plaza, Houston, TX 77030, USA
3 (bases I to 198037)
Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1063: contig of 1063 bp in length
1163: gap of unknown length
2325: contig of 1162 bp in length
2425: gap of unknown length
3556: contig of 1131 bp in length
3656: gap of unknown length
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of 1746
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/protein_id="AAH24519.1"
/protein_id="AAH24519.1"
/bc.xref="di:19353918"
/translation="PKGHVGSGSSGILAPPPALCGASACDVSMRVVVGEPPEARVVTGRICLDLAILDSAFLLSQVAPSLFMGSIVQLSHSVTAYMVSAAGLGLVAIYFATQVVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-rémail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 943

Web site: (Dickson, Mark) mcdépaxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 59 Row: p Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Colon, normal. 5 month old male mouse."
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B"
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Mus musculus, clone IMAGE:4984191, mRNA, partial cds.
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Patent: WO 0151633-A 11 19-JUL-2001; CORIXA CORPORATION (US)
                                                                                           Mismatches
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Sequence 11 from Patent W00173032.
AX267037 GI:16515822
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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Catarrhini; Hominidae; Homo.
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CORIXA CORPORATION.(US)
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/db_xref="taxon:9606"
202 c 170 g 16
            Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Pred. No. 3.6e-93;

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                                                                 195 TCCCTCAGCCCACAGCACTGTCTTTTGCTGATCCACCCCCCTCTTACCTTTTATCAGG 136
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A.
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CORIXA CORPORATION (US)
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Sequence 11 from Patent W00134802.
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/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

(bases 1 to 772)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Xto,J., Dillon,D.C., Mitcham,J.L., Mang,C.H., Retter,M.W.,

Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.

Compositions and methods for the therapy and diagnosis of prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent: WO 0125272-A 11 12-APR-2001;
CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 11 from Patent W00125272. AX106230.1 GI:13921916
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/db_xref="taxon:9606"
1.772
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202 c 170 g
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AX106230/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        695 GTGTGCTTCACTCCACTGGAGGCCCTGCTCTTGACCTCTTCCGGGACCCGGACCACTGT 754
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73651 81298: contig of 7648 bp in temper. 81299 81398: gap of 100 bp 91238: contig of 9840 bp in length 91239 91338: gap of 100 bp 91339 127752: contig of 36414 bp in length 127753 1277652: contig of 9640 bp 127753 177486: contig of 49634 bp in length 177487 177586: gap of 100 bp 177587 177586: gap of 100 bp 177587 177586: contig of 981 bp in length 177587 17667: contig of 981 bp in length.
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                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-272H13"
1. 58509
/clone_tab="RPCI-23 Female Mouse BAC"
/note="assembly_fragment
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vector_side:left"
S9610. :59459
//note="assembly_fragment"
59560. :60623 /-fragment"
60724. :6250
//note="assembly_fragment"
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//note="assembly_fragment"
65410. :67839
//note="assembly_fragment"
65410. :67839
//note="assembly_fragment"
67940. :69856
//note="assembly_fragment"
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73651. .81298
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Matches 686; Conservative
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170763 JGCTCTTTGGCCTCCTCACCCTCATTTCCTCATCTGCATGGCAGCCACTCTGTTTGTG 170704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 772)
Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
Compositions and methods for therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                            1055 CCCCGGCTGCACCTGTGCTGCCGCATGCCCCGCACCCTGCGCCCGGCTCTTCGTGGCT
                                                                                                                                   875 TGCCTCTTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG
                                                                                                                                                                                                                           935 GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCAGCAGAAGGGCTGTCGGCCCCCTCCTTG
                                                                                                                                                                                                                                                                                                                      995 TCGCCCCACTGCTGCTGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT
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A. (bases 1 to 1/85b).
A. (bases 1 to 1/85b).
Anderson.S., Barna, N. Bastlen, V. Boustlavkiy, L., Boukhgalter, B.,
Anderson.S., Barna, N. Bastlen, V., Boquslavkiy, L., Boukhgalter, B.
Erown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ginde, S., Gordet, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliau, G., MacLean, C.,
Inders, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C.,
Macdonald, P., Major, J., Levine, R., Liu, G., MacLean, C.,
McDwan, P., McKernan, K., Mellim, J., Matthews, C., McCarthy, M.,
McDwan, P., McKernan, K., Mellim, J., Menues, L., Mihova, T.,
McMenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Pierre, M., Pollara, V., Raymond, C.,
Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S.,
Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N.
Topham, K., Traves, M., Travis, N., Trafillo, J., Vassillev, H.,
Vola, R., Vola, R., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Direct, Submission
                               162177 CCCGGGTGCACCAGCTGTGCTGCCGAATGCCTCGCACCTGCGCCCGGCTCTTTGTGGCC 162236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1055 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCT 1114
                                                                                                                                                                                                                                                                                                                                                                                                                              1115 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 1174
                                                                                                                                                                                                                TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1175 GAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCCCGGAGGCCCGGAGACACTAT 1234
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Mus musculus clone RP23-272H13, WORKING DRAFT SEQUENCE, 13 ordered
                                                                                                           GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTG 994
875 IGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG 934
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-272H13
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Mus musculus.
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Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 14, 2002 this sequence version replaced gi:18308540. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ....... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIRR
Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contect: sequence_submissions@genome.wi.mit.edu
Contect clone name: 120597
Center clone name: 272_LL_13
Center clone name: 272_LL_13
Center clone name: 272_LL_13
Sequencing vector: Plasmid: n/a: 100% of reads
Sequencing vector: Plasmid: n/a: 100% of reads
Assembly program: Phrap: version 0.960731
Consensus quality: 175041 bases at least Q30
Consensus quality: 177048 bases at least Q30
Consensus quality: 177048 bases at least Q30
Consensus quality: 177028 bases at least Q30
Insert size: 182000; agarose-fp
Insert size: 173367; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58510 58609: gap of 100 bp 58610 59459: contig of 850 bp in length 59460 59559: gap of 100 bp 59560 60623: contig of 1064 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09: gap of 100 bp 67839: contig of 2430 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   op of 100 bp in length is contig of 2017 bp in length pp of 100 bp in length contig of 3494 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o of 100 bp contig of 2227 bp in length
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62950: cont
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65309: cont
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65310
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us-09-759-143-110.rge

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. bp in length length bp in length length bp in length length length bp in length of 1694 bp in length bp in length bp in length bp in length length bp in length length bp in length bp in length in length in length bp in length 1882 bp in length bp in length bp in length bp in length unknown length of 1131 bp in length length bp in length length bp in length in length in length bp in length in length bp in length in length of 1280 bp in length in length bp in length in length in length bp in length length unknown length of 1240 bp in l length length length unknown length length length length length length length length length length length length length length length length length length length ength ďq ďq ďq of 1918 bp unknown len ďq ďq unknown l of 2289 b unknown l of 2115 b unknown of 2376 h unknown] of 2061 b unknown] unknown of 2108 unknown of 1162 h unknown of 1348 unknown of 1576 unknown of 1149 unknown of 1575 contig of 1740 unknown of 1200 1672 2108 2014 of 1866 unknown unknown 1787 unknown of 1096 unknown of 1120 unknown of 1746 unknown 1248 of 1426 unknown unknown of 1635 unknown of 1671 unknown unknown of 1739 unknown of 1693 unknown 1611 unknown unknown unknown οţ oŧ of οĘ oţ oţ contig gap of gap of contig contig contig gap of contig contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of gap of contiq contig contig contig gap of gap of contig contig contig oţ. ō of gap of contig contig contig contig contig contig gap of contig oţ contig of contig gap of contig contig οĮ gap of gap of gap of gap of gap of gap of of of ot gap of gap of gap gap gap 37868: 58639: 58739: 30816: 32509: 1063: 23512: 25087: 26859: 26959: 28698: 41676: 21641: 2425: 3556: 3656: 4752: 5972: 12014: 20392: 23412: 12609: 35660: 9662: 13658: 18100: 5601: 6072: 7818: 7918: 17377: 0614 11914: 50490 50590 52430 54545 54645 56753 56853 58640 6073 7819 52330 1064 1164 2326 2426 3557 3657 4753 4853 5973 48101

unknown

161637 TGGCGTGGGCGCTATGGCCCCGGAGACCCTTTATCTGGGCTCTGTCCCTGGGTGTCCTG 161696 ö 574 634 814 AGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAG 694 695 GIGIGCIICACICCACIGGAGGCCCIGCICTCTGACCICITCCGGGACCCGGACCACIGI 754 815 CTGCCTGCCATTGACTGGGACACCCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAG 874 515 TGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTG 575 CTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCC CGCCAGGCCTACTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTC 455 GGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC 0; Gaps Length 198037; Indels length bp in length length bp in length in length in length length in length length in length in length in length in length bp in length bp in length length length length length length ength length ength Length ength ength ength ength. ength ength .86 length length length length length length unknown length DB 2; 다 ŗ ļ 디 무 Ţ 4e-98; unknown jour of 2164 kunknown joe 2045 E unknown of 3090 l unknown of 2419 h unknown of 2660 b unknown of 3479 unknown of 4640 unknown of 3279 unknown of 3189 unknown of 4159 2664 unknown of 2450 l unknown of 2839 unknown of 2717 Pred. No. 4e-9 0; Mismatches unknown 4269 2042 unknown unknown 5455 unknown unknown unknown Score 633.2; Pred. No. 4eof oţ oţ oţ oŧ ot οţ oţ οŧ of of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contig gap of contia contig contig contig contig gap of contig gap of contig qap of gap of gap of gap of of ō gap 18.6%; ilarity 87.6%; Conservative 123743: 61031: 63481: 66100: 613: 94992: 108313: 121079: 68860: .3868: 13968: 117889: 20979: 63581 Best Local Similarity Matches 692; Conserv 61032 63482 66018 66001 66101 66101 68761 68761 71025 71125 71125 73170 73270 94993 95093 100424 100524 104683 104783 108314 108414 113869 1113969 117790 120980 121080 123744 86874 91614 91714 86974 635 755 161877 Query Match q q q q g g ð g ð à ò δ ò ò

CAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCGGTGCCACATGCCTGTCC 1400 	ACAGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGC 1460	AGATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAGCAGGTGTTCCTGCCCA 1520 	AATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACCAGCTGATGACCAGCTTCCTGC 1580 	CAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC 1640 	TGCTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGG 1700 	TGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCG 1760 	CCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGCCCCATCCCTGTTTATGGGCTCCA 1820 	TTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGG 1880	TCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAG 1940 	CGTAGAAAACTICCAGCACATIGGGGTGGAGGCCTGCCTCACTGGGTCCCAGCTCCC 1998 	CGCTCCTGTTAGCCCCATGGGGCTGCCGGGCTGGCCGCAGTTTCTGTTGCTGCCAAAGT 2058 	AATGTGGCTCTCTGCTGCCACCCTGTGCT-GCTGAGTGCGTAGCTGCACAGCTGGGGGC 2117 	2128 788	AC126523 Ratius norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS AC126523 AC126523. AC126523. AC126523.1 GI:21700488 HTG: HTGS_PHASE1. NORWAY rat. Ratius norvegicus Ratius norvegicus Ratius. Ratius. Ratius. Ratius. Ratius. Ratius. Ratius. Ratius. Ratius. Ratius. AlionAdata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ratius. Ratius. AlionSes 1 to 198037) Ausny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
													TGGGGCGTCCC 212 TNGGGNGTTCC 788	AC126523 ***, 65 unordered p AC126523 AC126523 AC126523.1 GI:2170 HTG; HTGS PHASEI. Norway rat. Rattus norvegicus Eukaryota; Metazoa; Mammalia; Eutheria; Rattus. 1 (bases 1 to 1980 Muzny, D.M., Adams,C Alsbrooks,S.L., Ama
Qy 1341 Db 1	Qy 1401 Db 61	Qy 1461 Db 121	Oy 1521 Db 181	Qy 1581 Db 241	Qy 1641 Db 301	Qy 1701 Db 361	Qy 1761 Db 421	Oy 1821 Db 480	Oy 1881 Db 540	Oy 1941 Db 599	Qy 1999 Db 658	Qy 2059 Db 718	Oy 2118 Db 778	RESULT 32 AC126523 LOCUS DEFINITION RAY ACCESSION AV VERSION AV VE

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Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bulbay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, S., Chen, R., Chen, S., Chondhy, I., Christopoulos, C., Clen, G., Chen, R., Chen, S., Chowdhry, I., Christopoulos, C., Clen, G., Day, Carroll, L., Dady C., Ding, R., David, R., David, R., Douthwaite, K.J., Draper, H., Duyan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Duyan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagga, N., Poot, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gabisi, A., Guovara, W., Gunrarine, P., Hahe, S., Hamilton, K., Harris, C., Harris, K., Huber, J., Hayes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Howard, S., Huber, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Joline, J., Jackson, L.E., Jacobson, B., Jia, Y., Lucier, J., Lul, W., Loulesged, H., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, R., Luna, R., Mayuen, N., Mayuen, P., Matchell, T., Mohabbat, K., Morgan, M., Mayuer, N., Muyen, N., Naul, D., Newtson, J., Newtson, N., Naul, D., Newtson, J., Newtson, N., Naul, D., Newtson, R., Paton, S., Savery, G., Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, J., Schere, S., Sotton, R., Share, S., Wann, M., Stone, J., Sother, S., Sotton, R., Sotton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, R., Tamerisa, R., Tamerisa, R., Tamerisa, R., Tamerisa, R., Tamerisa, R., Tamerisa, R., Tamerisa, R., Tamerisa, R., Tang, R., Wulliamson, A., Williamson, A., Williamson, A., Williamson, A., Williamson, A., Williamson, R., Waond, S., Warren, R., Wang, S., Warren, S., Rock, R., Wang, S., Warren, S., Rock, R., Wang, S., Warren, S., Rock, R., Wang, 
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft, sequence. It currently

* consists of 65 contigs. The true order of the pieces

* is not known and thelir order in this sequence record is
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 149884 bases at least Q40
Consensus quality: 159599 bases at least Q20
Consensus quality: 166549 bases at least Q20
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Center code: BCM
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Unpublished
2 (bases 1 to 198037)
Worley, K.C.
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TITLE
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Db 421 CCATCCTGGATAGTG-CTTCCTGCTGCTGCCCCANGTGGCCCCATCCTGTTATGGGCTCCA 479 Qy 1821 TTGTCCAGCCAGTCTGTCACTGCCTATATGGGCTGGGGCTGGG 1880	Qy 1581	11 CAGGCCCTAAGCCTG
480 TIGLCCAGCTCAGCCAGTCTGTCACTGCCTATATGCTGTCTGCCGCAGGCCTGGGTCTGG 539	Н	1 TGCTCCCACCTCCAC
OY 1881 TCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAG 1940	Db 301 Qy 1701	1 TGGTGGGTGAGCCC
QY 1941 CGTAGAAAACTTCCAGCACATGGGGTGGAGGCCTGCCTCACTGGGTCCCAGCTCCC 1998 II IIII IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 361 Qy 1761	
Qy 1999 CGCTCCTGTTAGCCCCATGGGGCTGCCGGCTGGCCGCCAGTTTCTGTTGCTGCCAAAGT 2058	Db 421 Qy 1821	
Qy 2059 AATGTGGCTCTCTGCTGCCACCCTGTGCT - GCTGAGGTGCGTAGCTGCACAGCTGGGGGC 2117 Db 718 NATGTGGCTCTCTGCTGCTGTTGCTGGCTGAAGTGCNTACNGCNCANCTNGGGGGG 777	Db 480 Qy 1881	
	1	540 TC-CCATTTACTTTG 941 CGTAGAAAACTTCCA
AX200380 LOCUS AX200380 789 bp DNA linear PAT 29-AUG-2001 DEFINITION Sequence 10 from Patent WO0151633. ACCESSION AX200380 GI:15390176	Oy 1999 Oy 2050	CGTTAAAAA CGCTCCTGTT CGCTCCTGTT
KEYWORDS OORGE human saniens		
Entaryota; Metazoa; Chordata; Craniata; Vertebrata; Bute Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Hom 1 (bases 1 to 789) Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,	Qy 2118 Db 778	8 TGGGCGTCCC 212
<pre>reed.s.G., Kalos, W.D., Fanger,G.K., Day,C.H., Retter,M.W., Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. TITLE Compositions and methods for the therapy and diagnosis of prostate cancer</pre>	RESULT 31 AX267036	**************************************
JOURNAL Patent: WO 0151633-A 10 19-JUL-2001; CORIXA CORPORATION (US) FEATURES Location/Qualifiers Source 1 789 //organism="finno sapiens"	TTION SION ON SDS	Ax267036.1 GI:16 human.
BASE COUNT 122 a 250 c 221 g 182 t 14 others ORIGIN	ORGANISM	Homo sapiens Eukaryota; Metazo Mammalia; Eutheri
Query Match Best Local Similarity 94.2%; Pred. No. 3.3e-105; Matches 745; Conservative 0; Mismatches 40; Indels 6; Gaps 5;	REFERENCE AUTHORS	1 Xu,J., Dillon,D.C Kalos,M.D., Fange Vedvick,T.S., Car
OY 1341 CAGTGTATTTGGCCAGTGTGGCTGCTGTGGCTGCGGTGCCATGCCTGTCCC 1400	TITLE	and Henderson, K.A Compositions and cancer Patent: WO 017303
OY 1401 ACAGIGIGGCCGTGGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGC 1460	FEATURES SOUFCE	CORIXA CORPORATIO LOCATION 1789 /organis
OY 1461 AGATCCTGCCTACACACTGCCTCCTCTACCACGGGAGAAGCAGGTGTTCCTGCCCA 1520	BASE COUNT ORIGIN	700_x1e1 122 a 250
QY 1521 AATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGC 1580	Query Match Best Local Matches 74	Match 19. Local Similarity' 94. Hes 745; Conservative

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TGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCA 1820
                                                                                                                                                                                                                            CCCATGGGGCTGCGGGCTGGCCGGTTTCTGTTGCTGCCAAAGT 2058
IGGAGCTCCCTTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCC 1640
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              d methods for the therapy and diagnosis of prostate
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4.2%; Pred. No. 3.3e-105;
ve 0; Mismatches. 40; Indels 6
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ef="taxon:9606"
0 c 221 g 187
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CORIXA CORPORATION (US)
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Sequence 10 from Patent WO0134802.
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/db_xref="taxon:9606"
250 c 221 g 18:
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KEYWORDS
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Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A. Compositions and methods for therapy and diagnosis of prostate
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Best Local Similarity 94.2%; Pred. No. 3.3e-105;
Matches 745; Conservative 0; Mismatches 40; Indels 6
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Patent: WO 0125272-A 10 12-APR-2001;
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/organism-"Homo sapiens"
/db_xref="taxon:9606"
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/note="n = A,T,C or G"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 789)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Sked,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H.,
Skeiky,Y.A. and Wang,A.
Compositions and methods for the therapy and diagnosis of prostate
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Pred. No. 6.5e-126;
           methods for the therapy
                                 Patent: WO 0173032-A 851 04-OCT-2001; CORIXA CORPORATION (US)
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Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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	Db 2422 CICCCGCCAGAGCAGTGAGCTCATCACGTGAGGGGGATTTATTTGCAA 2479 Qy 3222 TAATGTCGTCTTATTATTAGCGGGGGAATTTATACTGTAACTAGCAA 3275 Db 2480 TAATGTTATTATTATTAGCAGAGTAAAATTTTATACGGTAAGTGAAAA 2539	QY 3276 TCAGAGTATAATGTTTATGCTGACAAAATTAAAGGCTTTCTTATATGTTTAAAAAAAA	Qy 3336 AAAAAAAAAAAA 3348 Db 2599 AAAAAAAAAAAA 2611	RESULT 25 AX343860 LOCUS LOCUS DEFINITION Sequence 6 from Patent W00200892. ACCESSION AX343860 VERSION AX343860. KEYWORDS SOURCE 7 Synthetic construct. ORGANISM Synthetic construct	artificial sequences. cabezon Silva,T.E. and Del Triple fusion proteins com thioredoxin and a polypept Patent: WO 0200892-A 6 03- Smithkline Beecham Biologia Location/Qualifie 1. 1593 //db_xref="taxon:3 //db_xref="taxon:3	28.2%; Score 961.2; rity 99.3%; Pred. No. 2.2 nservative 0; Mismatches TCCAGAGGCTGTGGGTGAGCCGCTGCT	523 ACGCTATGGCCGCCCCTCATCTGGGCACTGCCTTGGGCACCTGCTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATCTTGGGCATGTCTTGGGCATGTCTTGGGCATGTCTTGGGCATGTCTTGGGCATGTCTTGGGCATGTCTTGGGCATGTCTGCTGCTGGCCATGTCTTGGGCATGTCTGCTGCTGGCCTGCTGGCCTGCTGGCCTGCTGGCCTGCTG

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	3 GCACTCATGACCTTCAGGCTGTTTTACACGGATTTCGTGGGCGAGGGCCTGTACCAGGGC 	3 GGCAGCCTGGGGCTGTTCCTCCAGTCCCCTTCCTCCTGGTCTTCTCTCTGGTCATGGAC	3 GTGGCTGCCGGTGCCCACATGCCTGCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCC	3 CAC 1 -1 1 1 CAC 3 GAG		3 TCTGCCTGTGATGTCTCCGTACGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTT	GIGGCCCCATCCTGTTATGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTAT	3 GACAAGAGCGACTTGGCCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGG
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 43 Row: p Column: 14
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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RMGSLGLFLQCAISLVFSLVMDRLVQKFGTRSVYLASVMTFPVAAAATCLSHSVVVVT
ASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRGDAGGSSGEDSQTTSFLPGPKP
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SDLFRDPDHCRQAFSVYAFMISLGGCLGYLLPAIDWDTSVLAPYLGTQEECLFGLLTL
IFLICMAATLFVTEEAVLGPPEPAEGLLVSAVSRRCCPCHVGLAFRNLGTLFPRLQQL
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DSAFLLSQVAPSLFMGSIVQLSHSVTAYMVSAAGLGLVAIYFATQVVFDKNDLARYSV
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 943

Meb site: http://www-shgc.stanford.edu

Contact: (Dickson, Mark) mcd@paxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J.; Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Mammary tumor. Metallothionien-rGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam1" /lab_nost="DH108"
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0; Mismatches 568; Indels 179;
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/protein_id=*MA134084.1"
/bx.xref="G1:21707616"
/db_xref="LocusID:212980"
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/organism="Mus musculus"
/db_xref="taxon:10090"
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  Email: cgapbs-r@mail.nih.gov
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                                                                                                       GCCATCTCCCTGGTCTTCTCTCTGTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGA 1339
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Mus musculus, clone IMAGE:4457452, mRNA, partial cds.
BC034084
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Contact: MGC help desk
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2501 CACACACTGTTTTTTGCTGATCACCCCCCCTGTTTAATATTAATATTATTTTTTTT	Qy Dp	2441 GAC 2533 GG-	GACTTATITGIAGGGAAGACTCCTGAGGGCAACACACAAGAACCAGGTCCCCTCAGCC 2500	0 0
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2619 TAACAAAGTAGAAGGGAATCCATTCTTTTTTTTTTTTTT	Qy Db			7.
2691 TAACAAATCAGAGAAAATCATTCCAGCCTTTTTTTTTTT	٥y			7.
2678 GGGTGGGGGATCCCCAACAATCAGGTCCCTGAGATAGCTGGTCATGGGCTGATCATG 2750 [11 11 11 11 11 11 11 11	QQ			<u>م</u>
2750 GGGTGGGATTCCCCCAAAACTGGGTCCCCTAAAATAGCTGGTCACTGGTTAGATATG 28 2738 CCAGAATCCTCTTCTCCTGGGGTCTGGCCCCCAAAATGCCTAACCCAGGCCATACTCC 28 2734 CAAATCTACTCACTCTGGGTGATAGATGCCCCCCAAAACGCCTAACCCCGAGTAGCCTTG 28 2794 GAAATCTACTCACTCCTAATTGGGCCATAA	οy	m	27	- 21
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3034 AGCTCCACAACCCTGTTTGGAGCTACTGCAGACCAGAAGTGCGGTTTCCCAA 30	. ۵) 4'
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3094 GCCTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGA 31 11	۵	LC		7
3103 GCTTCTGCCCATCTCAGCCTTGTGCAGCCTGGGGAATCTCACAGCTGGGGAATCTCACAGCTGGGGAATCTCACAGCTGGGGAATCTCACAGCTGGGGAATCTCACAGCTGGGGAATCTCACAGCTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGT	> -	₹.	314	6
3150 AACTCAGGAGCACCCCTGCCTGAGCTAAGGAGGTTTATGAGGAGGCGTTTAAGGAGTTAAGGAGTTTAAGGAGTTTAAGGAGTTAAGGAGTTAAGGAGTTAAGGAGTAAGGAGTAAGGAGTACTCAGGAGCAGGAGGTTTAAGGAGTAAGGAGTTTAGGAGGAGTTTAAGGAGG	٩		. 6	0
3161 AACTCAGGACTACTCCCCCCCAGAGCCAGTGAGCCTCATCACGTCGAGGGGATTTCAG 3210 TGCCGTTTGCAATAATGTCGTCTATTTTAGCGGGGTGATATTTTATACT	>-			6
3210 TGCCGTTTGCAATAATGTCGTCTTATTTATGGGGGGGGGG	Db		321	8
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AX343857 2133 bp Sequence 3 from Patent WO0200892. AX343857

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AX343857
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AX343857.1 GI:18491926

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                                                                                                                                                                                                                            Gaps
                                                      Triple fusion proteins comprising ubiquitin fused between thioredoxin and a polypeptide of interest. Patent: WO 0200892-A 3 03-JAN-2002; SmithKline Beecham Biologics SA (BE)

Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 5.4e-247;
Matches 1503; Conservative 0; Mismatches 0;
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QQ	11	da Db	60 CTGGTCAT
Qy	281 ACTATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGGAACCCGGAAAGCCCAGCTCTTG	40	
ΟÞ	440 ATCATGATCCAGAGGCTGTGGGGCCAGCGGTCTGCTACGGCACCGGAAAGCTCAGCTCTG	qq 66	
Qy	341 CTGGTCAACCTGGTAACCTTTGGCCTGGAGGTGTTTGGCCGCAGGCATCACCTATGTG	00	
qq	500 CTGGTCAACCTGCTCACCTTTGGCCTGGAGGTGTGCCTGGCTGCCGGCATTACCTATGTG	26 GU 65	1000
οy	401 CCGCCTCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATT	60 Cy	1481 GCCTCCCTCT
qq	560 CCACCCCTTCTGCTGGAAGTCGGGGTGGAGAAATTCATGACCATGGTGTTGGGCATT	619	
οy	461 GGTCCAGTGGTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGGCGGTGACCACTGGCGT	.20 OY	1300 GGT&CGT&CCAG
qq	620 GGCCCAGTGCTAGGCCTGGTTCTACTCCTAGGCTCAGCCAGTGACCAGTGGCGT	679	1601 CCCTTCCCTAP
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අු	680 GGGCGCTATGGCCGCCGGAGACCCTTTATCTGGGCTTTGTCCCTGGGTGTCCTGCTAAGC	39	
λο t	581 CTCTTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGTGCCCGGATCCCAGGCCC	0 0	CTC
8 8	/40 CICIIICICAICCCGAGGGCIGGCIGGCIGGCIGGCIGGC	99 0y	1721 GCCAGGGTGGT
5 A		da 5	1880 GCCAGGGTTG
ò		60 QY	1781 CTGCTGTCCCA
. අ	860 TITACICCATIGGAGGCCTIACICCGACCICITCCGGGACCCAGACCACIGCGGCAA	da Db	1940 CIGCIGIC
οy		. 0	1841 GTCACTGCCTA
qq	920 GCCTTCTGTCTACGCCTTCATGATCAGCCTTGGGGGCTGCCTGGGCTACCTCTTACCT	979 Db	GTCACT
0y	21		1901 CAGGTAGTAT1
qq	80 GCCATTGACTGGGACACCAGCGTTCTGGCCCCCTACCTGGGTACTCAGGAAGAATG	039 Db	090
	81	940 QY	
qq	1040 TTTGGCCTCCTCACCCTCATTTCCTCATCTGCATGGCAGCCACTCTGTTTGTGACGGAG	90 G60	
δλ	41	VQ 000	
qq	1100 GAGGCAGTACTGGGCCCACCCGAGCCGGCAGAGGGTTGTTGGTCTCTGCCGTGTCGCGC	1159 Db	
٥y	01 CACTGCT	VO 090	
qq	9	219 Db	
δλ	61	1120 Qy	2141 CCAGTCTCTA(
qq	20 CTGCAGCAGCAGCTGCTGCCACCGCACCCTACGCCGACTCTTTGTGGCTGACGCT	1279 Db	2274 CTTCAGAGIC
٥y	21	1180 QY	Æ
QQ		1339 Db	
δλ	81	1240 Qy	
q	1340 CTGTACCAGGGTGTACCCAGCCGAGCCAGCCAGGCACGAGGCCGGAGACACTATGATGAA	399 Db	74 G
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ACAGGCTGGTACAGAAGTTCGGCACACGGTCAGTCTATCTGGCCAGTGTG 1519
                                                                                                ATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGCG 1660
                                                                                                                                                                                                                                                                                                                                                                          TICCGGGCCGGGGCAICTGCCTGGACCTCGCCAICCTGGAIAGTGCCTTC 1780
                         NGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCT
                                                                                                                                                                                                                 CCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGGTGAGCCCACCGAG
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                                                                                 CCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACTG
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                                                                                                                                          ACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGA
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/translation="MIQRLMASRLLRHRRAQLLLVNLLTFGLEVCLAAGITYVPPLLL
EVGVEEKFWTMVLGIGPVLGLVSVPLLGSASDQWRGRYGRRRPFIWALSLGVLLSLFL
IPRAGWLAGLLYPDTRPLELALLILGVGLLDFCGQVCFTPLEALLSDLFRDPDHCRQA
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BEAVLGPPEPARGLLVSAVSRRCPCFWGLAFRUGTLEFREKDGLCGWBFTLDRIFY
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GLIPFTLASLYHREKQYFLPKYRGGAGGSGEBOSTTSFLFGFRFGAL
SGILAPTLASCODVSMRVVGEPPEARVYTGGICLDLAILDSAFLLSQVAPST
PMGSIVQLSHSVTAYWVSAGLGLVAIYFATQVVFDKNDLAKYSV"
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                     Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 45 Row: 1 Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                  Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M. Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Liver, normal. 5 month old male mouse."
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 GCCTCGGCCAGGATCTGAGTGATGAGACGTGTCCCCACTGAG--GTGCCCCACAGCAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                            WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.4%; Score 1583.4; DB 10; Length 3354;
.larity 74.0%; Pred. No. 1e-260;
Conservative 0; Mismatches 671; Indels 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"Unknown (protein for MGC:32471)"

**Protein_id="Anal3181.1"

**Ab_xref="GI:31594809"

**Ab_xref="LocusID:212980"
                                                                                                                                                                                                                                             Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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                                                                                                                                                  GGATGTGGCCTGTTGGTCCTTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAA 2607
TITGAACATATGAC--TIATTTGTAGGGGAAGAGTCCTGAGGGGCCAACACACAGAACCA 2487
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3354)
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Best Local Similarity 98.7%;
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Homo sapiens chromosome l clone RP11-6B6, WORKING DRAFT SEQUENCE, 7
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Catarrhini; Hominidae; Homo.
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Direct Submission
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                                                                             6612 CTGATGAGGCACTGCCCAAAATTTCCCCTACCCCCAACTTTCCCCTACCCCCAACTTTC
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AC096533.1 GT:15638681
HTG: HTGS_PHASE1; HTGS_BRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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On Sep 18, 2001 this sequence version replaced gi:9931838
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Contact: uwgchtgs@u.washington.edu
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Center clone name: RP11-6B6 (sc0601)
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Mammalia, Eutheria, Primates,
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Sequencing vector: plasmid; L08752; 100% of reads

Summary Statistics

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GAACTTGGCCGTAACCTGCCAACCAAAGCGAGAACAAAACATAACATCAAACGAATCG
ACCGATTGTTAGGTAATCGTCACCTCCACAAAGAGCGACTCGCTGTATACCGTTGGCA
TGCTAGCTTTATCTGTTCGGGCAATACGATGCCCATTGTACTTGTTGACTGGTCTGAT
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FGATGAATCCCCTAATGATTTTGGTAAAAATCATTAAGTTAAGGTGGATACACATCTT
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TCGATATTTTACACGACTCTCTTTACCAATTCTGCCCCGGAATTACACTTAAAACGACT
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ACTGGTTAAGTCGAGTAAGAGGAAAAGTACAATATGCAGACCTAGGAGCGGAAAACTG
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/note="gi|154843|gb|J01829|TRN10IS13 excised from sc0601
Contig28 ( 10917 . . 12245 )
                                                                                                                                                                                                                                                                                                                                   arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                    Quality coverage: 7.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 1576... contig of 6264 bp in length 6364: gap of unknown length 6365 15785: contig of 9421 bp in length 1886 15885: gap of unknown length 1886 27947: contig of 12062 bp in length 948 28047: gap of unknown length 1993 52092: gap of unknown length 1993 52092: gap of unknown length 1955 18813: contig of 23062 bp in length 155 18813: contig of 37559 bp in length 1814 118913: gap of unknown length 1814 118913: gap of unknown length 1814 118913: gap of unknown length 1914 157988: contig of 39075 bp in length 157988: contig of 39075 bp in length 157988
Chemistry: Dye-terminator ET; 57% of reads Chemistry: Dye-terminator Big Dye; 4% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 154688 bases at least Q40 Consensus quality: 156347 bases at least Q30 Consensus quality: 157058 bases at least Q20 Insert size: 157388; sum-of-contigs
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/note="assembly_name:Cont1g23"
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/db_xref="taxon:9606"
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GAGCA 3274 Db 5532 ACTITGCTACACAGGTAGTATTGACAAGAGCGACTTGGCCAAATACTCAGCGTAGAA 11111 GAGCA 2396 Qy 1950 CTTCCAGCACATTGGGGTGGAGGGCCTGCCTCACTGGGTCCCCGGTCCTGT		ACCTGTGCTGC	2130 CTCCTCTCCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTT	Qy 2190 TGGACTTATACAGGAGGCCAGAAGGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGT	Qy 2250 GGATTACCCAGGCTCAGGGTTAACAGCTAGCCTAGCTTGAGACACACAC	Retter, M.W., 1.J. 1.J. 1.J. 1.J. 1.J. 1.J. 1.J. 1.	Oy 2370 AGCTTGGTTTAATGTAGCATGGAGAGTTTCTAGGATGAAACACTCCTCCATGGGA	Oy 2430 TITGAACATATGACTTATTIGTAGGGAAGAGCCTGAGGGGAACACACAAGAACCA	Dy 2488 GGTC Oy 2488 GGTC Oy 2482 GGTC Oy 2482 GGTC Oy CHILL OP CHILD OY CGTC OY CHILD OY CHILD OY CGTC OY CHILD OY CHILD OY CGTC OY CHILD	CCGAG 11	OY 2608 OY 2608 OCCTA 1589 Db 6252	CCCAC 1649 Qy 2668	GGGTG 17 GGGTG 53	CCTGG 17	さつつつつ
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/tissue_type="stomach"
/clone_lib="666 (synonym: hsto2). Vector pSportl; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
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CTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTT
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TCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGG	GCBGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGGTG	GGGTGGTTCCGGGCCGGGGATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCC 		0-0		GGTGGAGGGCCTGCCCCACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGG	CGGGCTGCCGCCAGTTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTVIIIIIIIIIIIIIIIIIIIIIIIII		TCTCTAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGTTTTTTTT	AGGCCACAAAGGCTCCATGCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGTCTCTTCTGCAGGTGGATTACCCAGGCTCTCTGTTTTTTTT	AGGGTTAACAGCTACCCCTAGTTGAGACACACCCTAGAGAAGGGTTTTTGGGAGCTGAA 	TAAACTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAAT(AGCTCTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATAT 	CTTATTTGTAGGGAAGAGTCCTGAGGGGCAACACACACAGAACCAG 	CAGCACTGTCTTTTGCTGATCCACCCCCTCTTACCTTTATCAGGAT(GTCCTTCTGTTGCCATCACAGAGACACAGGCATTTAAATATTTAACTTATTTAT	AAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTTGGTGTCTAATATTT	GGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGA
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Ansorge, W., Wirker, U., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
This chone (DKFZp66500110) is available at the RZPD in Berlin.
This chone (DKFZp66600110) is available at the RZPD in Berlin.
This chone contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
Information about the clone and the sequencing project is available
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HOMO Sapiens mRNA; cDNA DKFZp666D0110 (from clone DKFZp666D0110).
AL832933
                  1500 GGGGATCCCCAACAATCAGGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGA 1559
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1740 IGGITCCCCCCACTTCCACTCCCCTCTAGGACTGGGCTGATGAAGGCACTG
                                                                              2743 ATCTTCTTCTCCTGGGGTCTGGCCCCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTA
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2100 ATAATGTTTATGGTGACAAAATTAAAGGCTTTCTTATATGTTTA 2143
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Location/Qualifiers
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                               CCTTTGTCCATCTCAGCCCCCAGAGTATATCTGTGCTTGGGGAATCTCACACAGAACTC 3154
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Silling-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Silling-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Sordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
toberts-Rapp, L., Kussell, J.C., Stroupe, S.D. and Yu, H.
eagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 15 10-OCT-2000;
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GCTCCACAACCCTGTTTGGAGCTACTGCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAG 1920
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                                                                                                                                                                            TTTGCAATAATGTCGTCTTATTTATTTAGCGGGGGGAATATTTTATACTGTAAGTGAGCA 3274
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Pred. No. 0;
0; Mismatches
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2143 bp C

R112294.1 GI:14092194
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39; Conserv
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Unknown. Unclassified.

ORGANISM

SOURCE

REFERENCE AUTHORS

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CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATGTAGCT CTTGCATGGGAGTTTCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGTAGCT [ACT ACT TTC TTC	AGAAGGGAATCCATTGCTAGCTTTTTTGTGTGTTGGTGTAATATTTGGGTAGGGTGGGGGG	17CC 11CC 11CC 11CC 11CC 11CC 11CC	AATTTCCCCAGCCCCCCCCCCCCCCCCCCCCCCCCCCCC
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1 (bases 1 to 2152)
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.,
Roberts' Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 16 10-OCT-2000;
Location/Qualifiers
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Matches 2149; Conservative
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PAT 16-MAY-2001

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AR112295 2152 bp C Sequence 16 from patent US 6130043. AR112295.1 GI:14092195

RESULT 16
AR112295
LOCUS
DEFINITION
ACCESSION
VERSION

131		2811 GATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCT	1309 GGACCGGCTGGTGCAGCGATTCGGCACTCCAGCAGTTTGGCCAGTGTGGCCAGTGTTTTTGGCTGGC	1369 CCCTGTGGCCGGTGCCACATGCCTGTCCCACAGTGTGGCGCTGGTGACACCTTCAGC 1428	1429 CGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGCCTCCCT 1488 1111111111111111111111111111111111	1489 CTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAG 1548	1549 CAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCTTCCC 1608	1609 TAATGGACACGTGGGTGCTGGAGGAGTGGCCTGCTCCCACCTCCACCCGGGTCTGGG 1668 3171 TAATGGACACGTGGGTGYTGGAGGCAGTGGCCTGCTCCCACCTCCACCCGCGCTTGGGG 3230	16	3231 GGCCTCTGCCTGTGATGTCTCCGTACGTGGGGGGGGGGG	3291 GGTTCCGGGCCGGGCATCTGCCTCGCCATCCTGGAFAGTGCCTTGTGTGT	1789 CCAGGTGGCCCCATCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTCC 1848	1849 CTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGT 19	3411	1909 ATTTGACAAGACCACTTGACCAAATACTCAGCAAAAAAAA	1969 GAGGCCTGCCTCACTGGGTCCCAGCTCCCGCTCCTGTTAGCCCCATGGGGCTGCCGGG 202	3531	3591 CTGGCCGCAGTTTCTGTTGCTGCCAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTG 365	2089 CTGAGGTGCGTAGCTGCACAGCTGGGGCTGGGGCGTCCCTCCTCCTCCTCCCCAGTCTC	3651 CTGAGGTGCGTAGCTGCACAGCTGGGGGCTGGGGGGTCCCTCTCCTCTCCCCAGTCC 571	3711 TAGGGCTGCCTGACTGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGGGGG 3	2209		2269 TTAACAGCTAGCCTCCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAA 23	3831 TTAACAGCTAGCTCCTAGTTGAGACACCCTAGAGAAGGGTTTTTGGGAGCTGAATAAA 3	y 2329 CTCAGTCACCTGGTTTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAATCTAGCT 2388
915 TOCCUCTUTUGGCCTCCTCACCTCACCTCACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTACCTCGCTTCGCTTCTTCTTCGTTTTTTTT		д а .	da da	QQ Db	da da	QV dq	oy da	δ da	Qy.		q _Q	Qy	, vo	අ :	ф —	δō	යි :	7 d	δδ	ag *c		٥٧	qa —	Qy	qa —	П
	5 TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG 9		935 GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCAGAGGGCTGTCGGCCCCCTTG 99	1/91 GCTGAGGAGGCAGCCCCCCCCCCAGCCAGCAGCAGCCCGCCC	1851 TCGCCCCACTGCTGCTGCCGGGCCCGCCTTGGCTTTCCGGAACCTGGGCGCCCTGCTT 191. 1055 CCCCGGCTGCACCAGCTGCTGCCGCATGCCCGCACCCTGCGCCGGCTCTTCGTGGCT 111.	1911 CCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCCCC	1971 GAGCTGTGCAGCTGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCTGGGCTGGGAGCTGGGAGCTGGGAGCTGGGAGCTGAGGGGGGGG	2031 GAGGGGTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGGAGACTAT 209 1235 GATGA	GATGAAGGTAAGGCCTTGGCAGCCAGAGGCTGGTGTGGGGAGCCGCCCACCAGAGACG 215:	ACACTCGGGGCTGTGTGTGGGGGTGGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGG 221	. 12401230	ZZII AANGTGGGGARIGGACCCCATCTGCATACGGCTTCTCATGGGTGTGGAACATCTGTGT ZZI	2271 IGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTT 233	2331 TGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGG 23	1240 123	2391 ATTTCAGATCTGCCTGGTTCCAGCGGAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAA 245	2451 ATAATCTCACCAGCGCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCA 251	1240	2511 GCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTT 257 1240	2571 CAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGG 263	123	AAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGGCTG 269	1240 123	2691 GTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGAC 275	2751 TGCTCCGACCTTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTCG 281	, 1249 GATGGGCAGCCTGGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGTGTCAT 1

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3286
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Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 TGCCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGGTTTAAGTGCCGTTTGCAATAATG
                                                      TCGTCTTATTTATTTAGCGGGGGGAAATATTTATACTGTAAGTGAGCAATCAGAGTATAA
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CORIXA CORPORATION (US)
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Best Local Similarity 80.1%; Pred. No. 0;
Matches 2872; Conservative 1; Mismatches
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/db_xref="taxon:9606"
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1907 TANTOGOCICAMINETIC	40 da	90 90 PP	40 . 40 .	9 o o	RES LOC DEF ACC VER	SOC C C	T U	BAS ORI O	Oy M	DP QY DP
		9 CCAAATACTCAGCGTAGAAAACTTCCAGCACATTGGGGTGGAGGCCTGCCT	49 CTGCCAAAGTAATGTGGCTCTGCTGCCACCCTGTGCTGAGGTGCGTAGCTGCACA 210 [1	199 1996 1997 1	PATGAAACACTCCTCCATGGGATTTGAACATATGACTTATTTGTAGGGAAGAGTCCTG	27 CCCCCCTTACCTTTATCAGGATGTGCCCTGTTGGTCCTTCTGTTGCCATCACAGAGA 25	47 CTTTTCTGTGTTGTTGTTAATATTTGGTAGGGTGGGGGATCCCCAACAATCAGGTCC 222 1 CTTTCTGTGTTGTTGTTAATATTTGGTAGGTGGGGGATCCCCAACAATCAGGTCC 270 21 CTTTCTGTGTTGTTTGTTTTGGGTAGGGTGGGGGATCCCCAACAATCAGGTCC 228	07 CTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGTCTGGC 276 	67 CCCCAAAATGCCTAACCCAGGACCTTGGAAATTCTACTCATCCCAAATGATAATTCCAAA 282. 11111111111111111111111111111111111
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2401 TGCTGTTACCCAAGGTTAGGGTGTTGAAGGAAGGTAGAGGGTGGGGCCTTCAGGTCTCAAC 2460
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1 (bases I to 4894)

Xu, J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., Reed, S.G., Kalos, M.D., Fanger, G.R., Day, C.H., Retter, M.W., Stolk, J.A., Skeiky, Y.A., Wang, A. and Meagher, M.J.

Compositions and methods for the therapy and diagnosis of prostate
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                                3007 ITTCCCCTACCCCCAACTTTCCCCACCAGCTCCACAACCTGTTTGGAGCTACTGCAGGA
                                                                                                                                                                                                                                     3067 CCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTTGTCCATCTCAGCCCCCAGAGTATATCT
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Db 25		Oy	1070 CTGTGCTGCCGCA
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	TTATCTCTCAGGGGGGTTTAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT	QY	1241
	3247 GGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAATTA 3306	qa	481 CTGGCTGCTCTAG
	GGTGAATATTTTATACTGTGAGCAATCAGAGTATAATGTTTATGGTGACAAAATTA	QY	1241
	AAGGCTTCTTATATGTTTAAAAA	qa	541 GCTTATTCAAAGT
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RESULT 13		qq	601 CCAGCCGCAGTGT
AX267729 LOCUS		Οy	1241
DEFINITION ACCESSION	Sequence 703 from Patent WOUL/3032. AX267729	qa	661 CCAGCTCAGGCGT
VERSION KEYWORDS	AX267729.1 GI:16516401	Οy	1241
SOURCE ORGANISM		qa	721 TCACCCGCCTGTC
		Οy	1241
REFERENCE AUTHORS		qa	781 TTCAGCAAGGGG
	<pre>Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.</pre>	δλ	1269 TCCTGCAGTGCGC
TITLE	and Henderson, R.A. Compositions and methods for the therapy and diagnosis of prostate	qa	841 TCCTGCAGTGCGC
JOURNAL	Cancer Patent: WO 0173032-A 703 04-0CT-2001;	Qy	1329 TCGCCACTCGAGC
FEATURES	CORIXA CORPORATION (US) Location/Qualifiers	QQ	901 TCGCCACTCGAGG
source		Qy	1389 CATGCCTGTCCC
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1130	ATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCCTGTACCAG 1189 	on.
1190	TGCCCAGAGCTGAGCCGGCACCGAGCCCGGAGACACTATGATGAA 	0
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781	GAGGCGTTCGGATGGGCAGCCTGGGGCTG	
1269	TCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGTGCAGT 1328	ω _
7	GGCACTCGAGCAGTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCA 138:	ω.
901	CGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGG	_
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1629	GAGGCAGTGGCCTGCTCCCACCTCCACCGGGGCTCTGCGGGGCCTCTGCCTGTGATGTCT 168	88
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1689	CCGTACGTGTGGTGGGTGAGCCCACGAGGCCAGGGTGGTTCCGGGCCGGGGCATCT 174	
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1749	GCCIGGACCICGCCAICCIGGAIAGIGCCIICCIGCIGICCCAGGIGGCCCCAICCCIGI 180	8